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[Continued on next page]

(54) Title: ISOLATED G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES THEREOF AS INSECTICIDAL TARGETS

(57) Abstract: The present invention provides amino acid sequences of proteins that are encoded by genes within the *Drosophila melanogaster* genome, the GPCR proteins of the present invention. The present invention specifically provides isolated protein and nucleic acid molecules, methods of identifying orthologs and paralogs of the GPCR proteins and methods of identifying modulators of the GPCR proteins for use as insecticides.

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A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/12 C07K14/435 C07K14/705 C07K16/18 C12N5/10
C12Q1/68 G01N33/50

According to International Patent Classification (IPC) or to both national classification end IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C07K G01N C12N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

SEQUENCE SEARCH, EPO-Internal, BIOSIS, WPI Data, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL SEQUENCE LIBRARY [Online] 6 January 2000 (2000-01-06) ADAMS, M. AND VENTER, J.C.: "Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces" XP002182628 accession no AC020076 ---	1,2,4,5
A	WO 94 08006 A (ZYMOGENETICS INC) 14 April 1994 (1994-04-14) the whole document --- -/--	

X Further documents are listed in the continuation of box C. X Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
13 November 2001	15. 02. 2002

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Holtorf, S

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	LI X-J ET AL: "CLONING, FUNCTIONAL EXPRESSION, AND DEVELOPMENTAL REGULATION OF A NEUROPEPTIDE Y RECEPTOR FROM DROSOPHILA MELANOGASTER" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, US, vol. 267, no. 1, 5 January 1992 (1992-01-05), pages 9-12, XP000877443 ISSN: 0021-9258 the whole document ---	
A	WO 99 01468 A (DEN HEUVEL MARCEL VAN ;INGHAM PHILIP W (GB); ONTOGENY INC (US)) 14 January 1999 (1999-01-14) the whole document ---	
A	HAUSER FRANK ET AL: "Molecular cloning, genomic organization and developmental regulation of a novel receptor from Drosophila melanogaster structurally related to gonadotropin-releasing hormone receptors from vertebrates." BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 249, no. 3, 28 August 1998 (1998-08-28), pages 822-828, XP002182627 ISSN: 0006-291X the whole document ---	
A	FENG G ET AL: "CLONING AND FUNCTIONAL CHARACTERIZATION OF A NOVEL DOPAMINE RECEPTOR FROM DROSOPHILA MELANOGASTER" JOURNAL OF NEUROSCIENCE, NEW YORK, NY, US, vol. 15, no. 12, 15 June 1995 (1995-06-15), pages 3925-3933, XP002919142 ISSN: 0270-6474 the whole document ---	
P,X	ADAMS M D ET AL: "THE GENOME SEQUENCE OF DROSOPHILA MELANOGASTER" SCIENCE, AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE,, US, vol. 287, no. 5461, 24 March 2000 (2000-03-24), pages 2185-2195, XP000961051 ISSN: 0036-8075 the whole document ---	1,2,4,5

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	C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT	
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	DATABASE EMBL SEQUENCE LIBRARY [Online] 24 March 2000 (2000-03-24) ADAMS, M.D:, ETAL.: "Drosophila melanogaster genomic scaffold 142000013386053 section 8 of 30 complete sequence" XP002182629 accession no. AE003491 and AE002593 ---	1,2,4,5
P,X	DATABASE TREMBLREL. DATABASE [Online] 1 May 2000 (2000-05-01) ADAMS, M.D., ET AL.: "The genome sequence of Drosophila melanogaster - cross-reference to EMBL accession no. AE003491, AAF48216.1" XP002182630 accession no. Q9VYH9 ---	1,2
E	EP 1 136 501 A (BAYER AG) 26 September 2001 (2001-09-26) the whole document -----	1-20

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INTERNATIONAL SEARCH REPORT

Box I	**Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II	**Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

> see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

> 1-20 partially

Remark on Protest   ☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet (1)) (July 1998)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-20 partially

Isolated protein consisting or comprising an amino acid sequence as characterized by SEQID3, or an allelic variant or an ortholog of said amino acid sequence wherein said variant or ortholog is encoded by a nucleic acid molecule that hybridizes to the nucleic acid molecule as characterized by SEQID1 or 2; an antibody that binds to said protein; furthermore a nucleic acid molecule consisting or comprising of a nucleotide sequence that
1) encodes the amino acid sequence of SEQId3
2) encodes and allelic variant or an ortholog of an amino acid sequence of SEQId3 wherein said nucleotide sequence hybridizes to SEQID 1 or 2
3) encodes a fragment of said SEQID3
4) is the complement of the nucleotides of 1) to 3)

The recombinant expression of the same in host cells and methods for the detection of said proteins or said nucleic acids in a sample with the help of an agent that binds to said protein or an oligonucleotide and kits that contain such agent or oligonucleotide.
Furthermore, a method to identify an agent that binds to said protein by detecting a complex formed by an agent and the said protein.

Invention 2-66: claims 1-20 partially

as invention one but referring to the protein and nucleic acid sequences as characterized by SEQIDs
6,9,....,192,195,198; SEQIDs 4,7,....,190,193,196 and SEQIDs
5,8,.....,191,194,197, respectively.

International Application No

PCT/US 01/09341

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 9408006	A	14-04-1994	CA	2145866 A1	14-04-1994
			EP	0663006 A1	19-07-1995
			JP	8501942 T	05-03-1996
			WO	9408006 A1	14-04-1994
			US	5683884 A	04-11-1997
			US	5674981 A	07-10-1997
			US	5622839 A	22-04-1997
			US	5674689 A	07-10-1997
WO 9901468	A	14-01-1999	AU	8380898 A	25-01-1999
			WO	9901468 A2	14-01-1999
EP 1136501	A	26-09-2001	DE	10013618 A1	20-09-2001
			EP	1136501 A2	26-09-2001
			JP	2001299369 A	30-10-2001

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09/618,893   18 July 2000 (18.07.2000)   US

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(72) Inventor: CRAVCHIK, Anibal; Celera, 45 West Gude Drive, Rockville, MD 20850 (US).

(74) Agent: MILLMAN, Robert, A.; Celera Genomics Corp., 45 West Gude Drive C2-4, Rockville, MD 20850 (US).

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ISOLATED G-PROTEIN COUPLED RECEPTORS, NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES THEREOF AS INSECTICIDAL TARGETS

RELATED APPLICATIONS

5   The present application claims priority to U.S. Serial No. 60/191,638, filed March 23, 2000 (Atty. Docket CL000388) and U.S. Serial No. 09/618,893, filed July 18, 2000 (Atty. Docket CL000733).

FIELD OF THE INVENTION

10   The present invention is in the field of G-Protein coupled receptors (GPCRs), recombinant DNA molecules and protein production. The present invention specifically provides novel GPCR proteins and nucleic acid molecules encoding such protein molecules, for use in the development of insecticide and insecticide targets and as a source for identifying human therapeutics and human therapeutic development.

15

BACKGROUND OF THE INVENTION

The *Drosophila melanogaster* genome is 165 Mb, with about 120 Mb of this being euchromatic. The genome is organized in 4 chromosome pairs and is estimated to contain 10 - 12,000 genes. Model organisms, such as *Drosophila melanogaster,* share many genes with
20   humans whose sequences and functions have been conserved. In addition to myriad similarities in cellular structure and function, humans and Drosophila share pathways for intercellular signaling, developmental patterning, learning and behavior, as well as tumor formation and metastasis.

The genes involved in the development of Drosophila, with few exceptions, are the same
25   as those involved in the development of higher organisms. Developmental biology studies the sequential activation and interaction of genes, in relation to developing morphology. Right now, Drosophila is the only organism for which one can begin with a list of genes active in the egg and follow the morphological changes and gene activations through to adulthood.

Drosophila studies have provided the widest knowledge base available for any single
30   organism; accordingly, developmental biologists use the fly to ferret out the activity of genes with similar functions in higher organisms. Despite its small size, the fly is by no means a small developmental problem. If you know the genes involved in the development of the fly, you also

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know, to a reasonable approximation, the genes involved in the development of the worm, the fish, the mouse, and humans.

A major goal in drug/insecticide development is to understand and elucidate the molecular mechanisms that govern cell signaling and cell-cell interactions in higher eukaryotes.

5   GPCRs form major links in cellular communication/response systems. A complete list of GPCR proteins from Drosophila would therefore be invaluable in developing human therapeutic targets. Not only will the proteins serve as models for human cellular signaling and response, such molecules will also serve as molecular keys in identifying therapeutically important human orthologs.

10

G-protein coupled receptors

G-protein coupled receptors (GPCRs) constitute a major class of proteins responsible for transducing a signal within a cell. GPCRs have three structural domains: an amino terminal extracellular domain, a transmembrane domain containing seven transmembrane segments, three

15   extracellular loops, and three intracellular loops, and a carboxy terminal intracellular domain. Upon binding of a ligand to an extracellular portion of a GPCR, a signal is transduced within the cell that results in a change in a biological or physiological property of the cell. GPCRs, along with G-proteins and effectors (intracellular enzymes and channels modulated by G-proteins), are the components of a modular signaling system that connects the state of intracellular second

20   messengers to extracellular inputs.

GPCR genes and gene-products are potential causative agents of disease (Spiegel et al., J. Clin. Invest. 92:1119-1125 (1993); McKusick et al., J. Med. Genet. 30:1-26 (1993)). Specific defects in the rhodopsin gene and the V2 vasopressin receptor gene have been shown to cause various forms of retinitis pigmentosum (Nathans et al., Annu. Rev. Genet. 26:403-424(1992)), and

25   nephrogenic diabetes insipidus (Holtzman et al., Hum. Mol. Genet. 2:1201-1204 (1993)). These receptors are of critical importance to both the central nervous system and peripheral physiological processes. Evolutionary analyses suggest that the ancestor of these proteins originally developed in concert with complex body plans and nervous systems.

The GPCR protein superfamily can be divided into five families: Family I, receptors

30   typified by rhodopsin and the β2-adrenergic receptor and currently represented by over 200 unique members (Dohlman et al., Annu. Rev. Biochem. 60:653-688 (1991)); Family II, the parathyroid hormone/calcitonin/secretin receptor family (Juppner et al., Science 254:1024-1026 (1991); Lin et al., Science 254:1022-1024 (1991)); Family III, the metabotropic glutamate receptor family

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(Nakanishi, *Science 258* 597:603 (1992)); Family IV, the cAMP receptor family, important in the chemotaxis and development of *D. discoideum* (Klein *et al.*, *Science 241*:1467-1472 (1988)); and Family V, the fungal mating pheromone receptors such as STE2 (Kurjan, *Annu. Rev. Biochem. 61*:1097-1129 (1992)).

5   There are also a small number of other proteins, which present seven putative hydrophobic segments and appear to be unrelated to GPCRs; they have not been shown to couple to G-proteins. *Drosophila* expresses a photoreceptor-specific protein, bride of sevenless (boss), a seven-transmembrane-segment protein, which has been extensively studied and does not show evidence of being a GPCR (Hart *et al.*, *Proc. Natl. Acad. Sci. USA 90*:5047-5051 (1993)). The gene *frizzled (fz)*
10   in *Drosophila* is also thought to be a protein with seven transmembrane segments. Like boss, fz has not been shown to couple to G-proteins (Vinson *et al.*, *Nature 338*:263-264 (1989)).

           G proteins represent a family of heterotrimeric proteins composed of α, β and γ subunits, that bind guanine nucleotides. These proteins are usually linked to cell surface receptors, e.g., receptors containing seven transmembrane segments. Following ligand binding to the GPCR, a
15   conformational change is transmitted to the G protein, which causes the α-subunit to exchange a bound GDP molecule for a GTP molecule and to dissociate from the βγ-subunits. The GTP-bound form of the α-subunit typically functions as an effector-modulating moiety, leading to the production of second messengers, such as cAMP (e.g., by activation of adenyl cyclase), diacylglycerol or inositol phosphates. Greater than 20 different types of α-subunits are known in
20   humans. These subunits associate with a smaller pool of β and γ subunits. Examples of mammalian G proteins include Gi, Go, Gq, Gs and Gt. G proteins are described extensively in Lodish *et al.*, *Molecular Cell Biology*, (Scientific American Books Inc., New York, N.Y., 1995), the contents of which are incorporated herein by reference. GPCRs, G proteins and G protein-linked effector and second messenger systems have been reviewed in *The G-Protein Linked Receptor Fact*
25   *Book*, Watson *et al.*, eds., Academic Press (1994).

           Dopamine receptors

           The understanding of the dopaminergic system relevance in brain function and disease developed several decades ago from three diverse observations following drug treatments. These
30   were the observations that dopamine replacement therapy improved Parkinson's disease symptoms, depletion of dopamine and other catecholamines by reserpine caused depression and antipsychotic drugs blocked dopamine receptors. The finding that the dopamine receptor binding affinities of typical antipsychotic drugs correlate with their clinical potency led to the dopamine overactivity

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hypothesis of schizophrenia (Snyder, S.H., *Am J Psychiatry 133*, 197-202 (1976); Seeman, P. and

Lee, T., *Science 188*, 1217-9 (1975)). Today, dopamine receptors are crucial targets in the

pharmacological therapy of schizophrenia, Parkinson's disease, Tourette's syndrome, tardive

dyskinesia and Huntington's disease. The dopaminergic system includes the nigrostriatal,

5   mesocorticolimbic and tuberoinfundibular pathways. The nigrostriatal pathway is part of the striatal

motor system and its degeneration leads to Parkinson's disease; the mesocorticolimbic pathway

plays a key role in reinforcement and in emotional expression and is the desired site of action of

antipsychotic drugs; the tuberoinfundibular pathways regulates prolactin secretion from the

pituitary.

10   Dopamine receptors are members of the G protein coupled receptor superfamily, a large

group proteins that share a seven helical membrane-spanning structure and transduce signals

through coupling to heterotrimeric guanine nucleotide-binding regulatory proteins (G proteins).

Dopamine receptors are classified into subfamilies: D1-like (D1 and D5) and D2-like (D2, D3 and

D4) based on their different ligand binding profiles, signal transduction properties, sequence

15   homologies and genomic organizations (Civelli, O., Bunzow, J.R. and Grandy, D.K., *Annu Rev

Pharmacol Toxicol 33*, 281-307 (1993)). The D1-like receptors, D1 and D5, stimulate cAMP

synthesis through coupling with Gs-like proteins and their genes do not contain introns within their

protein coding regions. On the other hand, the D2-like receptors, D2, D3 and D4, inhibit cAMP

synthesis through their interaction with Gi-like proteins and share a similar genomic organization

20   which includes introns within their protein coding regions.

Serotonin receptors

Serotonin (5-Hydroxytryptamine; 5-HT) was first isolated from blood serum, where it was

shown to promote vasoconstriction (Rapport, M.M., Green, A.A. and Page, I.H., *J Biol Chem 176*,

25   1243-1251 (1948). Interest on a possible relationship between 5-HT and psychiatric disease was

spurred by the observations that hallucinogens such as LSD and psilocybin inhibit the actions of 5-

HT on smooth muscle preparations (Gaddum, J.H. and Hameed, K.A., *Br J Pharmacol 9*, 240-248

(1954)). This observation lead to the hypothesis that brain 5-HT activity might be altered in

psychiatric disorders (Wooley, D.W. and Shaw, E., *Proc Natl Acad Sci U S A 40*, 228-231 (1954);

30   Gaddum, J.H. and Picarelli, Z.P., *Br J Pharmacol 12*, 323-328 (1957)). This hypothesis was

strengthened by the introduction of tricyclic antidepressants and monoamine oxidase inhibitors for

the treatment of major depression and the observation that those drugs affected noradrenaline and 5-

HT metabolism. Today, drugs acting on the serotoninergic system have been proved to be effective

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in the pharmacotherapy of psychiatric diseases such as depression, schizophrenia, obsessive-compulsive disorder, panic disorder, generalized anxiety disorder and social phobia as well as migraine, vomiting induced by cancer chemotherapy and gastric motility disorders.

Serotonin receptors represent a very large and diverse family of neurotransmitter receptors.
5   To date thirteen 5-HT receptor proteins coupled to G proteins plus one ligand–gated ion channel receptor (5-HT3) have been described in mammals. This receptor diversity is thought to reflect serotonin's ancient origin as a neurotransmitter and a hormone as well as the many different roles of 5-HT in mammals. The 5-HT receptors have been classified into seven subfamilies or groups according to their different ligand-binding affinity profiles, molecular structure and intracellular
10   transduction mechanisms (Hoyer, D. et al., *Pharmacol. Rev. 46*, 157-203 (1994)).

GPCRs are a major target for drug/insecticide action and development. Accordingly, it is valuable to the field of pharmaceutical development to identify and characterize previously unknown GPCRs. The present invention advances the state of the art by providing a previously unidentified drosophila GPCRs.

15

Insecticides

About 10,000 species of the more than 1 million species of insects are crop-eating, and of these, approximately 700 species worldwide cause most of the insect damage to man's crops, in the field and in storage.
20   A detailed study of novel proteins from Drosophila and invertebrate orthologs thereof, will serve as targets for identifying new members of the known classes of insecticides as well as aiding in the identification of new classes of compounds.

SUMMARY OF THE INVENTION
25   The present invention is based in part on the identification of nucleic acid sequences that encode amino acid sequences of 66 GPCR proteins that are produced by *Drosophila melanogaster* and invertebrate, human and other mammalian orthologs thereof. These unique protein sequences, and nucleic acid sequences that encode these proteins, can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins
30   and serve as targets for the development of human therapeutic and insecticidal agents.

The proteins of the present inventions are GPCRs that participate in signaling pathways. As used herein, a "signaling pathway" refers to the modulation (e.g., stimulation or inhibition) of a cellular function/activity upon the binding of a ligand to the GPCR protein. Examples of such

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functions include mobilization of intracellular molecules that participate in a signal transduction pathway, e.g., phosphatidylinositol 4,5-bisphosphate (PIP_2), inositol 1,4,5-triphosphate (IP_3) and adenylate cyclase; polarization of the plasma membrane; production or secretion of molecules; alteration in the structure of a cellular component; cell proliferation, e.g., synthesis of DNA; cell

5   migration; cell differentiation; and cell survival

The response mediated by the receptor protein depends on the type of cell. For example, in some cells, binding of a ligand to the receptor protein may stimulate an activity such as release of compounds, gating of a channel, cellular adhesion, migration, differentiation, etc., through phosphatidylinositol or cyclic AMP metabolism and turnover while in other cells, the binding of the

10   ligand will produce a different result. Regardless of the cellular activity/response modulated by the receptor protein, it is universal that the protein is a GPCR and interacts with G proteins to produce one or more secondary signals, in a variety of intracellular signal transduction pathways, e.g., through phosphatidylinositol or cyclic AMP metabolism and turnover, in a cell.

As used herein, "phosphatidylinositol turnover and metabolism" refers to the molecules

15   involved in the turnover and metabolism of phosphatidylinositol 4,5-bisphosphate (PIP_2) as well as to the activities of these molecules. PIP_2 is a phospholipid found in the cytosolic leaflet of the plasma membrane. Binding of ligand to the receptor activates, in some cells, the plasma-membrane enzyme phospholipase C that in turn can hydrolyze PIP_2 to produce 1,2-diacylglycerol (DAG) and inositol 1,4,5-triphosphate (IP_3). Once formed IP_3 can diffuse to the endoplasmic reticulum surface

20   where it can bind an IP_3 receptor, e.g., a calcium channel protein containing an IP_3 binding site. IP_3 binding can induce opening of the channel, allowing calcium ions to be released into the cytoplasm. IP_3 can also be phosphorylated by a specific kinase to form inositol 1,3,4,5-tetraphosphate (IP_4), a molecule that can cause calcium entry into the cytoplasm from the extracellular medium. IP_3 and IP_4 can subsequently be hydrolyzed very rapidly to the inactive products inositol 1,4-biphosphate

25   (IP_2) and inositol 1,3,4-triphosphate, respectively. These inactive products can be recycled by the cell to synthesize PIP_2. The other second messenger produced by the hydrolysis of PIP_2, namely 1,2-diacylglycerol (DAG), remains in the cell membrane where it can serve to activate the enzyme protein kinase C. Protein kinase C is usually found soluble in the cytoplasm of the cell, but upon an increase in the intracellular calcium concentration, this enzyme can move to the plasma membrane

30   where it can be activated by DAG. The activation of protein kinase C in different cells results in various cellular responses such as the phosphorylation of glycogen synthase, or the phosphorylation of various transcription factors, e.g., NF-kB. The language "phosphatidylinositol activity", as used herein, refers to an activity of PIP_2 or one of its metabolites.

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Another signaling pathway in which the receptor may participate is the cAMP turnover

pathway. As used herein, "cyclic AMP turnover and metabolism" refers to the molecules

involved in the turnover and metabolism of cyclic AMP (cAMP) as well as to the activities of

these molecules. Cyclic AMP is a second messenger produced in response to ligand-induced

5   stimulation of certain G protein coupled receptors. In the cAMP signaling pathway, binding of a

ligand to a GPCR can lead to the activation of the enzyme adenyl cyclase, which catalyzes the

synthesis of cAMP. The newly synthesized cAMP can in turn activate a cAMP-dependent

protein kinase. This activated kinase can phosphorylate a voltage-gated potassium channel

protein, or an associated protein, and lead to the inability of the potassium channel to open

10   during an action potential. The inability of the potassium channel to open results in a decrease in

the outward flow of potassium, which normally repolarizes the membrane of a neuron, leading to

prolonged membrane depolarization.

By targeting an agent to modulate a GPCR, the signaling activity and biological process

mediated by the receptor can be agonized or antagonized. Such agonism and antagonism serves

15   as a basis for modulating a biological activity in a therapeutic context (mammalian therapy) or

toxic context (anti-invertebrate/insecticidal agent).

DESCRIPTION OF THE FIGURE SHEETS

FIGURE SHEETS 1-89 provides genomic nucleic acid sequences from Drosophila

20   melanogaster, predicted transcript, amino acid coding regions, information relating to the

subfamily of GPCR proteins to which the protein sequence belongs, e.g., BLAST hit homology,

presence of hidden Markov model, etc. Also provided are 5' promoter sequences, transciption

initiation sites and other structural features.

25   ## DETAILED DESCRIPTION OF THE INVENTION

General Description

The present invention is based on the sequencing of the *Drosophila melanogaster*

genome. During the sequencing and assembly of the *Drosophila melanogaster* genome, analysis

of the sequence information revealed previously unidentified nucleic acid molecules that encode

30   proteins that share structural and/or sequence homology to protein/peptide/domains identified

and characterized within the art as being a GPCR protein or part of a GPCR protein. Based on

this analysis, the present invention provides amino acid sequences of 66 GPCR proteins that are

produced by Drosophila melanogaster, nucleic acid sequences that encode these GPCR proteins,

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and the art known protein/peptide/domain that have structural or sequence homology to the Drosophila melanogaster protein.

In addition to being previously unknown, the proteins and nucleic acid molecules that are provided in the present invention are selected based on their ability to be used for the

5   development of commercially important products and services. Specifically, the present proteins are selected based on homology and/or structural relatedness to known GPCR proteins of commercial importance and/or the presence of genetic signals that define the protein as a GPCR protein. Some of the more specific features of the proteins of the present invention, and the uses thereof, are described in detail below, and are known within the art for each category of GPCR.

10

Specific Embodiments

Peptide Molecules

In the Figure sheets, the present invention provides nucleic acid sequences that encode 66 protein molecules that have been identified as being within the Drosophila melanogaster genome

15   (SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, encoded by nucleic acid molecules provided in SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196 (genomic sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)). These protein sequences will be referred herein as the GPCR proteins of the present invention, GPCR proteins, or the peptides or the proteins of the present invention. Table 1 provides a summary of the GPCRs of the present invention and the subfamily

20   assignment of each one.

The present invention provides isolated peptide and protein molecules that consist of, consist essentially of or are comprised of the amino acid sequences of the GPCR proteins disclosed in the Figure sheets (SEQ ID NO: 3, 6, 9, 189, 192, 195, 198, encoded by nucleic acid molecules provided in SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196 (genomic sequences) or SEQ ID

25   NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)), as well as all obvious variants of these proteins that are within the art to make and use. Some of these variants are described in detail below.

As used herein, a protein is said to be "isolated" or "purified" when it is substantially free of cellular material or free of chemical precursors or other chemicals. The proteins of the present

30   invention can be purified to homogeneity or other degrees of purity. The level of purification will be based on the intended use. The critical feature is that the preparation allows for the desired function of the protein, even if in the presence of considerable amounts of other components.

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In some uses, "substantially free of cellular material" includes preparations of the protein having less than about 30% (by dry weight) other proteins (i.e., contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins. When the protein is recombinantly produced, it can also be substantially free of culture medium,

5   i.e., culture medium represents less than about 20% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of the protein in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of the GPCR protein having less than about

10   30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

The isolated GPCR protein can be purified from cells that naturally express it, purified from cells that have been altered to express it (recombinant), or synthesized using known protein

15   synthesis methods. For example, a nucleic acid molecule encoding the GPCR protein is cloned into an expression vector, the expression vector introduced into a host cell and the protein expressed in the host cell. The protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Many of these techniques are described in detail below.

20   Accordingly, the present invention provides proteins that consist of one of the amino acid sequences encoded by the nucleic acid sequences shown in the Figure sheets (SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196 (genomic sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)). The amino acid sequences of such proteins are provided in the Figure Sheets along with an explanation of the protein type/family. A protein consists of an amino acid sequence when

25   the amino acid sequence is the final amino acid sequence of the protein.

The present invention further provides proteins that consist essentially of one of the amino acid sequences encoded by the nucleic acid sequences shown in the Figure sheets (SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196 (genomic sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)). A protein consists essentially of an amino acid sequence when such an

30   amino acid sequence is present with only a few additional amino acid residues in the final protein.

The present invention further provides proteins that are comprised of one of the amino acid sequences encoded by the nucleic acid sequences shown in the Figure sheets (SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196 (genomic sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript

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sequences)). A protein is comprised of an amino acid sequence when the amino acid sequence is at least part of the final amino acid sequence of the protein. In such a fashion, the protein can be only the protein or have additional amino acid molecules, such as amino acid residues (contiguous encoded sequence) that are naturally associated with it or heterologous amino acid residues/peptide

5   sequences. Such a protein can have a few additional amino acid residues or can comprise several hundred or more additional amino acids. The preferred classes of proteins that are comprised of the GPCR proteins of the present invention are the naturally occurring mature proteins.

The GPCR proteins of the present invention can be attached to heterologous sequences to form chimeric or fusion proteins. Such chimeric and fusion proteins comprise a GPCR protein

10   operatively linked to a heterologous protein having an amino acid sequence not substantially homologous to the GPCR protein. "Operatively linked" indicates that the GPCR protein and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the GPCR protein.

In some uses, the fusion protein does not affect the activity of the GPCR protein *per se*. For

15   example, the fusion protein can include, but is not limited to, enzymatic fusion proteins, for example beta-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions, MYC-tagged, HI-tagged and Ig fusions. Such fusion proteins, particularly poly-His fusions, can facilitate the purification of recombinant GPCR protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of a protein can be increased by using a heterologous signal sequence.

20   A chimeric or fusion protein can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different protein sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to

25   complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (e.g., a GST protein). A GPCR protein-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-

30   frame to the GPCR protein.

As mentioned above, the present invention also provides and enables obvious variants of the amino acid sequence of the proteins of the present invention, such as naturally occurring mature forms of the protein, allelic/sequence variants of the proteins, non-naturally occurring

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recombinantly derived variants of the proteins, and orthologs and paralogs of the proteins. Such variants can readily be generated using art know techniques in the fields of recombinant nucleic acid technology and protein biochemistry. It is understood, however, that variants exclude any amino acid sequences disclosed prior to the invention.

5   Such variants can readily be identified/made using molecular techniques and the sequence information disclosed herein. Further, such variants can readily be distinguished from other proteins based on sequence and/or structural homology to the GPCR proteins of the present invention. The degree of homology/identity present will be based primarily on whether the protein is a functional variant or non-functional variant, the amount of divergence present in the paralog

10   family and the evolutionary distance between the orthologs.

       To determine the percent identity of two amino acid sequences or two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In a

15   preferred embodiment, the length of a reference sequence aligned for comparison purposes is at least 30%, 40%, 50%, 60%, 70%, 80%, or 90% or more of the length of the reference sequence. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the

20   molecules are identical at that position (as used herein amino acid or nucleic acid "identity" is equivalent to amino acid or nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

25   The comparison of sequences and determination of percent identity and similarity between two sequences can be accomplished using a mathematical algorithm. (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New

30   Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm

which has been incorporated into the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the

5   GAP program in the GCG software package (Devereux, J., *et al., Nucleic Acids Res. 12(1)*:387 (1984)) (available at http://www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated

10   into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against sequence databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and

15   XBLAST programs (version 2.0) of Altschul, et al. (*J. Mol. Biol.* 215:403-10 (1990)). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the proteins of the invention. To obtain gapped

20   alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (*Nucleic Acids Res.* 25(17):3389-3402 (1997)). When utilizing BLAST and gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See http://www.ncbi.nlm.nih.gov.

Full-length pre-processed forms, as well as mature processed forms, of proteins that

25   comprise one of the proteins of the present invention can readily be identified as having complete sequence identity to one of the GPCR proteins of the present invention as well as being encoded by the same genetic locus as the GPCR protein provided herein.

Allelic variants of a GPCR protein can readily be identified as having a high degree (significant) of sequence homology/identity to at least a portion of the GPCR protein as well as

30   being encoded by the same genetic locus as the GPCR protein provided herein. As used herein, two proteins (or a region of the proteins) have significant homology when the amino acid sequences are typically at least about 70-75%, 80-85%, and more typically at least about 90-95% or more homologous. A significantly homologous amino acid sequence, according to the present

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invention, will be encoded by a nucleic acid sequence that will hybridize to a GPCR protein encoding nucleic acid molecule under stringent conditions as more fully described below.

Paralogs of a GPCR protein can readily be identified as having some degree of significant sequence homology/identity to at least a portion of the GPCR protein, as being encoded by a gene from Drosophila, and as having similar activity or function. Two proteins will typically be considered paralogs when the amino acid sequences are typically at least about 70-75%, 80-85%, and more typically at least about 90-95% or more homologous through a given region or domain. Such paralogs will be encoded by a nucleic acid sequence that will hybridize to a GPCR protein encoding nucleic acid molecule under stringent conditions as more fully described below.

Orthologs of a GPCR protein can readily be identified as having some degree of significant sequence homology/identity to at least a portion of the GPCR protein as well as being encoded by a gene from another organism. Preferred orthologs will be isolated from mammals, preferably human, for the development of human therapeutic targets and agents, or other invertebrates, particularly insects of economical/agriculture importance, e.g. members of the Lepidopteran and Coleopteran orders, for the development of insecticides and insecticidal targets. Such orthologs will be encoded by a nucleic acid sequence that will hybridize to a GPCR protein encoding nucleic acid molecule under moderate to stringent conditions, as more fully described below, depending on the degree of relatedness of the two organisms yielding the proteins.

Non-naturally occurring variants of the GPCR proteins of the present invention can readily be generated using recombinant techniques. Such variants include, but are not limited to deletions, additions and substitutions in the amino acid sequence of the GPCR protein. For example, one class of substitutions are conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a GPCR protein by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu, and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al., Science 247*:1306-1310 (1990).

Variant GPCR proteins can be fully functional or can lack function in one or more activities, e.g. ability to bind ligand, ability to bind G-protein, ability to mediate signaling, etc. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids

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that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree.

Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* *244*:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity such as receptor binding or in assays such as an *in vitro* proliferative activity. Sites that are critical for ligand-receptor binding can also be determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol. 224*:899-904 (1992); de Vos *et al. Science 255*:306-312 (1992)).

Polypeptides often contain amino acids other than the 20 amino acids commonly referred to as the 20 naturally-occurring amino acids. Further, many amino acids, including the terminal amino acids, may be modified by natural processes, such as processing and other post-translational modifications, or by chemical modification techniques well known in the art. Common modifications that occur naturally in polypeptides are described in basic texts, detailed monographs, and the research literature, and they are well known to those of skill in the art.

Accordingly, the polypeptides also encompass derivatives or analogs in which a substituted amino acid residue is not one encoded by the genetic code, in which a substituent group is included, in which the mature polypeptide is fused with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol), or in which the additional amino acids are fused to the mature polypeptide, such as a leader or secretory sequence or a sequence for purification of the mature polypeptide or a pro-protein sequence.

The present invention further provides fragments of the GPCR proteins, in addition to proteins and peptides that comprise and consist of such fragments. The fragments to which the invention pertains, however, are not to be construed as encompassing fragments that may be disclosed publicly prior to the present invention.

As used herein, a fragment comprises at least 8 or more contiguous amino acid residues from a GPCR protein. Such fragments can be chosen based on the ability to retain one or more of the biological activities of the GPCR protein or could be chosen for the ability to perform a function, e.g. act as an immunogen. Particularly important fragments are biologically active

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fragments, peptides which are, for example, about 8 or more amino acids in length. Such fragments will typically comprise a domain or motif of the GPCR protein, e.g., active site, a G-protein binding site, a transmembrane domain or a ligand binding domain. Further, possible fragments include, but are not limited to, domain or motif containing fragments, soluble peptide fragments, and fragments

5   containing immunogenic structures. Predicted domains and functional sites are readily identifiable by computer programs well-known and readily available to those of skill in the art (e.g., PROSITE analysis).

Polypeptides often contain amino acids other than the 20 amino acids commonly referred to as the 20 naturally-occurring amino acids. Further, many amino acids, including the terminal amino

10   acids, may be modified by natural processes, such as processing and other post-translational modifications, or by chemical modification techniques well known in the art. Common modifications that occur naturally in GPCR proteins are described in basic texts, detailed monographs, and the research literature, and they are well known to those of skill in the art.

Accordingly, the GPCR proteins of the present invention also encompass derivatives or

15   analogs in which a substituted amino acid residue is not one encoded by the genetic code, in which a substituent group is included, in which the mature GPCR protein is fused with another compound, such as a compound to increase the half-life of the GPCR protein (for example, polyethylene glycol), or in which the additional amino acids are fused to the mature GPCR protein, such as a leader or secretory sequence or a sequence for purification of the mature GPCR protein or a pro-

20   protein sequence.

Known modifications include, but are not limited to, acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond

25   formation, demethylation, formation of covalent crosslinks, formation of cystine, formation of pyroglutamate, formylation, gamma carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination.

30   Such modifications are well-known to those of skill in the art and have been described in great detail in the scientific literature. Several particularly common modifications, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation, for instance, are described in most basic texts, such as *Proteins - Structure and*

Molecular Properties, 2nd Ed., T.E. Creighton, W. H. Freeman and Company, New York (1993). Many detailed reviews are available on this subject, such as by Wold, F., *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York 1-12 (1983); Seifter *et al.* (*Meth. Enzymol. 182*: 626-646 (1990)) and Rattan *et al.* (*Ann. N.Y. Acad. Sci. 663*:48-62 (1992)).

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Protein/Peptide Uses

The proteins of the present invention can be used in assays to identify modulators as potential insecticides, to determine the biological activity of the protein, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune

10   response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its binding partner or receptor) in biological fluids; and as markers for tissues in which the corresponding protein is preferentially expressed. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the binding partner so as to develop a system to

15   identify inhibitors of the binding interaction. Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E. F. Fritsch and T. Maniatis eds., 1989,

20   and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S. L. and A. R. Kimmel eds., 1987 and can readily be determined using the information provided in Table 1.

The potential uses of the proteins of the present invention are based primarily on the source of the protein as well as the class/action of the protein. For example, GPCRs isolated

25   from Drosophila and other invertebrates serve as a target for identifying anti-invertebrate compounds, e.g. insecticides. GPCRs isolated from Drosophila and their human/mammalian orthologs serve as targets for identifying agents for use in mammalian therapeutic applications, e.g. a human drug. Approximately 70% of all pharmaceutical agents modulate the activity of a GPCR. A combination of the invertebrate and mammalian ortholog can be used in selective

30   screening methods to find agents specific for invertebrates. Table 1 provides specific context of use for each of the presently disclosed GPCRs. Particularly useful are GPCRs involved in neurotransmission for use as insecticide targets.

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The receptor polypeptides (including variants and fragments which may have been disclosed prior to the present invention) are useful for biological assays related to GPCRs. Such assays involve any of the known GPCR functions or activities or properties useful for diagnosis and treatment of GPCR-related conditions.

The receptor polypeptides are also useful in drug/insecticide screening assays, in cell-based or cell-free systems. Cell-based systems can be native, i.e., cells that normally express the receptor protein, as a biopsy or expanded in cell culture. In one embodiment, however, cell-based assays involve recombinant host cells expressing the receptor protein.

The polypeptides can be used to identify compounds that modulate receptor activity. Both the GPCRs of the present invention and appropriate variants and fragments can be used in high-throughput screens to assay candidate compounds for the ability to bind to the receptor. These compounds can be further screened against a functional receptor to determine the effect of the compound on the receptor activity. Further, these compounds can be tested in animal or invertebrate systems to determine activity/effectiveness. Compounds can be identified that activate (agonist) or inactivate (antagonist) the receptor to a desired degree.

Further, the receptor polypeptides can be used to screen a compound for the ability to stimulate or inhibit interaction between the receptor protein and a target molecule that normally interacts with the receptor protein. The target can be ligand or a component of the signal pathway that the receptor protein normally interacts (for example, a G-protein or other interactor involved in cAMP or phosphatidylinositol turnover and/or adenylate cyclase, or phospholipase C activation). Such assays typically include the steps of combining the receptor protein with a candidate compound under conditions that allow the receptor protein, or fragment, to interact with the target molecule, and to detect the formation of a complex between the protein and the target or to detect the biochemical consequence of the interaction with the receptor protein and the target, such as any of the associated effects of signal transduction such as G-protein phosphorylation, cAMP or phosphatidylinositol turnover, and adenylate cyclase or phospholipase C activation.

Candidate compounds include, for example, 1) peptides such as soluble peptides, including Ig-tailed fusion peptides and members of random peptide libraries (see, e.g., Lam *et al.*, *Nature* *354*:82-84 (1991); Houghten *et al.*, *Nature 354*:84-86 (1991)) and combinatorial chemistry-derived molecular libraries made of D- and/or L- configuration amino acids; 2) phosphopeptides (e.g., members of random and partially degenerate, directed phosphopeptide libraries, see, e.g., Songyang *et al.*, *Cell 72*:767-778 (1993)); 3) antibodies (e.g., polyclonal, monoclonal, humanized, anti-idiotypic, chimeric, and single chain antibodies as well as Fab, F(ab')$_2$, Fab expression library

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fragments, and epitope-binding fragments of antibodies); and 4) small organic and inorganic molecules (e.g., molecules obtained from combinatorial and natural product libraries).

One candidate compound is a soluble fragment of the receptor that competes for ligand binding. Other candidate compounds include mutant receptors or appropriate fragments containing

5   mutations that affect receptor function and thus compete for ligand. Accordingly, a fragment that competes for ligand, for example with a higher affinity, or a fragment that binds ligand but does not allow release, is encompassed by the invention.

The invention further includes other end point assays to identify compounds that modulate (stimulate or inhibit) receptor activity. The assays typically involve an assay of events in the signal

10   transduction pathway that indicate receptor activity. Thus, the expression of genes that are up- or down-regulated in response to the receptor protein dependent signal cascade can be assayed. In one embodiment, the regulatory region of such genes can be operably linked to a marker that is easily detectable, such as luciferase. Alternatively, phosphorylation of the receptor protein, or a receptor protein target, could also be measured.

15   Any of the biological or biochemical functions mediated by the receptor can be used as an endpoint assay. These include all of the biochemical or biochemical/biological events described herein, in the references cited herein, incorporated by reference for these endpoint assay targets, and other functions known to those of ordinary skill in the art.

Binding and/or activating compounds can also be screened by using chimeric receptor

20   proteins in which the amino terminal extracellular domain, or parts thereof, the entire transmembrane domain or subregions, such as any of the seven transmembrane segments or any of the intracellular or extracellular loops and the carboxy terminal intracellular domain, or parts thereof, can be replaced by heterologous domains or subregions. For example, a G-protein-binding region can be used that interacts with a different G-protein then that which is recognized by the

25   native receptor. Accordingly, a different set of signal transduction components is available as an end-point assay for activation. Alternatively, the entire transmembrane portion or subregions (such as transmembrane segments or intracellular or extracellular loops) can be replaced with the entire transmembrane portion or subregions specific to a host cell that is different from the host cell from which the amino terminal extracellular domain and/or the G-protein-binding region are derived.

30   This allows for assays to be performed in other than the specific host cell from which the receptor is derived. Alternatively, the amino terminal extracellular domain (and/or other ligand-binding regions) could be replaced by a domain (and/or other binding region) binding a different ligand, thus, providing an assay for test compounds that interact with the heterologous amino terminal

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extracellular domain (or region) but still cause signal transduction. Finally, activation can be detected by a reporter gene containing an easily detectable coding region operably linked to a transcriptional regulatory sequence that is part of the native signal transduction pathway.

The receptor polypeptides are also useful in competition binding assays in methods designed
5   to discover compounds that interact with the receptor. Thus, a compound is exposed to a receptor polypeptide under conditions that allow the compound to bind or to otherwise interact with the polypeptide. Soluble receptor polypeptide is also added to the mixture. If the test compound interacts with the soluble receptor polypeptide, it decreases the amount of complex formed or activity from the receptor target. This type of assay is particularly useful in cases in which
10   compounds are sought that interact with specific regions of the receptor. Thus, the soluble polypeptide that competes with the target receptor region is designed to contain peptide sequences corresponding to the region of interest.

To perform cell free drug/insecticide screening assays, it is sometimes desirable to immobilize either the receptor protein, or fragment, or its target molecule to facilitate separation of
15   complexes from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay.

Techniques for immobilizing proteins on matrices can be used in the drug/insecticide screening assays. In one embodiment, a fusion protein can be provided which adds a domain that allows the protein to be bound to a matrix. For example, glutathione-S-transferase/15625 fusion
20   proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the cell lysates (e.g., ^{35}S-labeled) and the candidate compound, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads are washed to remove any unbound label, and the matrix immobilized and radiolabel
25   determined directly, or in the supernatant after the complexes are dissociated. Alternatively, the complexes can be dissociated from the matrix, separated by SDS-PAGE, and the level of receptor-binding protein found in the bead fraction quantitated from the gel using standard electrophoretic techniques. For example, either the polypeptide or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin using techniques well known in the art. Alternatively,
30   antibodies reactive with the protein but which do not interfere with binding of the protein to its target molecule can be derivatized to the wells of the plate, and the protein trapped in the wells by antibody conjugation. Preparations of a receptor-binding protein and a candidate compound are incubated in the receptor protein-presenting wells and the amount of complex trapped in the well

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can be quantitated. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the receptor protein target molecule, or which are reactive with receptor protein and compete with the target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic

5   activity associated with the target molecule.

Agents that modulate one of the GPCRs of the present invention can be identified using one or more of the above assays, alone or in combination. It is generally preferable to use a cell-based or cell free system first and then confirm activity in an animal/insect model system. Such model systems are well known in the art and can readily be employed in this context.

10   Modulators of receptor protein activity identified according to these drug/insecticide screening assays can be used to treat a subject with a disorder mediated by the receptor pathway, by treating cells that express the GPCR. These methods of treatment include the steps of administering the modulators of protein activity in a pharmaceutical composition as described herein, to a subject in need of such treatment.

15   In yet another aspect of the invention, the GPCR proteins can be used as "bait proteins" in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos et al. (1993) *Cell* 72:223-232; Madura et al. (1993) *J. Biol. Chem.* 268:12046-12054; Bartel et al. (1993) *Biotechniques* 14:920-924; Iwabuchi et al. (1993) *Oncogene* 8:1693-1696; and Brent WO94/10300), to identify other proteins, which bind to or interact with the GPCR and are

20   involved in GPCR activity. Such GPCR-binding proteins are also likely to be involved in the propagation of signals by the GPCR proteins or GPCR targets as, for example, downstream elements of a GPCR-mediated signaling pathway, e.g., a signaling pathway. Alternatively, such GPCR-binding proteins are likely to be GPCR inhibitors.

The two-hybrid system is based on the modular nature of most transcription factors,

25   which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for a GPCR protein is fused to a gene encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known

30   transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a GPCR-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription

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factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the GPCR protein.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (e.g., a GPCR modulating agent, an antisense GPCR nucleic acid molecule, a GPCR-specific antibody, or a GPCR-binding partner) can be used in an animal or insect model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal or insect model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for insecticidal activity as described herein.

Antibodies

The invention also provides antibodies that selectively bind to one of the proteins of the present invention, a protein comprising such a peptide, as well as variants and fragments thereof. As used herein, an antibody selectively binds a target peptide when it binds the target peptide and does not significantly bind to unrelated proteins. An antibody is still considered to selectively bind a peptide even if it also binds to other proteins that are not substantially homologous with the target peptide so long as such proteins share homology with a fragment or domain of the peptide target of the antibody. In this case, it would be understood that antibody binding to the peptide is still selective despite some degree of cross-reactivity.

As used herein, an antibody is defined in terms consistent with that recognized within the art: they are multi-subunit proteins produced by a mammalian organism in response to an antigen challenge. The antibodies of the present invention include polyclonal antibodies and monoclonal antibodies, as well as fragments of such antibodies, including, but not limited to, Fab or $F(ab')_2$, and Fv fragments.

Many methods are known for generating and/or identifying antibodies to a given target peptide. Several such methods are described by Harlow, Antibodies, Cold Spring Harbor Press, (1989).

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In general, to generate antibodies, an isolated peptide is used as an immunogen and is administered to a mammalian organism, such as a rat, rabbit or mouse. Either the full-length protein, an antigenic peptide fragment or a fusion protein can be used.

Antibodies are preferably prepared from regions or discrete fragments of the GPCR proteins. Antibodies can be prepared from any region of the protein as described herein. However, preferred regions will include those involved in function/activity and/or receptor/binding partner interaction.

An antigenic fragment will typically comprise at least 10 contiguous amino acid residues. The antigenic peptide can comprise, however, at least 12, 14, 20 or more amino acid residues. Such fragments can be selected on a physical property, such as fragments correspond to regions that are located on the surface of the protein, e.g., hydrophilic regions or can be selected based on sequence uniqueness.

Detection on an antibody of the present invention can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I, ^{131}I, ^{35}S or ^{3}H.

Antibody Uses

The antibodies can be used to isolate one of the proteins of the present invention by standard techniques, such as affinity chromatography or immunoprecipitation. The antibodies can facilitate the purification of the natural protein from cells and recombinantly produced protein expressed in host cells. In addition, such antibodies are useful to detect the presence of one of the proteins of the present invention in cells or tissues to determine the pattern of expression of the protein among various tissues in an organism and over the course of normal development. Further, such antibodies can be used to detect protein *in situ*, *in vitro*, or in a cell lysate or supernatant in order to evaluate the abundance and pattern of expression. Also, such antibodies can be used to assess abnormal tissue

distribution or abnormal expression during development. Antibody detection of circulating fragments of the full length protein can be used to identify turnover.

The antibodies can also be used to assess normal and aberrant subcellular localization of cells in the various tissues in an organism. The diagnostic uses can be applied, not only in genetic testing, but also in monitoring a treatment modality. Accordingly, where treatment is ultimately aimed at correcting expression level or the presence of aberrant sequence and aberrant tissue distribution or developmental expression, antibodies directed against the or relevant fragments can be used to monitor therapeutic efficacy.

The antibodies are also useful for inhibiting protein function, for example, blocking the binding of the GPCR protein to a binding partner such as a ligand. An antibody can be used, for example, to block binding, thus modulating (agonizing or antagonizing) the peptides activity. Antibodies can be prepared against specific fragments containing sites required for function or against intact protein that is associated with a cell or cell membrane.

The invention also encompasses kits for using antibodies to detect the presence of a protein in a biological sample. The kit can comprise antibodies such as a labeled or labelable antibody and a compound or agent for detecting protein in a biological sample; means for determining the amount of protein in the sample; means for comparing the amount of protein in the sample with a standard; and instructions for use.

Nucleic Acid Molecules

The present invention further provides isolated nucleic acid molecules that encode a GPCR protein or protein of the present invention (SEQ ID NO: 3, 6, 9, ..., 192, 195, 198, encoded by nucleic acid molecules provided in SEQ ID NOs: 1, 4, 7, ..., 190, 193, 196 (genomic sequences) or SEQ ID NOs: 2, 5, 8, ..., 191, 194, 197 (transcript sequences)). Such nucleic acid molecules will consist of, consist essentially of, or comprise a nucleotide sequence that encodes one of the GPCR proteins of the present invention, an allelic variant thereof, or an ortholog or paralog thereof.

As used herein, an "isolated" nucleic acid molecule is one that is separated from other nucleic acid present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. However, there can be some flanking nucleotide sequences, for example up to about 5KB, 4KB, 3KB, 2KB, or 1KB or less, particularly contiguous protein encoding sequences and protein

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encoding sequences within the same gene but separated by introns in the genomic sequence. The important point is that the nucleic acid is isolated from remote and unimportant flanking sequences such that it can be subjected to the specific manipulations described herein such as recombinant expression, preparation of probes and primers, and other uses specific to the nucleic acid sequences.

5   Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. However, the nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated.

10   For example, recombinant DNA molecules contained in a vector are considered isolated. Further examples of isolated DNA molecules include recombinant DNA molecules maintained in heterologous host cells or purified (partially or substantially) DNA molecules in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the isolated DNA molecules of the present invention. Isolated nucleic acid molecules according to the present invention further include

15   such molecules produced synthetically.

Accordingly, the present invention provides nucleic acid molecules that consist of one of the nucleotide sequences shown in the Figure sheets (SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196 (genomic sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)). A nucleic acid molecule consists of a nucleotide sequence when the nucleotide sequence is the

20   complete nucleotide sequence of the nucleic acid molecule.

The present invention further provides nucleic acid molecules that consist essentially of one of the nucleotide sequences shown in the Figure sheets (SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196 (genomic sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)). A nucleic acid molecule consists essentially of a nucleotide sequence when such a nucleotide

25   sequence is present with only a few additional nucleic acid residues in the final nucleic acid molecule.

The present invention further provides nucleic acid molecules that are comprised of one of the nucleotide sequences shown in the Figure sheets (SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196 (genomic sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)). A

30   nucleic acid molecule is comprised of a nucleotide sequence when the nucleotide sequence is at least part of the final nucleotide sequence of the nucleic acid molecule. In such a fashion, the nucleic acid molecule can be only the nucleotide sequence or have additional nucleic acid residues, such as nucleic acid residues that are naturally associated with it or heterologous nucleotide

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sequences. Such a nucleic acid molecule can have a few additional nucleotides or can comprises several hundred or more additional nucleotides. The preferred classes of nucleic acid molecules that are comprised of the nucleotide sequences of the present are the naturally occurring full-length cDNA molecules and genes and genomic clones since some of the nucleic acid molecules provided

5   in the Figure sheets are fragments of the complete gene that exists in nature. A brief description of how various types of these nucleic acid molecules can be readily made/isolated is provided below.

In the Figures, both coding and non-coding sequences are provided for each protein encoding nucleic acid sequence. Because of the source of the present invention, Drosophila genomic sequences, the nucleic acid molecules in the figures will contain genomic intronic

10   sequences, 5' and 3' non-coding sequences, gene regulatory regions and non-coding intergenic sequences. In general such sequence features are either noted or can readily be identified using computational tools known in the art. As discussed below, some of the non-coding regions, particularly gene regulatory elements such as promoters, are useful for a variety of purposes, e.g. control of heterologous gene expression, target for identifying gene activity modulating

15   compounds.

Full-length genes may be cloned from known sequence using any one of a number of methods known in the art. For example, a method which employs XL-PCR (Perkin-Elmer, Foster City, Calif.) to amplify long pieces of DNA may be used. Other methods for obtaining full-length sequences are well known in the art.

20   The isolated nucleic acid molecules can encode the mature protein plus additional amino or carboxyl-terminal amino acids, or amino acids interior to the mature protein (when the mature form has more than one protein chain, for instance). Such sequences may play a role in processing of a protein from precursor to a mature form, facilitate protein trafficking, prolong or shorten protein half-life or facilitate manipulation of a protein for assay or production, among other things. As

25   generally is the case *in situ*, the additional amino acids may be processed away from the mature protein by cellular enzymes.

As mentioned above, the isolated nucleic acid molecules include, but are not limited to, the sequence encoding the GPCR protein alone, the sequence encoding the mature protein and additional coding sequences, such as a leader or secretory sequence (e.g., a pre-pro or pro-protein

30   sequence), the sequence encoding the mature protein, with or without the additional coding sequences, plus additional non-coding sequences, for example introns and non-coding 5' and 3' sequences such as transcribed but non-translated sequences that play a role in transcription, mRNA processing (including splicing and polyadenylation signals), ribosome binding and stability of

mRNA. In addition, the nucleic acid molecule may be fused to a marker sequence encoding, for example, a protein that facilitates purification.

Isolated nucleic acid molecules can be in the form of RNA, such as mRNA, or in the form DNA, including cDNA and genomic DNA obtained by cloning or produced by chemical synthetic techniques or by a combination thereof. The nucleic acid, especially DNA, can be double-stranded or single-stranded. Single-stranded nucleic acid can be the coding strand (sense strand) or the non-coding strand (anti-sense strand).

The invention further provides nucleic acid molecules that encode fragments of the proteins of the present invention as well as nucleic acid molecules that encode obvious variants of the GPCR proteins of the present invention that are described above. Such nucleic acid molecules may be naturally occurring, such as allelic variants (same locus), paralogs (different locus), and orthologs (different organism), or may be constructed by recombinant DNA methods or by chemical synthesis. Such non-naturally occurring variants may be made by mutagenesis techniques, including those applied to nucleic acid molecules, cells, or organisms. Accordingly, as discussed above, the variants can contain nucleotide substitutions, deletions, inversions and insertions. Variation can occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions.

The present invention further provides non-coding fragments of the nucleic acid molecules provided in the Figures. Preferred non-coding fragments include, but are not limited to, promoter sequences, enhancer sequences, gene modulating sequences and gene termination sequences. Such fragments are useful in controlling heterologous gene expression and in developing screens to identify gene modulating agents. Particularly useful are fragments from about 100 to about 1,000 nucleotides taken 5' from the start ATG in the genomic sequences provided in the Figures (SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196,).

A fragment comprises a contiguous nucleotide sequence greater than 12 or more nucleotides. Further, a fragment could at least 30, 40, 50, 100, 250 or 500 nucleotides in length. The length of the fragment will be based on its intended use. For example, the fragment can encode epitope bearing regions of the protein, or can be useful as DNA probes and primers. Such fragments can be isolated using the known nucleotide sequence to synthesize an oligonucleotide probe. A labeled probe can then be used to screen a cDNA library, genomic DNA library, or mRNA to isolate nucleic acid corresponding to the coding region. Further, primers can be used in PCR reactions to clone specific regions of gene.

A probe/primer typically comprises substantially a purified oligonucleotide or oligonucleotide pair. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 20, 25, 40, 50 or more consecutive nucleotides.

5   Orthologs, homologs, and allelic variants can be identified using methods well known in the art. As described in the protein Section, these variants comprise a nucleotide sequence encoding a protein that is typically 60-65%, 70-75%, 80-85%, and more typically at least about 90-95% or more homologous to the nucleotide sequence shown in the Figure sheets or a fragment of this sequence. Such nucleic acid molecules can readily be identified as being able to hybridize under

10   moderate to stringent conditions, to the nucleotide sequence shown in the Figure sheets or a fragment of the sequence.

As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences encoding a protein at least 50-55% homologous to each other typically remain hybridized to each other. The conditions

15   can be such that sequences at least about 65%, at least about 70%, or at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. One example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45C, followed by one or more

20   washes in 0.2 X SSC, 0.1% SDS at 50-65C.

Nucleic Acid Molecule Uses

The nucleic acid molecules of the present invention are useful for probes, primers, chemical intermediates, and in biological assays. The nucleic acid molecules are useful as a hybridization

25   probe for cDNA and genomic DNA to isolate full-length cDNA and genomic clones encoding the protein described in the Figures and to isolate cDNA and genomic clones that correspond to variants (alleles, orthologs, etc.) producing the same or related proteins shown in the Figures.

The probe can correspond to any sequence along the entire length of the nucleic acid molecules provided in the Figures. Accordingly, it could be derived from 5' noncoding regions, the

30   coding region, and 3' noncoding regions. However, as discussed, fragments are not to be construed as encompassing fragments disclosed prior to the present invention.

The nucleic acid molecules are also useful as primers for PCR to amplify any given region of a nucleic acid molecule and are useful to synthesize antisense molecules of desired length and sequence.

The nucleic acid molecules are also useful for constructing recombinant vectors. Such

5   vectors include expression vectors that express a portion of, or all of, the protein sequences. Vectors also include insertion vectors, used to integrate into another nucleic acid molecule sequence, such as into the cellular genome, to alter *in situ* expression of a gene and/or gene product. For example, an endogenous coding sequence can be replaced via homologous recombination with all or part of the coding region containing one or more specifically introduced mutations.

10   The nucleic acid molecules are also useful for expressing antigenic portions of the proteins.

The nucleic acid molecules are also useful in making vectors containing the gene regulatory regions of the nucleic acid molecules of the present invention.

The nucleic acid molecules are also useful for designing ribozymes corresponding to all, or a part, of the mRNA produced from the nucleic acid molecules described herein.

15   The nucleic acid molecules are also useful for constructing host cells expressing a part, or all, of the nucleic acid molecules and proteins.

The nucleic acid molecules are also useful for constructing transgenic animals expressing all, or a part, of the nucleic acid molecules and proteins.

The nucleic acid molecules are also useful for making vectors that express part, or all, of the

20   proteins.

The nucleic acid molecules are also useful as hybridization probes for determining the presence, level, form and distribution of nucleic acid expression. Accordingly, the probes can be used to detect the presence of, or to determine levels of, a specific nucleic acid molecule in cells, tissues, and in organisms. The nucleic acid whose level is determined can be DNA or RNA.

25   Accordingly, probes corresponding to the proteins described herein can be used to assess expression and/or gene copy number in a given cell, tissue, or organism. These uses are relevant for efficacy of insecticides involving an increase or decrease in GPCR protein expression relative to normal results.

In vitro techniques for detection of mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detecting DNA includes Southern hybridizations and *in situ*

30   hybridization.

Probes can be used as a part of a diagnostic test kit for identifying cells or tissues that express a GPCR protein, such as by measuring a level of a receptor-encoding nucleic acid in a

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sample of cells from a subject e.g., mRNA or genomic DNA, or determining if a receptor gene has been mutated.

Nucleic acid expression assays are useful for drug/insecticide screening to identify compounds that modulate GPCR nucleic acid expression.

The invention thus provides a method for identifying a compound that can be used to treat a block the activity of the GPCR by modulating the expression of the GPCR gene. The method typically includes assaying the ability of the compound to modulate the expression of the GPCR nucleic acid and thus identifying a compound that can be used to kill insects by altering GPCR nucleic acid expression. The assays can be performed in cell-based and cell-free systems. Cell-based assays include cells naturally expressing the GPCR nucleic acid or recombinant cells genetically engineered to express specific nucleic acid sequences.

The assay for GPCR nucleic acid expression can involve direct assay of nucleic acid levels, such as mRNA levels, or on collateral compounds involved in the signal pathway. Further, the expression of genes that are up- or down-regulated in response to the GPCR protein signal pathway can also be assayed. In this embodiment the regulatory regions of these genes can be operably linked to a reporter gene such as luciferase.

Thus, modulators of GPCR gene expression can be identified in a method wherein a cell is contacted with a candidate compound and the expression of mRNA determined. The level of expression of GPCR mRNA in the presence of the candidate compound is compared to the level of expression of GPCR mRNA in the absence of the candidate compound. The candidate compound can then be identified as a modulator of nucleic acid expression based on this comparison and be used, for example to treat a disorder characterized by aberrant nucleic acid expression. When expression of mRNA is statistically significantly greater in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of nucleic acid expression. When nucleic acid expression is statistically significantly less in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of nucleic acid expression.

The nucleic acid molecules are also useful in diagnostic assays for qualitative changes in GPCR nucleic acid, and particularly in qualitative changes that lead to insecticidal activity/tolerance. The nucleic acid molecules can be used to detect mutations in GPCR genes and gene expression products such as mRNA.

The nucleic acid molecules are thus useful as antisense constructs to control GPCR gene expression in cells, tissues, and organisms. A DNA antisense nucleic acid molecule is designed to

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be complementary to a region of the gene involved in transcription, preventing transcription and hence production of GPCR protein. An antisense RNA or DNA nucleic acid molecule would hybridize to the mRNA and thus block translation of mRNA into GPCR protein.

The invention also encompasses kits for detecting the presence of a GPCR nucleic acid in a
5   biological sample. For example, the kit can comprise reagents such as a labeled or labelable nucleic acid or agent capable of detecting GPCR nucleic acid in a biological sample; means for determining the amount of GPCR nucleic acid in the sample; and means for comparing the amount of GPCR nucleic acid in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect GPCR protein mRNA
10   or DNA.

Vectors/host cells

The invention also provides vectors containing the nucleic acid molecules described herein. The term "vector" refers to a vehicle, preferably a nucleic acid molecule, that can transport the
15   nucleic acid molecules. When the vector is a nucleic acid molecule, the nucleic acid molecules are covalently linked to the vector nucleic acid. With this aspect of the invention, the vector includes a plasmid, single or double stranded phage, a single or double stranded RNA or DNA viral vector, or artificial chromosome, such as a BAC, PAC, YAC, OR MAC.

A vector can be maintained in the host cell as an extrachromosomal element where it
20   replicates and produces additional copies of the nucleic acid molecules. Alternatively, the vector may integrate into the host cell genome and produce additional copies of the nucleic acid molecules when the host cell replicates.

The invention provides vectors for the maintenance (cloning vectors) or vectors for expression (expression vectors) of the nucleic acid molecules. The vectors can function in
25   procaryotic or eukaryotic cells or in both (shuttle vectors).

Expression vectors contain cis-acting regulatory regions that are operably linked in the vector to the nucleic acid molecules such that transcription of the nucleic acid molecules is allowed in a host cell. The nucleic acid molecules can be introduced into the host cell with a separate nucleic acid molecule capable of affecting transcription. Thus, the second nucleic acid molecule
30   may provide a trans-acting factor interacting with the cis-regulatory control region to allow transcription of the nucleic acid molecules from the vector. Alternatively, a trans-acting factor may be supplied by the host cell. Finally, a trans-acting factor can be produced from the vector itself. It

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is understood, however, that in some embodiments, transcription and/or translation of the nucleic acid molecules can occur in a cell-free system.

The regulatory sequence to which the nucleic acid molecules described herein can be operably linked include promoters for directing mRNA transcription. These include, but are not
5   limited to, the left promoter from bacteriophage λ, the lac, TRP, and TAC promoters from *E. coli*, the early and late promoters from SV40, the CMV immediate early promoter, the adenovirus early and late promoters, and retrovirus long-terminal repeats.

In addition to control regions that promote transcription, expression vectors may also include regions that modulate transcription, such as repressor binding sites and enhancers.
10   Examples include the SV40 enhancer, the cytomegalovirus immediate early enhancer, polyoma enhancer, adenovirus enhancers, and retrovirus LTR enhancers.

In addition to containing sites for transcription initiation and control, expression vectors can also contain sequences necessary for transcription termination and, in the transcribed region a ribosome binding site for translation. Other regulatory control elements for expression include
15   initiation and termination codons as well as polyadenylation signals. The person of ordinary skill in the art would be aware of the numerous regulatory sequences that are useful in expression vectors. Such regulatory sequences are described, for example, in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual. 2nd. ed.*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, (1989).

20   A variety of expression vectors can be used to express a nucleic acid molecule. Such vectors include chromosomal, episomal, and virus-derived vectors, for example vectors derived from bacterial plasmids, from bacteriophage, from yeast episomes, from yeast chromosomal elements, including yeast artificial chromosomes, from viruses such as baculoviruses, papovaviruses such as SV40, Vaccinia viruses, adenoviruses, poxviruses, pseudorabies viruses, and
25   retroviruses. Vectors may also be derived from combinations of these sources such as those derived from plasmid and bacteriophage genetic elements, e.g. cosmids and phagemids. Appropriate cloning and expression vectors for prokaryotic and eukaryotic hosts are described in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual. 2nd. ed.*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, (1989).

30   The regulatory sequence may provide constitutive expression in one or more host cells (i.e. tissue specific) or may provide for inducible expression in one or more cell types such as by temperature, nutrient additive, or exogenous factor such as a hormone or other ligand. A variety of

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vectors providing for constitutive and inducible expression in prokaryotic and eukaryotic hosts are well known to those of ordinary skill in the art.

The nucleic acid molecules can be inserted into the vector nucleic acid by well-known methodology. Generally, the DNA sequence that will ultimately be expressed is joined to an expression vector by cleaving the DNA sequence and the expression vector with one or more restriction enzymes and then ligating the fragments together. Procedures for restriction enzyme digestion and ligation are well known to those of ordinary skill in the art.

The vector containing the appropriate nucleic acid molecule can be introduced into an appropriate host cell for propagation or expression using well-known techniques. Bacterial cells include, but are not limited to, *E. coli*, *Streptomyces*, and *Salmonella typhimurium*. Eukaryotic cells include, but are not limited to, yeast, insect cells such as *Drosophila*, animal cells such as COS and CHO cells, and plant cells.

As described herein, it may be desirable to express the protein as a fusion protein. Accordingly, the invention provides fusion vectors that allow for the production of the proteins. Fusion vectors can increase the expression of a recombinant protein, increase the solubility of the recombinant protein, and aid in the purification of the protein by acting for example as a ligand for affinity purification. A proteolytic cleavage site may be introduced at the junction of the fusion moiety so that the desired peptide can ultimately be separated from the fusion moiety. Proteolytic enzymes include, but are not limited to, factor Xa, thrombin, and enterokinase. Typical fusion expression vectors include pGEX (Smith *et al.*, *Gene 67*:31-40 (1988)), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, *Gene 69*:301-315 (1988)) and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology 185*:60-89 (1990)).

Recombinant protein expression can be maximized in a host bacteria by providing a genetic background wherein the host cell has an impaired capacity to proteolytically cleave the recombinant protein. (Gottesman, S., *Gene Expression Technology: Methods in Enzymology 185*, Academic Press, San Diego, California (1990) 119-128). Alternatively, the sequence of the nucleic acid molecule of interest can be altered to provide preferential codon usage for a specific host cell, for example *E. coli*. (Wada *et al.*, *Nucleic Acids Res. 20*:2111-2118 (1992)).

The nucleic acid molecules can also be expressed by expression vectors that are operative in yeast. Examples of vectors for expression in yeast e.g., *S. cerevisiae* include pYepSec1 (Baldari, *et*

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*al., EMBO J. 6:*229-234 (1987)), pMFa (Kurjan *et al., Cell 30:*933-943(1982)), pJRY88 (Schultz *et al., Gene 54:*113-123 (1987)), and pYES2 (Invitrogen Corporation, San Diego, CA).

The nucleic acid molecules can also be expressed in insect cells using, for example, baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured

5   insect cells (e.g., Sf 9 cells) include the pAc series (Smith *et al., Mol. Cell Biol. 3:*2156-2165 (1983)) and the pVL series (Lucklow *et al., Virology 170:*31-39 (1989)).

In certain embodiments of the invention, the nucleic acid molecules described herein are expressed in mammalian cells using mammalian expression vectors. Examples of mammalian expression vectors include pCDM8 (Seed, B. *Nature 329:*840(1987)) and pMT2PC (Kaufman *et al.,*

10   *EMBO J. 6:*187-195 (1987)).

The expression vectors listed herein are provided by way of example only of the well-known vectors available to those of ordinary skill in the art that would be useful to express the nucleic acid molecules. The person of ordinary skill in the art would be aware of other vectors suitable for maintenance propagation or expression of the nucleic acid molecules described herein.

15   These are found for example in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

The invention also encompasses vectors in which the nucleic acid sequences described herein are cloned into the vector in reverse orientation, but operably linked to a regulatory sequence

20   that permits transcription of antisense RNA. Thus, an antisense transcript can be produced to all, or to a portion, of the nucleic acid molecule sequences described herein, including both coding and non-coding regions. Expression of this antisense RNA is subject to each of the parameters described above in relation to expression of the sense RNA (regulatory sequences, constitutive or inducible expression, tissue-specific expression).

25   The invention also relates to recombinant host cells containing the vectors described herein. Host cells therefore include prokaryotic cells, lower eukaryotic cells such as yeast, other eukaryotic cells such as insect cells, and higher eukaryotic cells such as mammalian cells.

The recombinant host cells are prepared by introducing the vector constructs described herein into the cells by techniques readily available to the person of ordinary skill in the art. These

30   include, but are not limited to, calcium phosphate transfection, DEAE-dextran-mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, lipofection, and other techniques such as those found in Sambrook, *et al. (Molecular Cloning: A*

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Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

Host cells can contain more than one vector. Thus, different nucleotide sequences can be introduced on different vectors of the same cell. Similarly, the nucleic acid molecules can be introduced either alone or with other nucleic acid molecules that are not related to the nucleic acid molecules such as those providing trans-acting factors for expression vectors. When more than one vector is introduced into a cell, the vectors can be introduced independently, co-introduced or joined to the nucleic acid molecule vector.

In the case of bacteriophage and viral vectors, these can be introduced into cells as packaged or encapsulated virus by standard procedures for infection and transduction. Viral vectors can be replication-competent or replication-defective. In the case in which viral replication is defective, replication will occur in host cells providing functions that complement the defects.

Vectors generally include selectable markers that enable the selection of the subpopulation of cells that contain the recombinant vector constructs. The marker can be contained in the same vector that contains the nucleic acid molecules described herein or may be on a separate vector. Markers include tetracycline or ampicillin-resistance genes for prokaryotic host cells and dihydrofolate reductase or neomycin resistance for eukaryotic host cells. However, any marker that provides selection for a phenotypic trait will be effective.

While the mature proteins can be produced in bacteria, yeast, mammalian cells, and other cells under the control of the appropriate regulatory sequences, cell- free transcription and translation systems can also be used to produce these proteins using RNA derived from the DNA constructs described herein.

Where secretion of the protein is desired, which is difficult to achieve with multi-transmembrane domain containing proteins such as GPCRs, appropriate secretion signals are incorporated into the vector. The signal sequence can be endogenous to the proteins or heterologous to these proteins.

Where the protein is not secreted into the medium, which is typically the case with GPCRs, the protein can be isolated from the host cell by standard disruption procedures, including freeze thaw, sonication, mechanical disruption, use of lysing agents and the like. The protein can then be recovered and purified by well-known purification methods including ammonium sulfate precipitation, acid extraction, anion or cationic exchange chromatography, phosphocellulose chromatography, hydrophobic-interaction chromatography, affinity chromatography,

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hydroxylapatite chromatography, lectin chromatography, or high performance liquid chromatography.

It is also understood that depending upon the host cell in recombinant production of the proteins described herein, the proteins can have various glycosylation patterns, depending upon the cell, or maybe non-glycosylated as when produced in bacteria. In addition, the proteins may include an initial modified methionine in some cases as a result of a host-mediated process.

Nucleic Acid Arrays

The present invention further provides arrays or microarrays of nucleic acid molecules that are based on the sequence information provided in the Figure Sheets SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196 (genomic sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)).

As used herein "Arrays" or "Microarrays" refers to an array of distinct polynucleotides or oligonucleotides synthesized on a substrate, such as paper, nylon or other type of membrane, filter, chip, glass slide, or any other suitable solid support. In one embodiment, the microarray is prepared and used according to the methods described in US Patent 5,837,832, Chee et al., PCT application WO95/11995 (Chee et al.), Lockhart, D. J. et al. (1996; Nat. Biotech. 14: 1675-1680) and Schena, M. et al. (1996; Proc. Natl. Acad. Sci. 93: 10614-10619), all of which are incorporated herein in their entirety by reference. In other embodiments, such arrays are produced by the methods described by Brown et. al., US Patent No. 5,807,522.

The microarray is preferably composed of a large number of unique, single-stranded nucleic acid sequences, usually either synthetic antisense oligonucleotides or fragments of cDNAs, fixed to a solid support. The oligonucleotides are preferably about 6-60 nucleotides in length, more preferably 15-30 nucleotides in length, and most preferably about 20-25 nucleotides in length. For a certain type of microarray, it may be preferable to use oligonucleotides that are only 7-20 nucleotides in length. The microarray may contain oligonucleotides that cover the known 5', or 3', sequence, sequential oligonucleotides which cover the full length sequence; or unique oligonucleotides selected from particular areas along the length of the sequence. Polynucleotides used in the microarray may be oligonucleotides that are specific to a gene or genes of interest.

In order to produce oligonucleotides to a known sequence for a microarray, the gene(s) of interest (or an ORF identified from the contigs of the present invention) is typically examined using a computer algorithm which starts at the 5' or at the 3' end of the nucleotide sequence.

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Typical algorithms will then identify oligomers of defined length that are unique to the gene, have a GC content within a range suitable for hybridization, and lack predicted secondary structure that may interfere with hybridization. In certain situations it may be appropriate to use pairs of oligonucleotides on a microarray. The "pairs" will be identical, except for one

5   nucleotide that preferably is located in the center of the sequence. The second oligonucleotide in the pair (mismatched by one) serves as a control. The number of oligonucleotide pairs may range from two to one million. The oligomers are synthesized at designated areas on a substrate using a light-directed chemical process. The substrate may be paper, nylon or other type of membrane, filter, chip, glass slide or any other suitable solid support.

10   In another aspect, an oligonucleotide may be synthesized on the surface of the substrate by using a chemical coupling procedure and an ink jet application apparatus, as described in PCT application W095/251116 (Baldeschweiler et al.) which is incorporated herein in its entirety by reference. In another aspect, a "gridded" array analogous to a dot (or slot) blot may be used to arrange and link cDNA fragments or oligonucleotides to the surface of a substrate using a

15   vacuum system, thermal, UV, mechanical or chemical bonding procedures. An array, such as those described above, may be produced by hand or by using available devices (slot blot or dot blot apparatus), materials (any suitable solid support), and machines (including robotic instruments), and may contain 8, 24, 96, 384, 1536, 6144 or more oligonucleotides, or any other number between two and one million which lends itself to the efficient use of commercially

20   available instrumentation.

In order to conduct sample analysis using a microarray, the RNA or DNA from a biological sample is made into hybridization probes. The mRNA is isolated, and cDNA is produced and used as a template to make antisense RNA (aRNA). The aRNA is amplified in the presence of fluorescent nucleotides, and labeled probes are incubated with the microarray so that

25   the probe sequences hybridize to complementary oligonucleotides of the microarray. Incubation conditions are adjusted so that hybridization occurs with precise complementary matches or with various degrees of less complementarity. After removal of nonhybridized probes, a scanner is used to determine the levels and patterns of fluorescence. The scanned images are examined to determine degree of complementarity and the relative abundance of each oligonucleotide

30   sequence on the microarray. The biological samples may be obtained from any bodily fluids (such as blood, urine, saliva, phlegm, gastric juices, etc.), cultured cells, biopsies, or other tissue preparations. A detection system may be used to measure the absence, presence, and amount of hybridization for all of the distinct sequences simultaneously. This data may be used for large

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scale correlation studies on the sequences, expression patterns, mutations, variants, or polymorphisms among samples.

Using such arrays, the present invention provides methods to identify the expression of one or more of the proteins/peptides of the present invention. In detail, such methods comprise
5   incubating a test sample with one or more nucleic acid molecules and assaying for binding of the nucleic acid molecule with components within the test sample. Such assays will typically involve arrays comprising many genes, at least one of which is a gene of the present invention.

Conditions for incubating a nucleic acid molecule with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the
10 type and nature of the nucleic acid molecule used in the assay. One skilled in the art will recognize that any one of the commonly available hybridization, amplification or array assay formats can readily be adapted to employ the novel fragments of the Drosophila genome disclosed herein. Examples of such assays can be found in Chard, T, *An Introduction to Radioimmunoassay and Related Techniques,* Elsevier Science Publishers, Amsterdam, The
15 Netherlands (1986); Bullock, G. R. *et al., Techniques in Immunocytochemistry,* Academic Press, Orlando, FL Vol. 1 (1 982), Vol. 2 (1983), Vol. 3 (1985); Tijssen, P., *Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology,* Elsevier Science Publishers, Amsterdam, The Netherlands (1985).

The test samples of the present invention include cells, protein or membrane extracts of
20 cells. The test sample used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing nucleic acid extracts or of cells are well known in the art and can be readily be adapted in order to obtain a sample that is compatible with the system utilized.

In another embodiment of the present invention, kits are provided which contain the
25 necessary reagents to carry out the assays of the present invention.

Specifically, the invention provides a compartmentalized kit to receive, in close confinement, one or more containers which comprises: (a) a first container comprising one of the nucleic acid molecules that can bind to a fragment of the Drosophila genome disclosed herein; and (b) one or more other containers comprising one or more of the following: wash reagents,
30 reagents capable of detecting presence of a bound nucleic acid. Preferred kits will include chips that are capable of detecting the expression of 10 or more, or 50 or more, or all of the GPCR genes expressed in Drosophila.

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In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers, strips of plastic, glass or paper, or arraying material such as silica. Such containers allows one to efficiently transfer reagents from one compartment to another compartment such that the

5   samples and reagents are not cross-contaminated, and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the nucleic acid probe, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, etc.), and containers which contain the reagents used to detect the bound probe. One skilled in

10   the art will readily recognize that the previously unidentified GPCR genes of the present invention can be routinely identified using the sequence information disclosed herein can be readily incorporated into one of the established kit formats which are well known in the art, particularly expression arrays.

15   ### Uses of vectors and host cells

The recombinant host cells expressing the proteins described herein have a variety of uses. First, the cells are useful for producing a GPCR protein or protein that can be further purified to produce desired amounts of GPCR protein or fragments. Thus, host cells containing expression vectors are useful for protein production.

20   Host cells are also useful for conducting cell-based assays involving the GPCR protein or GPCR protein fragments, such as those described above as well as other formats known in the art. Thus, a recombinant host cell expressing a native GPCR protein is useful for assaying compounds that stimulate or inhibit GPCR protein function.

Host cells are also useful for identifying GPCR protein mutants in which these functions are

25   affected. If the mutants naturally occur and give rise to a pathology, host cells containing the mutations are useful to assay compounds that have a desired effect on the mutant GPCR protein (for example, stimulating or inhibiting function) which may not be indicated by their effect on the native GPCR protein.

Genetically engineered host cells can be further used to produce non-human transgenic

30   animals. A transgenic animal is preferably a mammal, for example a rodent, such as a rat or mouse, in which one or more of the cells of the animal include a transgene. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal in one or more cell types or tissues of the transgenic

animal. These animals are useful for studying the function of a GPCR protein and identifying and evaluating modulators of GPCR protein activity. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, and amphibians.

A transgenic animal can be produced by introducing nucleic acid into the male pronuclei of a fertilized oocyte, e.g., by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. Any of the GPCR protein nucleotide sequences can be introduced as a transgene into the genome of a non-human animal, such as a mouse.

Any of the regulatory or other sequences useful in expression vectors can form part of the transgenic sequence. This includes intronic sequences and polyadenylation signals, if not already included. A tissue-specific regulatory sequence(s) can be operably linked to the transgene to direct expression of the GPCR protein to particular cells.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, both by Leder *et al.*, U.S. Patent No. 4,873,191 by Wagner *et al.* and in Hogan, B., *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the transgene in its genome and/or expression of transgenic mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene can further be bred to other transgenic animals carrying other transgenes. A transgenic animal also includes animals in which the entire animal or tissues in the animal have been produced using the homologously recombinant host cells described herein.

In another embodiment, transgenic non-human animals can be produced which contain selected systems which allow for regulated expression of the transgene. One example of such a system is the *cre/loxP* recombinase system of bacteriophage P1. For a description of the *cre/loxP* recombinase system, see, e.g., Lakso *et al. PNAS 89*:6232-6236 (1992). Another example of a recombinase system is the FLP recombinase system of *S. cerevisiae* (O'Gorman *et al. Science 251*:1351-1355 (1991). If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein is required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

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Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut, I. *et al. Nature 385*:810-813 (1997) and PCT International Publication Nos. WO 97/07668 and WO 97/07669. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G_0 phase.

5   The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyst and then transferred to pseudopregnant female foster animal. The offspring born of this female foster animal will be a clone of the animal from which the cell, e.g., the somatic cell, is isolated.

10   Transgenic animals containing recombinant cells that express the proteins described herein are useful to conduct the assays described herein in an *in vivo* context. Accordingly, the various physiological factors that are present *in vivo* and that could effect ligand binding, GPCR protein activation, and signal transduction, may not be evident from *in vitro* cell-free or cell-based assays. Accordingly, it is useful to provide non-human transgenic animals to assay *in vivo* GPCR protein

15   function, including ligand interaction, the effect of specific mutant GPCR proteins on GPCR protein function and ligand interaction, and the effect of chimeric GPCR proteins. It is also possible to assess the effect of null mutations, that is mutations that substantially or completely eliminate one or more GPCR protein functions.

All publications and patents mentioned in the above specification are herein incorporated

20   by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the above-

25   described modes for carrying out the invention which are obvious to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Left column

Gene	Transcript	Similar to	F (E Value)	W (E Value)	V (E Value)
A. Rhodopsin-like receptor family					
Opsin-like					
CG5638	CT17820	Rh3	e-57	c-14	e-44
Receptors for biogenic amines and related compounds					
5-HT receptor-like					
CG8007	CT24060	5-HT2	e-21	e-35	e-27
Muscarinic Acetylcholine receptor-like					
CG7918	CT23924	mAcR-60C	e-32	e-49	e-41
Unclassifiable biogenic amine receptor-like					
CG17004	CT37739	5-HT7	e-18	e-20	e-28
CG7431	CT22855	CG16766	e-70	e-45	e-37
CG16766	CT37292	CG7431	e-53	e-31	e-22
CG12796	CT38338	CG6919	e-23	e-20	e-30
CG6919	CT21432	CG6989	e-82	e-46	e-57
CG6989	CT21650	CG6919	e-82	e-39	e-46
CG7078	CT21843	CG6919	e-73	e-46	e-38
CG18314	CT41076	CG6919	e-21	e-48	e-25
CG7994	CT24036		>e-10	>e-10	e-10
Purine receptors					
Adenosine receptor-like					
CG9753	CT27563	CG6989	e-19	e-29	e-42
Peptide receptors					
Allatostatin receptor-like					
CG10001	CT28187	EG:121E7.2	e-62	e-35	e-34
FSH/TSH/LH receptor-like					
CG4187	CT13764	CG5042	e-48	e-23	e-24
CG5042	CT16185	CG4187	e-44	e-25	e-23
Gastrin/CCK receptor-like					
CG6857	CT21155	CG6881	e-96	e-33	e-19
CG6881	CT21314	CG6857	e-96	e-23	e-33
Gonadotropin releasing hormone receptor-like					
CG10698	CT29989	GRHR	e-43	e-34	e-39
Growth hormone secretagoge receptor-like					
CG8784	CT25324	CG8795	e-165	e-38	e-35
CG8795	CT25350	CG8784	e-165	e-40	e-37
CG9918	CT27924	CG8795	e-83	e-53	e-33
Tachykinin receptor-like					
CG1147	CT1960	NepYr	e-31	c-43	e-40
CG10626	CT29768	Takr99D	e-53	e-41	c-44
Somatostatin receptor-like					
CG7285	CT22465	CG13702	e-96	e-24	e-51
CG13702	CT33159	CG7285	e-96	e-26	e-46
Vasopressin receptor-like					
CG6111	CT19191	GRHR	e-36	e-26	e-45
Unclassifiable peptide receptors					
CG13575	CT32957	CG10626	e-08	e-08	e-8#
CG14003	CT33559	Takr99D	c-14	e-12	e-14#
CG5911	CT18539	Takr86C	c-18	e-19	e-26#
CG10823	CT18916	CG6857	e-10	e-10	e-12

Right column

Gene	Transcript	Similar to	F (E Value)	W (E Value)	V (E Value)
Orphan receptors					
Related to C. elegans orphan receptors					
CG2114	CT2366		>e-10	e-27	e-10
CG3171	CT10621	EG:22E5.10	e-50	e-16	e-26
CG5936	CT18637		>e-10	e-18	>e-10
CG8985	CT25824	CG13803	e-162	e-31	>e-10
CG13803	CT33298	CG8985	e-162	e-36	>e-10
CG13229	CT32473	CG13803	e-58	e-35	e-10
Other orphan receptors					
CG9569	CT17758		>e-10	>e-10	>e-10
CG12290	CT19320		>e-10	>e-10	>e-10
CG6986	CT21642	CG16726	e-10	>e-10	>e-10
CG13579	CT32961		>e-10	e-18	>e-10
CG13995	CT33551		>e-10	e-13	e-11
CG7497	CT23019		>e-10	>e-10	>e-10
Calcitonin receptor-like					
CG4395	CT4121	CG17415	e-46	e-16	e-41
CG17415	CT38445	CG4395	e-42	e-20	e-61
CG13758	CT33238	CG8422	e-40#	e-65	e-66
B. Se *Diuretic hormone receptor-like*					
CG8422	CT24513	CG12370	e-122	e-25	e-65
CG12370	CT24959	CG8422	e-122	e-30	e-101
HE6 receptor-like					
CG11318	CT31591	CG15556	e-104	e-11	e-20
CG15556	CT35672	CG11318	e-103	>e-11	e-6
Latrophilin-like					
CG8639	CT8755		>e-10	e-47	e-45
Methuselah-like					
CG4521	CT14539	CG6965	e-30	e-13	
CG17795	CT16507	mth	e-132	>e-10	>e-10
CG6530	CT20339	CG6536	e-104	>e-10	>e-10
CG6536	CT20351	CG6530	e-115	>e-10	
CG6965	CT21585	CG17795	e-12	>e-10	e-10
CG7476	CT22963	mth	e-66	>e-10	>e-10
CG13406	CT32762	CG17084	e-47	>e-10	>e-10
CG17084	CT33414	CG13406	e-47	>e-10	>e-10
CG17061	CT33415	mth	e-80	>e-10	>e-10
CG16992	CT37715	mth	e-32	>e-10	>e-10
C. Metabotropic glutamate receptor family					
GABA-B receptor-like					
CG3022	CT9836	CG6706	e-96	e-56	e-85
CG6706	CT20836	CG3022	e-120	e-61	e-169
CG15274	CT35221	CG3022	e-49	e-156	e-129
Metabotropic glutamate receptor-like					
CG8692	CT5032	Glu-RA	e-152	e-115	e-157
Other					
CG7155	CT22117		>e-10	>e-10	>e-10
CG11923	CT35779	CG17215	e-17	>e-10	e-17
D. Atypical 7 TM proteins					
Frizzled-like					
CG4626	CT9057	fz	e-36	e-54	e-76

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Claims

That which is claimed is:

1.   An isolated protein consisting of an amino acid sequence selected from the group consisting of:

      (a)   the amino acid sequence shown in SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198;

      (b)   the amino acid sequence of an allelic variant of the amino acid sequence shown in SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, wherein said allelic variant is encoded by a nucleic acid molecule that hybridizes to the nucleic acid molecule shown in SEQ ID NOs: 1, 4, 7, . . . , 795, 798, 801 (genomic sequences); SEQ ID NOs: 2, 5, 8, . . . , 796, 799, 802 (transcript sequences), under stringent conditions;

      (c)   the amino acid sequence of an ortholog of an amino acid sequence shown in SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, wherein said ortholog is encoded by a nucleic acid molecule that hybridizes to the nucleic acid molecule shown in SEQ ID NOs: 1, 4, 7, . . . , 795, 798, 801 (genomic sequences); SEQ ID NOs: 2, 5, 8, . . . , 796, 799, 802 (transcript sequences), under stringent condition;

      (d)   a fragment of the amino acid sequence shown in SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, wherein the fragment comprises at least 10 contiguous amino acids.

2.   An isolated protein comprising an amino acid sequence selected from the group consisting of:

      (a)   the amino acid sequence shown in SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198;

      (b)   the amino acid sequence of an allelic variant of the amino acid sequence shown in SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, wherein said allelic variant is encoded by a nucleic acid molecule that hybridizes to the nucleic acid molecule shown in SEQ ID NOs: 1, 4, 7, . . . , 795, 798, 801 (genomic sequences); SEQ ID NOs: 2, 5, 8, . . . , 796, 799, 802 (transcript sequences), under stringent conditions;

      (c)   the amino acid sequence of an ortholog of an amino acid sequence shown in the SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, wherein said ortholog is encoded by a nucleic acid molecule that hybridizes to the nucleic acid molecule shown in SEQ ID NOs: 1, 4, 7, . . . , 795, 798, 801 (genomic sequences); SEQ ID NOs: 2, 5, 8, . . . , 796, 799, 802 (transcript sequences), under stringent condition;

(d)   a fragment of the amino acid sequence shown in the SEQ ID NOs: 3, 6, 9,
. . . , 192, 195, 198, wherein the fragment comprises at least 10 contiguous amino acids.

3.   An isolated antibody that selectively binds to a protein of claim 1.

4.   An isolated nucleic acid molecule consisting of a nucleotide sequence selected from
the group consisting of:

(a)   a nucleotide sequence that encodes the amino acid sequence shown in SEQ
ID NOs: 3, 6, 9, . . . , 192, 195, 198;

(b)   a nucleotide sequence that encodes of an allelic variant of the amino acid
sequence shown in SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, wherein said nucleic acid molecule
hybridizes to the nucleic acid molecule shown in SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196
(genomic sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)), under
stringent conditions;

(c)   a nucleotide sequence that encodes an ortholog of an amino acid sequence
shown in SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, wherein said nucleic acid molecule hybridizes
to the nucleic acid molecule shown in SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196 (genomic
sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)), under stringent
condition;

(d)   a nucleotide sequence that encodes a fragment of the amino acid sequence
shown in the SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, wherein said the fragment comprises at
least 10 contiguous amino acids; and

(e)   A nucleic acid molecule that is the complement of a nucleic acid molecule
of (a)-(d).

5.   An isolated nucleic acid molecule comprising a nucleotide sequence selected from
the group consisting of:

(a)   a nucleotide sequence that encodes the amino acid sequence shown in SEQ
ID NOs: 3, 6, 9, . . . , 192, 195, 198;

(b)   a nucleotide sequence that encodes of an allelic variant of the amino acid
sequence shown in SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, wherein said nucleic acid molecule
hybridizes to the nucleic acid molecule shown in SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196

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(genomic sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)), under stringent conditions;

      (c)   a nucleotide sequence that encodes an ortholog of an amino acid sequence shown in the SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, wherein said nucleic acid molecule hybridizes to the nucleic acid molecule shown in SEQ ID NOs: 1, 4, 7, . . . , 190, 193, 196 (genomic sequences) or SEQ ID NOs: 2, 5, 8, . . . , 191, 194, 197 (transcript sequences)), under stringent condition;

      (d)   a nucleotide sequence that encodes a fragment of the amino acid sequence shown in the SEQ ID NOs: 3, 6, 9, . . . , 192, 195, 198, wherein said the fragment comprises at least 10 contiguous amino acids; and

      (f)   A nucleic acid molecule that is the complement of a nucleic acid molecule of (a)-(d).

6.   A nucleic acid vector comprising the nucleic acid sequences of claim 4.

7.   A nucleic acid vector comprising the nucleic acid sequences of claim 5.

8.   A host cell containing the vector of claim 6.

9.   A host cell containing the vector of claim 7.

10.   A method for producing any of the proteins of claim 1 comprising introducing a nucleotide sequence encoding any of the protein sequences in (a)-(d) into a host cell, and culturing the host cell under conditions in which the proteins are expressed from the nucleic acid.

11.   A method for producing any of the proteins of claim 2 comprising introducing a nucleotide sequence encoding any of the protein sequences in (a)-(d) into a host cell, and culturing the host cell under conditions in which the proteins are expressed from the nucleic acid.

12.   A method for detecting the presence of any of the proteins of claim 1 in a sample, said method comprising contacting said sample with an agent that specifically allows detection of the presence of the protein in the sample and then detecting the presence of the protein.

13.   A method for detecting the presence of any of the proteins of claim 2 in a sample, said method comprising contacting said sample with an agent that specifically allows detection of the presence of the protein in the sample and then detecting the presence of the protein.

14.   A kit comprising reagents used for the method of claim 12, wherein the reagents comprise an agent that specifically binds to said protein.

15.   A method for detecting the presence of a nucleic acid sequence of claim 4 in a sample, the method comprising contacting the sample with an oligonucleotide that hybridizes to the nucleic acid sequences under stringent conditions and determining whether the oligonucleotide binds to the nucleic acid sequence in the sample.

16.   A method for detecting the presence of a nucleic acid sequence of claim 5 in a sample, the method comprising contacting the sample with an oligonucleotide that hybridizes to the nucleic acid sequences under stringent conditions and determining whether the oligonucleotide binds to the nucleic acid sequence in the sample.

17.   A kit comprising reagents used for the method of claim 15, wherein the reagents comprise a compound that hybridizes under stringent conditions to any of the nucleic acid molecules.

18.   A kit comprising reagents used for the method of claim 16, wherein the reagents comprise a compound that hybridizes under stringent conditions to any of the nucleic acid molecules.

19.   A method for identifying an agent that binds to any of the proteins of claim 1, said method comprising contacting the protein with an agent and assaying the contacted mixture to determine whether a complex is formed with the agent bound to the protein.

20.   A method for identifying an agent that binds to any of the proteins of claim 2, said method comprising contacting the protein with an agent and assaying the contacted mixture to determine whether a complex is formed with the agent bound to the protein.

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SEQUENCE LISTING

<110> Cravchik, Anibal

<120> ISOLATED G-PROTEIN COUPLED RECEPTORS,
     NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
     THEREOF AS INSECTICIDAL TARGETS

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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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9

SUBSTITUTE SHEET (RULE 26)

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    50                  55                  60
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11

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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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                20                  25                  30
Ile Glu Cys Asp Pro Gly Asp Val Ile Asn Leu Ile Arg Ala Asn Tyr
            35                  40                  45
Gly Arg Phe Ser Ile Thr Ile Cys Asn Asp His Gly Asn Val Glu Trp
        50                  55                  60
Ser Val Asn Cys Met Phe Pro Lys Ser Leu Ser Val Leu Asn Ser Arg
65                  70                  75                  80
Cys Ala His Lys Gln Ser Cys Gly Val Leu Ala Ala Thr Ser Met Phe
                85                  90                  95
Gly Asp Pro Cys Pro Gly Thr His Lys Tyr Leu Glu Ala His Tyr Gln
            100                 105                 110
Cys Ile Ser Ala Ala Gln Thr Ser Thr Thr Thr Asn Arg Pro Ser Pro
        115                 120                 125
Pro Pro Trp Val Leu Ser Asn Gly Pro Pro Ile Phe Gly Asn Gly Ser
    130                 135                 140
Gly Leu Ile His Pro Pro Gly Val Gly Ala Gly Ala Pro Pro Pro Pro
145                 150                 155                 160
Arg Leu Pro Thr Leu Pro Gly Val Val Gly Ile Ser Gly Asn Pro Gly
                165                 170                 175
Leu Phe Asn Val Pro Pro Gln His Thr Ala Val Thr His Ser Thr Pro
                180                 185                 190
Ser Ser Ser Thr Thr Ala Val Gly Gly Gly Arg Leu Lys Gly Gly Ala
            195                 200                 205
Thr Ser Thr Thr Thr Thr Lys His Pro Ala Gly Arg His Asp Gly Leu
        210                 215                 220
Pro Pro Pro Gln Leu His His His His Asn His His Gly Glu Asp
225                 230                 235                 240
Thr Ala Ser Pro Thr Lys Pro Ser Ser Lys Leu Pro Ala Gly Gly Asn
                245                 250                 255
Ala Thr Ser Pro Ser Asn Thr Arg Ile Leu Thr Gly Val Gly Gly Ser
```

16

SUBSTITUTE SHEET (RULE 26)

```
                    260                     265                     270
Gly Thr Asp Asp Gly Thr Leu Leu Thr Thr Lys Ser Ser Pro Asn Arg
        275                     280                     285
Pro Pro Gly Thr Ala Ala Ser Gly Ser Val Val Pro Gly Asn Gly Ser
        290                     295                     300
Val Val Arg Thr Ile Asn Asn Ile Asn Leu Asn Ala Ala Gly Met Ser
305                     310                     315                     320
Gly Gly Asp Asp Glu Ser Lys Leu Phe Cys Gly Pro Thr His Ala Arg
                325                     330                     335
Asn Leu Tyr Trp Asn Met Thr Arg Val Gly Asp Val Asn Val Gln Pro
                340                     345                     350
Cys Pro Gly Gly Ala Ala Gly Ile Ala Lys Trp Arg Cys Val Leu Met
        355                     360                     365
Lys Arg Ile Pro Asp Ser Gly Tyr Asp Glu Tyr Asp Asp Asp Ile Ser
        370                     375                     380
Ser Thr Thr Pro Ala Pro Ser Gly Gly Asp Cys Leu His Asn Ser Ser
385                     390                     395                     400
Ser Cys Glu Pro Pro Val Ser Met Ala His Lys Val Asn Gln Arg Leu
                405                     410                     415
Arg Asn Phe Glu Pro Thr Trp His Pro Ala Thr Pro Asp Leu Thr Gln
                420                     425                     430
Cys Arg Ser Leu Trp Leu Asn Asn Leu Glu Met Arg Val Asn Gln Arg
        435                     440                     445
Asp Ser Ser Leu Ile Ser Ile Ala Asn Asp Met Ser Glu Val Thr Ser
        450                     455                     460
Ser Lys Thr Leu Tyr Gly Gly Asp Met Leu Val Thr Thr Lys Ile Ile
465                     470                     475                     480
Gln Thr Val Ser Glu Lys Met Met His Asp Lys Glu Thr Phe Pro Asp
                485                     490                     495
Gln Arg Gln Arg Glu Ala Met Ile Met Glu Leu Leu His Cys Val Val
        500                     505                     510
Lys Thr Gly Ser Asn Leu Leu Asp Glu Ser Gln Leu Ser Ser Trp Leu
        515                     520                     525
Asp Leu Asn Pro Glu Asp Gln Met Arg Val Ala Thr Ser Leu Leu Thr
        530                     535                     540
Gly Leu Glu Tyr Asn Ala Phe Leu Leu Ala Asp Thr Ile Ile Arg Glu
545                     550                     555                     560
Arg Ser Val Val Gln Lys Val Lys Asn Ile Leu Leu Ser Val Arg Val
                565                     570                     575
Leu Glu Thr Lys Thr Ile Gln Ser Ser Val Val Phe Pro Asp Ser Asp
                580                     585                     590
Gln Trp Pro Leu Ser Ser Asp Arg Ile Glu Leu Pro Arg Ala Ala Leu
        595                     600                     605
Ile Asp Asn Ser Glu Gly Gly Leu Val Arg Ile Val Phe Ala Ala Phe
        610                     615                     620
Asp Arg Leu Glu Ser Ile Leu Lys Pro Ser Tyr Asp His Phe Asp Leu
625                     630                     635                     640
Lys Ser Ser Arg Ser Tyr Ala Ile Leu Ser Asn Asp Ser Asp Val Asn
                645                     650                     655
Ala Gly Glu Ile Gln Gln Arg Leu Arg Ile Leu Asn Ser Lys Val Ile
        660                     665                     670
Ser Ala Ser Leu Gly Lys Gly Arg His Ile Gln Leu Ser Gln Pro Ile
        675                     680                     685
Thr Leu Thr Leu Lys His Leu Lys Thr Glu Asn Val Thr Asn Pro Thr
        690                     695                     700
Cys Val Phe Trp Asn Tyr Ile Asp His Ala Trp Ser Ala Asn Gly Cys
705                     710                     715                     720
Ser Leu Glu Ser Thr Asn Arg Thr His Ser Val Cys Ser Cys Asn His
                725                     730                     735
Leu Thr Asn Phe Ala Ile Leu Met Asp Val Val Asp Glu His Gln His
```

17

SUBSTITUTE SHEET (RULE 26)

```
                  740                    745                    750
Ser Leu Phe Thr Met Phe Asp Gly Asn Met Arg Ile Phe Ile Tyr Ile
        755                    760                    765
Ser Ile Gly Ile Cys Val Val Phe Ile Val Ile Ala Leu Leu Thr Leu
        770                    775                    780
Lys Leu Phe Asn Gly Val Phe Val Lys Val Arg Asn Gly Ser Asn Pro
785                    790                    795                    800
Leu Pro His Gln Arg Ser Gly Ser Arg Arg Gln Gln Asn Asn Ile Arg
                  805                    810                    815
Asp Gln Thr His Glu Ser Leu Thr Leu Thr Thr Pro Thr Ser Gln Ser
                  820                    825                    830
Asn Val Pro Pro Pro Ser His Gly Asn Thr Asn Phe Ile Gln His Asn
            835                    840                    845
Ser Ile Arg Asn Ser His Arg Asn Asn Leu Asn Tyr Asn Val Gln Gln
    850                    855                    860
Gln Gln Gln Gln Gln Gln Gln Gln Val Val Ala Ala Ala Ala Ala Ala
865                    870                    875                    880
Val Val Leu Ser Asn Gln Pro Gln Arg Asn Met Gln His Ala Met Asn
                  885                    890                    895
Asn Leu Asn Leu Asn Leu His Gln His Gly Gln Gln Thr Ala Ala Ala
                  900                    905                    910
Ala Ala Ala Ala Ala Ser Ile Ala Ala Ala Leu Gln Gln His Ala Val
        915                    920                    925
Gln Ala Ser Asn Ala Ser Asn Asn Leu Asn Ile Ser His Asn Tyr Leu
        930                    935                    940
Gln Gln Gln His Val Gln Gln Gln Gln Gln Gln Arg Gly Gln Gln
945                    950                    955                    960
Pro Gln Pro His Pro His Arg Asn His Asn Leu Asn Val Asp Gly Asn
                  965                    970                    975
Gly Leu Asp Asn Thr Asn Asn Ile Ile Met Gln Ala Asn Met Asp Asp
            980                    985                    990
Leu Gln Tyr Lys Trp Trp Trp Cys Ile Tyr Leu Cys Leu Leu Ala Ile
        995                    1000                   1005
Glu Leu Leu Phe Leu Leu Gly Ile Glu Gln Thr Glu Thr Ser Ile Phe
    1010                   1015                   1020
Cys Gly Phe Ile Thr Ile Phe Leu His Cys Ala Ile Leu Ser Gly Thr
1025                   1030                   1035                   1040
Ala Trp Phe Cys Tyr Glu Ala Phe His Ser Tyr Ser Thr Leu Thr Ser
                  1045                   1050                   1055
Asp Glu Leu Leu Leu Glu Val Asp Gln Thr Pro Lys Val Asn Cys Tyr
            1060                   1065                   1070
Tyr Leu Leu Ser Tyr Gly Leu Ser Leu Ser Val Val Ala Ile Ser Leu
        1075                   1080                   1085
Val Ile Asp Pro Ser Thr Tyr Thr Gln Asn Asp Tyr Cys Val Leu Met
1090                   1095                   1100
Glu Ala Asn Ala Leu Phe Tyr Ala Thr Phe Val Ile Pro Val Leu Val
1105                   1110                   1115                   1120
Phe Phe Val Ala Ala Ile Gly Tyr Thr Phe Leu Ser Trp Ile Ile Met
                  1125                   1130                   1135
Cys Arg Lys Ser Arg Thr Gly Leu Lys Thr Lys Glu His Thr Arg Leu
            1140                   1145                   1150
Ala Ser Val Arg Phe Asp Ile Arg Cys Ser Phe Val Phe Leu Leu Leu
        1155                   1160                   1165
Leu Ser Ala Val Trp Cys Ser Ala Tyr Phe Tyr Leu Arg Gly Ala Lys
        1170                   1175                   1180
Met Asp Asp Asp Thr Ala Asp Val Tyr Gly Tyr Cys Phe Ile Cys Phe
1185                   1190                   1195                   1200
Asn Thr Leu Leu Gly Leu Tyr Ile Phe Val Phe His Cys Ile Gln Asn
                  1205                   1210                   1215
Glu Lys Ile Arg Arg Glu Tyr Arg Lys Tyr Val Arg Gln His Ala Trp
```

18

SUBSTITUTE SHEET (RULE 26)

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                1220               1225               1230
Leu Pro Lys Cys Leu Arg Cys Ser Lys Thr Ser Ile Ser Ser Gly Ile
        1235               1240               1245
Val Thr Gly Asn Gly Pro Thr Ala Gly Thr Leu Cys Ser Val Ser Thr
        1250               1255               1260
Ser Lys Lys Pro Lys Leu Pro Leu Gly Val Ser Glu Glu Ala His Asp
1265               1270               1275               1280
Asp Pro Gln Gln Gln Gln Gln Thr Pro Val Pro Ile Thr Glu Asp Ala
                1285               1290               1295
Ile Met Gly Ala Thr Ser Asp Cys Glu Leu Asn Glu Ala Gln Gln Arg
                1300               1305               1310
Arg Thr Leu Lys Ser Gly Leu Met Thr Gly Thr Leu Gln Ala Pro Pro
        1315               1320               1325
Gln Thr Leu Gly Gly His Val Val Leu Glu Arg Gly Ser Thr Leu Arg
        1330               1335               1340
Ser Thr Gly His Ala Ser Pro Thr Ser Ser Ala Gly Ser Thr His Leu
1345               1350               1355               1360
Ile Phe Ala His Lys Gln Gln Gln Gln Gln Gln Gln Gly Pro Leu
        1365               1370               1375
Gly Glu Ser Tyr Tyr His Gln Pro Asp Tyr Tyr Ser Trp Lys Gln Pro
        1380               1385               1390
Ser Thr Gly Thr Gly Gly Leu Lys Thr Pro Arg Glu Tyr Tyr Asn Asn
        1395               1400               1405
Ala Gly Ala Ala Ala Ser Ser Pro Gln Gln Ala His Glu Val Phe Tyr
        1410               1415               1420
Trp Thr Gln Lys Pro Asn Ser Gly His Asn Gly Lys Lys Lys Arg Gly
1425               1430               1435               1440
Ala Gly Gly Val Pro Ala Ser Pro Ser Gly Ser Leu His Ser Arg Thr
        1445               1450               1455
Ala Ala Ala Ser Gln Val Leu Phe Tyr Pro Ser Tyr Lys Lys Thr Lys
        1460               1465               1470
Pro Gly Gln Pro Thr Gly Tyr Pro Gln Tyr Ala Glu Ala Leu Asp Pro
        1475               1480               1485
Pro Leu Ala Thr Gly Asn Ala Ala Ala Tyr Tyr Gln Gln Gln Gln Gln
        1490               1495               1500
Leu Arg Arg Gln Gln Leu His Gln Gln Gln Gln Gln Gln Gln Gln Gln
1505               1510               1515               1520
Gln Leu Ser Ser Asp Glu Glu Gln Ala Glu Gln His Ala His Leu Leu
        1525               1530               1535
His Leu Gln Arg Arg Ala Gly Ser Gln Gln Gln Leu Pro Ala Pro Pro
        1540               1545               1550
Pro His Met Ala Gln Tyr Gln Gln Glu Phe Met Gln Arg Gln Tyr Arg
        1555               1560               1565
Asn Lys His Ser Asn Cys Asp Leu Gly Met Gly Asp Ala Tyr Tyr Asn
        1570               1575               1580
Gln Gly Ser Val Gly Gly Ala Asp Gly Gly Pro Val Tyr Glu Glu Ile
1585               1590               1595               1600
Leu Ser Asn Arg Asn Ser Asp Val Gln His Tyr Glu Val Gly Asp Phe
        1605               1610               1615
Asp Val Asp Glu Val Tyr Asn Asn Ser Val Gly Thr Gly Val Phe Asn
        1620               1625               1630
Asn Met Arg Ala Ala Val Ala Ala Gly Gly Ser Arg Tyr Gly Gly Gly
        1635               1640               1645
Ser Leu Ser Gly Gly Ser Val Ser Ser Arg Ser Gln Gln Gln Gln Leu
        1650               1655               1660
Lys Lys Gln Gln Gln Gln Gln Ser Leu Ala Gln Gln Arg Ser Ala Arg
1665               1670               1675               1680
Arg Cys Thr Ala Asp Asp Asp Asp Asp Glu Asp Glu Glu Glu Asp Glu
        1685               1690               1695
Glu Ala Thr Ala Ala Glu Gln Leu His Asp Ser Val Cys Asp Glu Asp
```

SUBSTITUTE SHEET (RULE 26)

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         Glu Glu Glu Asp Glu Ser Asp Leu Glu Asp Asp Ala His Gly Leu Pro
             1715                1720                1725
         Pro Gln Ser Asp Glu Arg Met Arg Arg Leu Met Ala Met Gln Asp Glu
             1730                1735                1740
         Asp Phe Lys Arg Arg Phe Gln Arg Gln Leu Arg Lys His Gly Ala Pro
         1745                1750                1755                1760
         Leu Asp Tyr Gly Ala Leu Pro Pro Gly Ala Gly Pro Gln Pro Glu His
                     1765                1770                1775
         Asn Gly Ala Val Phe Gly Val Ser Gly Gly Val Gly Glu Gly Ser Leu
                     1780                1785                1790
         Arg Gly Ala Phe Arg Gln Gln Gln Gln Gln Ala Leu Asn Ala Lys Ser
                     1795                1800                1805
         Pro Gly Gly Arg Leu Ala Val Asn Glu Leu Phe Gly His Gly Asn Ser
             1810 .              1815                1820
         Gly Pro Pro Leu Pro Pro Ala Asn Gln Thr Pro Ala Gln Lys Arg Gln
         1825                1830                1835                1840
         Gln Leu Gln Lys Leu Ser Pro Gln Ser Thr Thr Ser Ser Ser Ser His
                     1845                1850                1855   .
         Thr Ser His Ser Asn Pro Asn Pro His Pro His Gln Leu Thr His Pro
                     1860                1865                1870
         His Pro His Gln His Pro Pro His His Gln Gln Arg His Leu Ser Ala
             1875                1880                1885
         Met Leu Asp Glu Asn Asn Thr Val Arg Cys Tyr Leu Glu Pro Leu Ala
             1890                1895                1900
         Lys
         1905


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20

SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

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<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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Ile Arg Ile Glu Met Cys Arg Lys Ile Gly Tyr Asn Glu Thr Ser Met
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Pro Asn Leu Val Gly Asn Glu Met Gln Thr Asp Val Glu Tyr Thr Leu
65                    70                    75                    80
Gln Thr Phe Ala Pro Leu Ile Glu Tyr Asp Cys Ser Ser Gln Leu Lys
                85                    90                    95
Leu Phe Leu Cys Ala Ala Tyr Val Pro Met Cys Thr Pro Lys Ala Pro
                100                   105                   110
Val His Ala Ile Gly Pro Cys Arg Ser Leu Cys Glu Ser Val Arg Ile
        115                   120                   125
Arg Cys His Pro Val Leu Gln Gly Phe Gly Phe Pro Trp Pro Pro Ala
        130                   135                   140
Leu Asp Cys Asp Lys Phe Pro Arg Glu Asn Asn His Glu Thr Met Cys
145                   150                   155                   160
Met Glu Gly Pro Gly Glu Leu His Gln Pro Gln Gln Glu Gln Asp Leu
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Tyr Gly Leu Pro Gly Gln Gly Ile Pro Gly Gly Leu Gly Gly Lys Leu
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Pro Met Asp Cys Ser Gly Leu Ala Lys Ser His Leu Tyr Val Arg Leu
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Pro Arg Ser Gly Arg Cys Ala Pro Leu Cys Glu Ala Asp Ile Leu Phe
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Thr Pro Ala Glu Lys His Leu Ala Glu Ile Trp Val Ser Thr Trp Ala
225                   230                   235                   240
Tyr Ala Ala Leu Gly Leu Ala Leu Val Ala Thr Val Cys Leu Leu Ala
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Ser Asp Gly Ser Arg Leu Ala Ser Ala Lys Trp Ser Arg Leu Leu Ser
                260                   265                   270
Pro Leu Ile Trp Cys His Asn Met Val Thr Leu Gly Trp Ala Val Arg
        275                   280                   285
Phe Met Val Gly Arg Thr Gly Thr Ala Cys Gly Thr Asp Pro Gln Ala
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Pro Asn Glu Ser Leu Leu Thr Val Asp Gly Leu Ser Asn Ala Ser Cys
305                   310                   315                   320
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Trp Trp Ala Val Leu Cys Leu Gly Trp His Arg Asp Ile Arg Arg His
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Gln Asn Asn Phe Val Cys Phe Val Ala Trp Gly Leu Pro Ala Phe Gln
385                   390                   395                   400
Thr Ser Ala Val Ile Val Ala Arg Phe Val Asp Ala Asp Glu Leu Leu
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Gly Asn Gln Ser Asp Lys Ala Leu Gln Ile Leu Val Ala Thr Pro Val
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Phe Cys Tyr Trp Ile Phe Gly Ser Met Asn Leu Ile Ser Gly Tyr Leu
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Val His Cys Arg Thr Lys Glu Ile Leu Arg Asn Ser Asn Ala Leu Ser
        450                   455                   460
Val Gln Gln Gln Leu Gln Gln Leu Ser Ala His Ser Ser Ser Gly Ile
465                   470                   475                   480
Gly Ile Phe Leu Phe Ile Tyr Gly Leu Ala Cys Ala Met Leu Leu Leu
                485                   490                   495
Ala Val Ile Tyr Glu Phe Ala Asn Ile Asp Val Trp Leu Gly Ser Gly
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23

SUBSTITUTE SHEET (RULE 26)

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Leu Met Leu Gly Ile Cys Cys Phe Ala Trp Val Leu Gly Pro Ser Ile
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Ser Thr Leu Tyr Lys Arg Gln Val Ser Asn Gly Lys Met Val Lys His
545                        550                        555                        560
Thr Ser Ala Gly Ala Ala Thr Gly His Leu Asp Gly His Ser Ser Ser
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Arg Gly Ser His Ala Ala Cys Asn Ser Thr Val Val Ser Tyr His Ser
            580                        585                        590
Val Arg Thr Ser Met Ala Ser Val Pro Leu Pro Pro Ser Pro Tyr Lys
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Leu Lys Thr Ser Pro Gly Thr Gly Ser Ile Ser Leu Asn Gln Met Ser
    610                        615                        620
Asn Tyr Ser Leu Gly Arg Ser Val His His Gln Gln Arg His Ser Pro
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His His His His His Gln Gln Gln Gln His His Gln Phe His Pro His
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His Asn His Gln His His Ser Thr Ser Ser His Arg Leu Tyr Tyr Pro
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<213> Drosophila

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25

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SUBSTITUTE SHEET (RULE 26)

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Arg	Gln	Gln	Arg	Leu	Asn	Ser	His	Ser	Asn	Leu	Pro	Gly	Ser	Thr	Asn
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Leu	Lys	Val	Asn	Gln	Val	Phe	Glu	Ser	Glu	Arg	Arg	Met	Ser	Pro	Ala
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Leu	Ser	Thr	Ser	Arg	Gly	Pro	Arg	Pro	Asp	Gly	Leu	Ser	Glu	Leu	Gly

28

SUBSTITUTE SHEET (RULE 26)

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Val Gly Val Asp Arg Phe Phe His Ala Ile Tyr Thr Gln Pro Ser Thr
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Arg Met Val Met Leu Leu Gly Ser Ala Cys Ser Glu Val Thr Glu Ser
225                 230                 235                 240
Leu Ala Lys Val Val Pro Tyr Trp Asn Ile Val Gln Val Ser Phe Gly
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Ser Thr Ser Pro Ala Leu Ser Asp Arg Arg Glu Phe Pro Tyr Phe Tyr
            260                 265                 270
Arg Thr Val Ala Pro Asp Ser Ser His Asn Pro Ala Arg Ile Ala Phe
            275                 280                 285
Ile Arg Lys Phe Gly Trp Gly Thr Val Thr Thr Phe Ser Gln Asn Glu
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Glu Val His Ser Leu Ala Val Asn Asn Leu Val Thr Glu Leu Glu Ala
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Lys Glu Gln Leu Leu Leu Leu Arg Glu Thr Asp Thr Arg Ile Ile Ile
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Arg Leu Arg Met Phe Gly Ala Asp Tyr Ala Trp Ile Leu His Glu Ser
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Met Gly Ala Pro Trp Trp Pro Asp Gln Arg Thr Ala Cys Ser Asn His
385                 390                 395                 400
Glu Leu Gln Leu Ala Val Glu Asn Leu Ile Val Val Ser Thr His Asn
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Ser Ile Val Gly Asn Asn Val Ser Tyr Ser Gly Leu Asn Asn His Met
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Phe Asn Ser Gln Leu Arg Lys Gln Ser Ala Gln Phe His Gly Gln Asp
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Gly Phe Gly Ser Gly Tyr Gly Ser Arg Ile Ser Ile Ala Ala Thr Gln
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Ser Asp Ser Arg Arg Arg Arg Arg Gly Val Gly Gly Thr Ser Gly
465                 470                 475                 480
Gly His Leu Phe Pro Glu Ala Ile Ser Gln Tyr Ala Pro Gln Thr Tyr
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Arg Ser Asp Met Ala Trp Glu Phe Leu Gln Gln Met Gly Lys Leu His
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Phe Leu Gly Val Ser Gly Pro Val Ser Phe Ser Gly Pro Asp Arg Val
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Gly Thr Thr Ala Phe Tyr Gln Ile Gln Arg Gly Leu Leu Glu Pro Val
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Ala Leu Tyr Tyr Pro Ala Thr Asp Ala Leu Asp Phe Arg Cys Pro Arg
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Cys Arg Pro Val Lys Trp His Ser Gly Gln Val Pro Ile Ala Lys Arg
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Val Phe Lys Leu Arg Val Ala Thr Ile Ala Pro Leu Ala Phe Tyr Thr
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Ala Phe Asn Leu His Phe Arg Lys Leu Lys Ala Ile Lys Leu Ser Ser
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SUBSTITUTE SHEET (RULE 26)

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Gly Phe Ser Leu Ala Phe Gly Ser Met Phe Ala Lys Thr Tyr Arg Val
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His Arg Ile Phe Thr Arg Thr Gly Ser Val Phe Lys Asp Lys Met Leu
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Gln Asp Ile Gln Leu Ile Leu Leu Val Gly Gly Leu Leu Leu Val Asp
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Tyr Met Ala Trp Glu Thr Arg His Val Lys Ile Pro Ala Leu Asn Asp
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Ser Gln Tyr Ile Gly Val Ser Val Tyr Ser Val Val Ile Thr Ser Ala
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Ile Val Val Val Leu Ala Asn Leu Ile Ser Glu Arg Val Thr Leu Ala
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Thr Arg Arg Phe Val Val Asp Asp Arg Arg Glu Leu Gln Tyr Arg Val
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SUBSTITUTE SHEET (RULE 26)

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Pro Asn Phe Leu Pro Ile Pro Thr Ile Ser Gly Gly Glu Gln Gly Asp
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Gln Thr Leu Gly Gly Lys Tyr Val Lys Leu Leu Glu Thr Lys Val Asn
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Phe Gln Leu Pro Ser Asn Arg Arg Pro Ser Val Val Gln Gln Pro Pro
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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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                85                  90                  95
Thr Phe Gly Thr Thr Leu Cys Lys Ile Phe Pro Val Ile Phe Tyr Gly
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           115                 120                 125
Tyr Ile Leu Ile Ala Cys His Ser Arg Tyr Ser Gln Ile Tyr Lys Pro
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Lys Phe Ile Thr Leu Gln Leu Leu Phe Val Trp Ala Val Ser Phe Leu
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               165                 170                 175
Glu Ala Thr Phe Ser Cys Thr Ile Leu Lys Lys Glu Gly Arg Ser Ile
               180                 185                 190
Lys Lys Thr Leu Phe Val Ile Gly Phe Leu Leu Pro Cys Leu Val Ile
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Ile Val Ser Tyr Ser Cys Ile Tyr Ile Thr Val Leu His Gln Lys Lys
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Ala Arg Glu Asp Asn Arg Leu Thr Val Met Met Val Thr Ile Phe Leu
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Cys Phe Leu Val Cys Phe Leu Pro Leu Met Leu Ala Asn Val Val Asp
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SUBSTITUTE SHEET (RULE 26)

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Ser Lys Asn Ser Lys Glu Leu Ser Gly Val Ile Arg Ser Thr Pro Leu
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SUBSTITUTE SHEET (RULE 26)

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<212> PRT
<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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Leu Val Asn Asn Glu Thr Arg Ser Gln Thr Gln Thr Ala Tyr Glu Ser
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<212> DNA
<213> Drosophila

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37

SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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<210> 23
<211> 2153
<212> DNA
<213> Drosophila

<400> 23
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<400> 24
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40

SUBSTITUTE SHEET (RULE 26)

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65                    70                    75                    80
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               85                    90                    95
Pro His Gly Ala Ser Pro Arg Phe Leu Lys Phe Leu Pro Asn Thr Arg
               100                   105                   110
Pro Thr Cys Arg Lys Asp Gln Thr Thr Glu Ile Phe Arg Ser Arg Gly
               115                   120                   125
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       210                   215                   220
Leu Leu Arg Leu Ser Pro Gln Leu Pro Glu Gly Ser Tyr Gln Thr Ser
225                   230                   235                   240
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               245                   250                   255
Asp Trp Gln Asp Ala Lys Leu Asp Arg Asn Thr Ala Met Leu Gln Leu
               260                   265                   270
Pro His Lys Asn Leu Ser Ala Gly Gln Tyr Cys Leu Glu His Thr Gln
       275                   280                   285
Arg Glu Gly Glu Val Lys Ile Ile Ala Cys Gln His Leu Phe Ser Ser
       290                   295                   300
Ala Ala Gly Ala Gly Ile His Asp Gly Ser Ile Gly Gly Thr Ile Glu
305                   310                   315                   320
Gln Ala Asn Gly Gln Asn Leu Gln Lys Ala Val Leu Thr Gly Gly Ile
               325                   330                   335
Leu Val Ser Ile Val Phe Leu Ser Ala Thr Leu Val Ala Gly Phe Leu
       340                   345                   350
Leu Pro Ala Val His His Ala Leu His Trp Arg Cys Gln Ile Cys Tyr
       355                   360                   365
Val Thr Cys Leu Leu Phe Gly Lys Ile Leu Leu Ala Ile Glu Glu Leu
       370                   375                   380
Ser Ser Ser Leu Gln Pro Gly Ser Ala Ala Cys His Thr Leu Ala Ile
385                   390                   395                   400
Thr Met Gln Phe Phe Phe Leu Ala Ala Phe Phe Trp Leu Asn Thr Met
               405                   410                   415
Cys Phe Asn Ile Trp Trp Thr Phe Arg Asp Phe Arg Pro Ser Ser Leu
               420                   425                   430
Glu Arg Asn Gln Glu Ala Leu Arg Arg Tyr Leu Tyr Ser Leu Tyr Ala
       435                   440                   445
Trp Gly Gly Pro Leu Leu Ile Thr Phe Val Ala Ala Cys Val Asp Gln
       450                   455                   460
Leu Pro Glu Thr Thr Leu Leu Arg Pro Gly Phe Gly Gln Leu Tyr Cys
465                   470                   475                   480
Trp Phe Asp Asn Arg Asn Leu Ser Ile Phe Ala Tyr Phe Tyr Gly Pro
               485                   490                   495
Ile Gly Leu Leu Leu Cys Ala Asn Ile Ala Leu Phe Val Ser Thr Thr
               500                   505                   510
His Gln Leu Thr Cys Gly Leu Trp Lys Arg Asp Asp Val Lys Ser Ser
```

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SUBSTITUTE SHEET (RULE 26)

```
         515                  520                  525
Ser Glu Lys Ser Ala Leu Gly Arg Val Cys Leu Lys Leu Val Val Val
    530                  535                  540
Met Gly Val Thr Trp Ile Ala Asp Ile Leu Ser Trp Leu Val Gly Gly
545                  550                  555                  560
Pro His Gly Val Trp Phe Phe Thr Asp Leu Ile Asn Ala Leu Gln Gly
                565                  570                  575
Val Phe Ile Phe Ile Val Val Gly Cys Gln Pro Gln Val Trp Thr Ala
            580                  585                  590
Cys Arg Arg Ile Phe Cys Pro Arg Leu Arg His Asp Ile Thr Asn Thr
    595                  600                  605
Thr Asn Gly Val Gln His Ser Ser Ser Ser Gln Gly Leu Pro Ser Met
    610                  615                  620
Ala Gly Gly Thr Glu Ile Thr Gln Asn Thr Thr Thr Thr Thr Thr Thr
625                  630                  635                  640
Thr Asn Thr Thr Ala Thr His Met Pro Ser Asn Pro Ala Glu Asp Glu
                645                  650                  655
Val Pro Glu Lys Ala Pro Ile Ala Pro Val Ala Pro Ile Val Lys Met
                660                  665                  670
Glu Thr Ile Cys
            675
```

```
<210> 25
<211> 3187
<212> DNA
<213> Drosophila
```

```
<400> 25
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ggacgtgaca cggtggagcg gtggagaaaa catcatcata ataataataa agccgaataa 180
ctttctccac acgtagtgtg tgtcaataaa tcggttgttt ctcgcagagt ttgaaaggaa 240
actttttagag ttcttaaaca aagaatgtgg ttttggaacc actgtgccgc atcctgtctg 300
ccatgaatga tgcgtccttt cctgccagca cataaagccc cggccagttg catctattcc 360
acacactgat agacaatgtt tgtgcactga tttatactca gccagctatt aaataagaat 420
tttcgttatt acgctgccgg ggatttttatt atgtgacttt caaaagcccc cgccaacttg 480
ttgtggcttt ggcttaaagc cgcgccaagc tgaaaattgt tattttaacc ttttaaagtc 540
agctttatca gcaccaaatg cagggccatt atgcgtggcc cacgcggcgt atgagcaacg 600
ttaaatctgc gaataattca aagacgtgcg tttcttttta cagccgcctt gtcggtaatc 660
ccattaagga gttatctggc gaaacatttt tgcacaacac tcgactggag gcactgtgag 720
tatactttgt ttgtttttaat ttaaaaaatc acaaatatata tcatgaagtt gttaaaacgg 780
gattgaattt gatttgaata tatgatttca tttaatttct caccaatatt taagttcgtt 840
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gaatctcacg ggaattcggt atgatcacat cgacttcgag gccatcaatt caatgcgcaa 960
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gtgcaagccg tccaccgatg gagtcagctc ctttcaagat cttctgagca aaccagtgtt 1080
acgttactcc gcctgggtga tggccacgtt gacaatagct ggaaatgtgc tagtcctatg 1140
gggacgcttt atctaccgcg atgagaatgt ggctgtgaca atggtgattc ggaatctggc 1200
tctggctgat atgctgatgg gcttctattt ggtcaccatt ggagtgcagg actatcgcta 1260
ccgcaacgag tattacaagt aagtcaaatg tgatggattg gcatttgtta cgccccaatc 1320
ttttagggtt gtgctggact ggataacctc gtggcagtgc acactgattg gaacgctggc 1380
cgtgagctcc tcggaggttt cgatgcttat cctggctttt atgtcgctgg agcggtttct 1440
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tttgatttgc atttggatta cgggcgtggg cttggctgtg caccggtgc tcctgtggcg 1560
gaccagtacc ctaccctact acggatccta ttccggaacc tgtgagcaca atgtttatga 1620
taaaatgtag tttaccaagt gacgaaatta aacttaacag gctttccatt gcacatccac 1680
gaggccttcc cgatgggctg gctttactcg gctttcgtgt cctgggcgt caatctgctg 1740
ctgctggtga tgattgcgat gctctacacg gcactcctta tttcgatatg gcgaacgagg 1800
agcgccactc cgctcactct gttggattgc gaattcgctg tgcgattctt tttcatcgtg 1860
```

```
ctgaccgact tcctgtgctg ggtgcccatc atcgttatga agatctgggt ttttttcaac 1920
tacaatatct ccgatgacat ctacgcctgg ttggtggtct ttgtgctgcc acttaactcg 1980
gcggttaatc ctctcttgta caccttcacc acgcccaagt accgaaatca aatcttcctt 2040
cgcggctgga agaagataac ttctagaaag cgagcggagg ctggcaatgg aaatgtggcc 2100
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gccaaagccg cgatgagatg ccattaggtc ctaacgctgt cgaactgaag gattcttgtg 2220
gcgcagatcg aacttgtata ccaccagatt tagcagcatt tattttgtct atgatatcga 2280
aaatctatat atgtatgtga atatctatcc ctgtccgtgt aagataacca aatgaaagtg 2340
tgaaataaat tgaatgtgat atttgtaagg caattttacg gaatttaaaa tgggatgcga 2400
gttagtgtaa gattaagcta ttatctaagt tttggtaata gtttttaaata ctttttattt 2460
agaaatagca gcgctatcat ttttggcatg gtgtgattct ttctggtccg agtaaatctt 2520
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ctgcaccacc atgttatgct tacgctccag gtgcatgcgt agtctaaaaa attattaagg 2640
agtgttactt tcaaataatg tacactttaa acaaaataac taacttgtta cgagctggat 2700
agctctgatg gcagtgggcg cactcaaatg gcatggccgt atgcgtgcac tcgtgattcc 2760
tgagagatga agatgaggta aaggacttct ggcagccggg aaactcgcaa atgaagcgag 2820
atccagagtg cttaacctgc tggtggacag tcaaatggga tcgctgtgcg aaacgacgat 2880
cacagagatc acaggaatag ggaaagtctc tgttatgata gcgtttatga atctccaggg 2940
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tcgaatcgac gtgaactttc agcgcctgct ttgtgaggta aacccggtcg cactggctgc 3060
aacgaaagtt gggacgattg gccaaatgaa tcatctggtg cttggccatg cgggaatggt 3120
tcctgaactc cttgtggcag aacttgcagt tggattttcc cgtatgccga ttgcgtggca 3180
caatgtc                                                            3187
```

<210> 26
<211> 1080
<212> DNA
<213> Drosophila

<400> 26
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cttctgagca aaccagtgtt acgttactcc gcctgggtga tggccacgtt gacaatagct 120
ggaaatgtgc tagtcctatg gggacgcttt atctaccgcg atgagaatgt ggctgtgaca 180
atggtgattc ggaatctggc tctggctgat atgctgatgg gcttctattt ggtcaccatt 240
ggagtgcagg actatcgcta ccgcaacgag tattacaagg ttgtgctgga ctggataacc 300
tcgtggcagt gcacactgat tggaacgctg gccgtgagct cctcggaggt ttcgatgctt 360
atcctggctt ttatgtcgct ggagcggttt ctcttgatcg ccgatccctt tcgcggccat 420
cgcagcattg gaaatcgggt gatgtggctg gctttgattt gcatttggat tacgggcgtg 480
ggcttggctg tggcaccggt gctcctgtgg cggaccagta ccctacccta ctacggatcc 540
tattccggaa cctgctttcc attgcacatc cacgaggcct tcccgatggg ctggctttac 600
tcggctttcg tgttcctggg cgtcaatctg ctgctgctgg tgatgattgc gatgctctac 660
acggcactcc ttatttcgat atggcgaacg aggagcgcca ctccgctcac tctgttggat 720
tgcgaattcg ctgtgcgatt cttttttcatc gtgctgaccg acttcctgtg ctgggtgccc 780
atcatcgtta tgaagatctg ggttttttttc aactacaata tctccgatga catctacgcc 840
tggttggtgg tctttgtgct gccacttaac tcggcggtta atcctctctt gtacaccttc 900
accacgccca agtaccgaaa tcaaatcttc cttcgcggct ggaagaagat aacttctaga 960
aagcgagcgg aggctggcaa tggaaatgtg gccaccacaa cgacgggcac ggcaactgga 1020
tcctctcagc atccggatga cttcacgatc tttgccaaag ccgcgatgag atgccattag 1080
```

<210> 27
<211> 359
<212> PRT
<213> Drosophila

<400> 27
```
Met Thr Pro Arg Val Arg Met Cys Lys Pro Ser Thr Asp Gly Val Ser
1               5                  10                  15
Ser Phe Gln Asp Leu Leu Ser Lys Pro Val Leu Arg Tyr Ser Ala Trp
             20                  25                  30
```

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SUBSTITUTE SHEET (RULE 26)

```
Val Met Ala Thr Leu Thr Ile Ala Gly Asn Val Leu Val Leu Trp Gly
        35                      40                  45
Arg Phe Ile Tyr Arg Asp Glu Asn Val Ala Val Thr Met Val Ile Arg
    50                      55                  60
Asn Leu Ala Leu Ala Asp Met Leu Met Gly Phe Tyr Leu Val Thr Ile
65                      70                  75                  80
Gly Val Gln Asp Tyr Arg Tyr Arg Asn Glu Tyr Tyr Lys Val Val Leu
            85                      90                  95
Asp Trp Ile Thr Ser Trp Gln Cys Thr Leu Ile Gly Thr Leu Ala Val
            100                 105                 110
Ser Ser Ser Glu Val Ser Met Leu Ile Leu Ala Phe Met Ser Leu Glu
            115                 120                 125
Arg Phe Leu Leu Ile Ala Asp Pro Phe Arg Gly His Arg Ser Ile Gly
    130                 135                 140
Asn Arg Val Met Trp Leu Ala Leu Ile Cys Ile Trp Ile Thr Gly Val
145                 150                 155                 160
Gly Leu Ala Val Ala Pro Val Leu Leu Trp Arg Thr Ser Thr Leu Pro
            165                 170                 175
Tyr Tyr Gly Ser Tyr Ser Gly Thr Cys Phe Pro Leu His Ile His Glu
            180                 185                 190
Ala Phe Pro Met Gly Trp Leu Tyr Ser Ala Phe Val Phe Leu Gly Val
    195                 200                 205
Asn Leu Leu Leu Leu Val Met Ile Ala Met Leu Tyr Thr Ala Leu Leu
    210                 215                 220
Ile Ser Ile Trp Arg Thr Arg Ser Ala Thr Pro Leu Thr Leu Leu Asp
225                 230                 235                 240
Cys Glu Phe Ala Val Arg Phe Phe Phe Ile Val Leu Thr Asp Phe Leu
            245                 250                 255
Cys Trp Val Pro Ile Ile Val Met Lys Ile Trp Val Phe Phe Asn Tyr
            260                 265                 270
Asn Ile Ser Asp Asp Ile Tyr Ala Trp Leu Val Val Phe Val Leu Pro
            275                 280                 285
Leu Asn Ser Ala Val Asn Pro Leu Leu Tyr Thr Phe Thr Thr Pro Lys
    290                 295                 300
Tyr Arg Asn Gln Ile Phe Leu Arg Gly Trp Lys Lys Ile Thr Ser Arg
305                 310                 315                 320
Lys Arg Ala Glu Ala Gly Asn Gly Asn Val Ala Thr Thr Thr Thr Gly
            325                 330                 335
Thr Ala Thr Gly Ser Ser Gln His Pro Asp Asp Phe Thr Ile Phe Ala
            340                 345                 350
Lys Ala Ala Met Arg Cys His
            355
```

```
<210> 28
<211> 3759
<212> DNA
<213> Drosophila

<400> 28
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ggaatcgtcg atgtttttcag cgcatagaaa cagcaaagtg tgtaaattgt aagtctaaat 180
taatttccat attttctaat acaattatta atagcatatt gcatatttat tgtgactcgc 240
cggtggtgta ggctggtgtc ttggaagaca tggataaata tctgaaatgt aagttttttt 300
tttaaagatc aatttatttg ttttttgcca aagacatcga aaacatggat gttcgccaac 360
atcgatgttt ctccacttct aatgccaacg aaaacgtgac tgggaacgta tcgatgggaa 420
aaacgttaca aaaataccaa ctatcgcata gcggaatcac cttggcgggc tattcgaatg 480
tatctcacaa atagttttta aggaacctac agtcagtacc aaatacttaa aattccattt 540
atattttatt ttatgctaca gaaaactgat aagctgcatt acttttgaaa agttaaaaat 600
```

44

SUBSTITUTE SHEET (RULE 26)

```
tgtgtttttt aaatgattta tttatataaa taagcttatg taatactatt gttaatatgt 660
aaaaaaaaaa gaataaaaga aaaagaatag tttacctaag cagttgcttg aataatacat 720
acataattta agttttatac ataatttatc aaccctcgct cagtaggaaa aaaagatggc 780
tcagaaatga gcaacgaatt ggaatgtccg ataagccttt tttatcaaaa taataatttt 840
tacattccct tttcataacg ctttcccagt tagtttgtgc caatcgtaaa acagcatccg 900
caaagtgaag tcgctgctat tttgtagtac cactacattc ttatttattt aagtaatatt 960
taaagaatgt ccagctaact atatgattgc tagttcaaaa atgttacttt ctgcatcgat 1020
cctaatatat ttcttgctga atctgcaatc ttcgagtgct gagattgccg actgcagttt 1080
ctatgatacc gttgatatct cggaaggcca gaggctctcg aatggatcat acctctacga 1140
gggattactt attcccgccc atttgacggc caagtatgaa ttcaagcttc tggcgaatgg 1200
agataaggag caggtgccaa gtcacgtgag aggatgtgtg tgcaagctaa ggacttgcgt 1260
caggttttgc tgcccacatg accacataat ggatatgggc gaatgctacg ccaacatgac 1320
gacggaggag aacgaattac tggaccccat gctaaatgtg accctggacg acggatcagt 1380
ggtgcaaagg cactataaga aggagctcat ggtgcagtgg gatctgccaa agccctgcga 1440
tgatatgttt tacctagaca accgggatat aatggatgag tacaccttgt tcgaggtatg 1500
gctgctcgaa aaataagcat ttttgggcag gatttattta tgctttggct ctctgcagaa 1560
tggaagattg ctgcgccact acgatcaagt gtatttggac aagtcggagt actgtctgca 1620
gcaccgaaca ttcggcgaag gtaacaacaa ctccattcgc attatacccc acaactgctt 1680
gatactgcca tccagaacgg gacagaccgt tggtaagatg atgcccattg cttgcatggt 1740
agctcccagt tctatatctt tcctatttcc atagtgatga tcacatcgtt gatatgcttg 1800
gttcttacca tcgccgtgta cctgtgcgtt aagaagctaa tgaatttgga gggcaagtgt 1860
ttcatctgtt acatgatgtg cctatttttc ggatacctgt tcctactcct tgatctgtgg 1920
gagttatcgc tcgatttctg taaagcagca ggttagctta gaggggatgc atttcaacac 1980
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gcgttctttt ggctatctat catcagtcgg cactattgga aatgtcttac caatccctgt 2100
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agaaactgtg ggtcaatatc tttctggtag ctgactactt caactggtcc caaggcgtca 2700
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tcttatagtt catagttcgg gtaaccagtt ccctaaaatg tctcttttca gaatatttcc 2820
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tatagaattc atttaatcac aaaatgtatg aatatttttc tttatatgac gtgcatcgac 3060
tatagaaaat cgactatagt gtgccacaat atattttact catcatttcc taatcaaact 3120
attgcaaact taactttgag ccgaggaaaa accctgtatg tctatcaaaa ctatgagtca 3180
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caaattttaa tttaaaaact ttgaaggtaa atagtgcttt atcagatgcg gattacacgg 3360
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aagcgctaaa gttgaatctc aatgtgctgt gctgccttac cctttttcgtc tttcggtgtg 3660
ctcttgattg tcgtggttcc gtcgtgggcc gttgtggtgt tctgattgat tgagatctga 3720
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```

<210> 29
<211> 1449
<212> DNA
<213> Drosophila

<400> 29

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aatggatcat acctctacga gggattactt attcccgccc atttgacggc caagtatgaa 180
ttcaagcttc tggcgaatgg agataaggag caggtgccaa gtcacgtgag aggatgtgtg 240
tgcaagctaa ggacttgcgt caggtttttgc tgcccacatg accacataat ggatatgggc 300
gaatgctacg ccaacatgac gacggaggag aacgaattac tggaccccat gctaaatgtg 360
accctggacg acggatcagt ggtgcaaagg cactataaga aggagctcat ggtgcagtgg 420
gatctgccaa agccctgcga tgatatgttt tacctagaca accgggatat aatggatgag 480
tacaccttgt tcgagaatgg aagattgctg cgccactacg atcaagtgta tttggacaag 540
tcggagtact gtctgcagca ccgaacattc ggcgaaggta acaacaactc cattcgcatt 600
ataccccaca actgcttgat actgccatcc agaacgggac agaccgttgt gatgatcaca 660
tcgttgatat gcttggttct taccatcgcc gtgtacctgt gcgttaagaa gctaatgaat 720
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ctccttgatc tgtgggagtt atcgctcgat ttctgtaaag cagcaggttt cttgggatac 840
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gtgcaacgcg agaaactgtg ggtcaatatc tttctggtag ctgactactt caactggtcc 1380
caaggcgtca ttatatttgt gctattcatt ctgcggcgca aaactcttgt actattcaag 1440
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```

```
<210> 30
<211> 482
<212> PRT
<213> Drosophila
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<400> 30
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1               5                   10                  15
Ser Ser Ser Ala Glu Ile Ala Asp Cys Ser Phe Tyr Asp Thr Val Asp
                20                  25                  30
Ile Ser Glu Gly Gln Arg Leu Ser Asn Gly Ser Tyr Leu Tyr Glu Gly
            35                  40                  45
Leu Leu Ile Pro Ala His Leu Thr Ala Lys Tyr Glu Phe Lys Leu Leu
        50                  55                  60
Ala Asn Gly Asp Lys Glu Gln Val Pro Ser His Val Arg Gly Cys Val
65                  70                  75                  80
Cys Lys Leu Arg Thr Cys Val Arg Phe Cys Cys Pro His Asp His Ile
                85                  90                  95
Met Asp Met Gly Glu Cys Tyr Ala Asn Met Thr Thr Glu Glu Asn Glu
                100                 105                 110
Leu Leu Asp Pro Met Leu Asn Val Thr Leu Asp Asp Gly Ser Val Val
            115                 120                 125
Gln Arg His Tyr Lys Lys Glu Leu Met Val Gln Trp Asp Leu Pro Lys
        130                 135                 140
Pro Cys Asp Asp Met Phe Tyr Leu Asp Asn Arg Asp Ile Met Asp Glu
145                 150                 155                 160
Tyr Thr Leu Phe Glu Asn Gly Arg Leu Leu Arg His Tyr Asp Gln Val
                165                 170                 175
Tyr Leu Asp Lys Ser Glu Tyr Cys Leu Gln His Arg Thr Phe Gly Glu
                180                 185                 190
Gly Asn Asn Asn Ser Ile Arg Ile Ile Pro His Asn Cys Leu Ile Leu
            195                 200                 205
Pro Ser Arg Thr Gly Gln Thr Val Val Met Ile Thr Ser Leu Ile Cys
        210                 215                 220
```

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SUBSTITUTE SHEET (RULE 26)

```
Leu Val Leu Thr Ile Ala Val Tyr Leu Cys Val Lys Lys Leu Met Asn
225             230             235             240
Leu Glu Gly Lys Cys Phe Ile Cys Tyr Met Met Cys Leu Phe Phe Gly
            245             250             255
Tyr Leu Phe Leu Leu Leu Asp Leu Trp Glu Leu Ser Leu Asp Phe Cys
            260             265             270
Lys Ala Ala Gly Phe Leu Gly Tyr Phe Phe Val Met Ala Ala Phe Phe
            275             280             285
Trp Leu Ser Ile Ile Ser Arg His Tyr Trp Lys Cys Leu Thr Asn Pro
        290             295             300
Cys Ala Ser Met Asn Ile Arg Ser Glu Arg Ala Phe Leu Leu Tyr Ser
305             310             315             320
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Phe Tyr Gly Pro Met Val Leu Leu Ile Leu Phe Asn Ile Thr Met Phe
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Val Leu Thr Ala Lys His Ile Ile Asp Ser Lys Arg Thr Leu Arg Lys
385             390             395             400
Ile Ala Arg Asn Glu Gly Arg Ile Gln Lys Leu Asn Ser Asp Lys Gln
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Ser Phe Glu Ile Phe Ser Tyr Leu Val Gln Arg Glu Lys Leu Trp Val
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Asn Ile Phe Leu Val Ala Asp Tyr Phe Asn Trp Ser Gln Gly Val Ile
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<210> 31
<211> 4469
<212> DNA
<213> Drosophila

<400> 31
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47

SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

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<211> 462
<212> PRT
<213> Drosophila

<400> 33
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Thr Ser Ala Thr Leu Ser Thr Ala Ala Ala Ser Thr Ser Thr Thr Ala
    50                  55                  60
Ala Pro Ser Ala Gly Ala Thr Trp Ile Asn His His Leu Ala Val Glu
65                  70                  75                  80
Ala Asp Ser Ser Gln Pro Ala Asn Gly Ser Asp Ala Gln Ala Gly Val
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Glu Gly Pro Thr Met Pro Ala Gly Tyr Leu Pro Leu Tyr Glu Asp Val
            100                 105                 110
Glu Thr Ala Ala Glu Asp Ala Gly Tyr Ala Leu Ile Asp Asp Ile Ser
        115                 120                 125
Glu Trp Leu Leu Gly Ser Val Gly Ser Glu Ala Ala Val Gly Gly Pro
    130                 135                 140
Glu Asn Ser Thr Asn Leu Ala Val Thr Gly Ala Asn Gly Thr Leu Ala
145                 150                 155                 160
Trp Leu Glu Ala Leu Asn Ser Thr Gln Pro Ala Gln Ser Asn Ser Ser
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Ala Glu Asp Gly Glu Arg Gly Arg Tyr Ser Leu Arg Ser Phe Val Glu
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Gln Gln Leu Ala Gly Gly Gly Ala Ala Gly Ala Gly Asp Gly Gly Asp
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225                    230                    235                    240
Ala Glu Leu Leu Gln Arg Thr Ala Thr Val Ala Arg Glu Thr Leu Gly
                245                    250                    255
Asn Arg Thr Ala Pro Ser Thr Thr Ser Tyr Asp Gly Gly Gly Ser Gly
                260                    265                    270
Asp Val Gly Val Ala Gly Gly Leu Ala Gly Thr Ala Gly Gly Gly Val
        275                    280                    285
Gly Gly Ala Gly Gly Ser Gly Gly Ser Thr Phe Met Leu Leu Leu Glu
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Asn Phe Asn Asp Tyr Phe Pro Asn Tyr Asn Gly Ser Thr Val Ser Gly
305                    310                    315                    320
Thr Ser Thr Ile Ala Pro Gly Val Ala Ile Thr Gly Ser Arg Gly Ser
                325                    330                    335
Gly Leu Leu Leu Glu Gln Asn Leu Thr Gly Leu Tyr Leu Asp Gly Tyr
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Arg Leu Asn Cys Thr Asn Glu Thr Leu Asn Leu Thr Asp Ser Cys Gly
                355                    360                    365
Glu Leu Arg Val Val Asp His Asn Tyr Trp Ala Leu Ile Leu Ile Leu
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Phe Pro Ile Leu Thr Leu Phe Gly Asn Ile Leu Val Ile Leu Ser Val
385                    390                    395                    400
Cys Arg Glu Arg Ser Leu Gln Thr Val Thr Asn Tyr Phe Ile Val Ser
                405                    410                    415
Leu Ala Ile Ala Asp Leu Leu Val Ala Val Val Val Met Pro Phe Ala
                420                    425                    430
Val Tyr Phe Leu Glu Pro Val Glu Pro Thr Thr Cys Ile Met Gly Ser
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<211> 11501
<212> DNA
<213> Drosophila
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SUBSTITUTE SHEET (RULE 26)

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52

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<211> 2177
<212> DNA
<213> Drosophila

<400> 35

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<212> DNA
<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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<213>  Drosophila
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<212> PRT
<213> Drosophila

<400> 39
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            20                  25                  30
Thr Arg Pro Glu Thr Trp Val Leu Gly His Glu Met Cys Lys Ala Val
        35                  40                  45
Pro Phe Val Glu Leu Thr Val Ala His Ala Ser Val Leu Thr Ile Leu
    50                  55                  60
Ala Ile Ser Phe Glu Arg Tyr Tyr Ala Ile Cys Glu Pro Leu Lys Ala
65                  70                  75                  80
Gly Tyr Val Cys Thr Lys Gly Arg Ala Ile Leu Ile Cys Val Leu Ala
                85                  90                  95
Trp Gly Ile Ala Ala Leu Phe Thr Ser Pro Ile Leu Trp Val Ala Glu
            100                 105                 110
Tyr Lys Leu Ala Glu Tyr Ile Asp Gly Ser Ser Val Ala Val Cys Leu
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Thr Gln Ala Ile Ser Asp Trp Thr Leu Ala Phe Phe Leu Met Thr Ile
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Ser Val Phe Phe Val Val Pro Phe Val Thr Leu Val Val Leu Tyr Gly
145                    150                    155                    160
Ile Ile Ala Arg Asn Leu Val Ser Asn Arg Ala Ala Met Leu Arg Ala
             165                    170                    175
Arg Pro Thr Lys Pro Glu Leu Ser Leu Lys Ala Arg Lys Gln Val Val
             180                    185                    190
Leu Met Leu Gly Ala Val Val Leu Ser Phe Phe Val Cys Leu Leu Pro
    195                    200                    205
Phe Arg Val Leu Thr Leu Trp Ile Ile Leu Ser Thr Asp Gln Thr Leu
    210                    215                    220
His Asp Leu Gly Leu Val Arg Tyr Tyr Ser Leu Leu Tyr Phe Cys Arg
225                    230                    235                    240
Ile Met Leu Tyr Leu Asn Ser Ala Met Asn Pro Ile Leu Tyr Asn Leu
             245                    250                    255
Met Ser Thr Lys Phe Arg Arg Gly Phe Lys Arg Leu Cys Gln Asp Ala
             260                    265                    270
Gly Arg Leu Leu Leu Glu Leu Val Thr Leu Gly Arg Arg Lys Glu Asp
             275                    280                    285
Ser Ser Arg Gly Arg Arg Gly Thr Leu Ser Leu Gly Met Gly Thr Asn
    290                    295                    300
Thr Asn Thr Asn Thr Asn Ser Ser Asn Ala Thr Gly Ala Thr Ser Ser
305                    310                    315                    320
Ser Ile Leu Ser Arg Ser Ser Asn Arg Arg Cys Ser Glu Asp Ile Ser
             325                    330                    335
Arg Thr Arg Leu Lys Ile Glu Met Gln Met Pro Cys Gly Ser Asp Leu
             340                    345                    350
Glu Ala Met Ala Met Leu Gln His Ser Thr Leu Gly Lys Gly Ile Ala
             355                    360                    365
Arg Arg Val Ser Asp Ser Arg Leu Met Pro Leu Arg Asn His Gln Pro
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Arg Arg His Lys Pro Gln Ile Ser Phe Asp Glu Glu Ser Leu Glu Glu
385                    390                    395                    400
Asn Lys Arg Arg Leu Gly Val Gln Ile Ser Thr Gly Ser Lys Gly Pro
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Ile Ile Ala Ile Ser Thr Tyr Ser Val Glu Pro Tyr Gly Asp Gly Thr
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Asp Ala Pro Val Cys Thr Thr Ala Ala Asp Gly Phe Trp Ser Ile Phe
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Tyr Phe Val Gly Cys Ile Thr Val Phe Phe Phe Leu Pro Phe Gly Ile
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Leu Val Leu Leu Tyr Ala Ala Ile Ala Tyr Lys Leu Leu Arg Pro Asn
465                    470                    475                    480
Asn Ala Phe His Arg Pro Thr Ser Pro Gln Pro Gln Gln Pro Ser Gly
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Gly Ala Thr Ser Gly Ser Ser Gln Val Pro Ser Thr Lys Gly Asn Ser
             500                    505                    510
His Gln Gln Ser Asn Gly Met Arg Lys His Arg Lys Gln Val Ile Phe
    515                    520                    525
Met Leu Val Ala Val Val Ser Ser Phe Phe Val Cys Leu Leu Pro Phe
    530                    535                    540
Arg Ala Phe Thr Leu Trp Val Ile Leu Ala Ser Ala Glu Asp Val Glu
545                    550                    555                    560
Gly Leu Gly Ile Ala Gly Tyr Tyr Asn Leu Leu Tyr Phe Ser Arg Phe
             565                    570                    575
Met Leu Tyr Leu Asn Ser Ala Met Asn Pro Ile Leu Tyr Asn Leu Met
             580                    585                    590
Ser Ser Lys Phe Arg Ser Gly Phe Trp Arg Leu Leu Leu Thr Cys Leu
```

```
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    His Pro Thr Ala Gly Gly Ser Gly Arg Asn Ala Ser Thr Arg Gln Glu
    625                    630                    635                    640
    Gln Asp Ala Glu Glu Gly Ala Ala Leu Ala Gly Thr Thr Ser Ala Arg
                    645                    650                    655
    His Pro Arg Arg Thr Leu Arg Arg Glu Ala Thr Phe Leu Ile Asn Ser
                    660                    665                    670
    Ile Ser Thr Ser Ser Gly Thr Asp Arg Thr Thr Ser Ser Ser Ala Trp
                    675                    680                    685
    Arg Ser Asn Ser Leu Ser Ile Ser Gly Leu Ser Glu Arg Glu Arg Gly
        690                    695                    700
    Ile Leu Gly Ala Ala Ile Ile Gly Thr Thr Ala Ala Thr Val Thr Thr
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<211> 3821
<212> DNA
<213> Drosophila
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SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

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<210> 42
<211> 385
<212> PRT

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<213> Drosophila

<400> 42

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Thr Ala Ala Leu Leu Ala Ile Val Phe Ala Ile Pro Phe Gly Ile Arg
            35   40   45
Met Leu Val His Lys Asp Arg Gly Gln Trp Glu Glu Phe Gly Pro Ala
        50   55   60
Phe Tyr Thr Ala His Leu Glu Leu Tyr Leu Gly Asn Gly Cys Leu Gly
65   70   75   80
Val Gly Val Met Met Leu Leu Val Leu Thr Ile Glu Arg Tyr Val Ser
                85   90   95
Val Cys His Pro Gly Phe Ala Arg Pro Val Met Gly Pro Pro Gly Val
            100   105   110
Val Val Phe Leu Thr Cys Leu Ala Thr Val Ile Val Tyr Leu Pro Ser
            115   120   125
Ile Phe Arg Gly Glu Leu Ile Lys Cys Ile Leu Gly Ser Ser Asp Val
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<211> 1525
<212> DNA
<213> Drosophila

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ctgcggacgc ctcaggttag ttaat 1525

<210> 45
<211> 507
<212> PRT
<213> Drosophila

<400> 45
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            35   40   45
Ala Ala Leu Ala Gly Asp Tyr Asn Asn Phe Thr His Asn Phe Val Asp
        50   55   60
Leu Gln Asn Leu Leu Ser Phe Asn Glu Leu Asn Gly Thr Ser Gly Ser
65   70   75   80
Gly Gly Thr Ala Val Ser Ser Leu Gly Ser Ser Ser Ala Ile Lys Leu
                85   90   95
Asn Asn Ser Ala Ile Thr Asp Thr Leu Leu Gly Thr Val Leu Thr Thr
                100   105   110
Ala Thr Ala Thr Val Ala Pro Ala Ala Ser Ser Leu Leu Ala Thr Leu
            115   120   125
Ala Ala Thr Thr Thr Ala Ser Ala Arg Gly Ser Leu Ala Gly Lys Ser
        130   135   140
Leu Ala Ile Ala Asp Ala Thr Ser Ser Thr Tyr Tyr Ser Asn Leu Leu
145   150   155   160
Asn Leu Ser Pro Ala Thr Thr Ser Leu Ile Ser Ala Ala Ala Ala Thr

67

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Val Asp Phe Gly Phe Asp Pro Leu Tyr Arg His Ser Leu Ala Met Ser
            195                  200                  205
Met Val Tyr Cys Val Ala Tyr Ile Val Val Phe Leu Val Gly Leu Ile
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Gly Asn Ser Phe Val Ile Ala Val Val Leu Arg Ala Pro Arg Met Arg
225                  230                  235                  240
Thr Val Thr Asn Tyr Phe Ile Val Asn Leu Ala Ile Ala Asp Ile Leu
                245                  250                  255
Val Ile Val Phe Cys Leu Pro Ala Thr Leu Ile Gly Asn Ile Phe Val
                260                  265                  270
Arg Lys Tyr Leu Phe Asn Ser Ala Arg Cys Arg Arg Asp Leu Phe Ala
            275                  280                  285
Thr Gly Gly His Val His Cys His Leu Val Ala Pro Glu Ala Asp Asp
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Lys Ala Thr Cys Pro His His Asp Asn Arg His Met Gly Asn Arg Ala
305                  310                  315                  320
Gly Asp His His Ser Leu Ala Ala Leu Leu Arg Pro Gly Ala Arg Arg
                325                  330                  335
Gly Gly Leu Leu Arg Arg Pro Gly Leu Gly Leu Leu Ala Ala Ala Val
            340                  345                  350
Pro Leu Pro Gly Gly Val Ala Pro Gly His Gly Trp Glu Pro Leu Leu
            355                  360                  365
Pro Ala Ser Gln Pro Gly Gly Leu Leu Pro Ala Ala His Val Pro Asp
        370                  375                  380
His Ala Leu Leu Arg Ala His Leu Asp Gln Gly Leu His Glu Val His
385                  390                  395                  400
Pro Arg Arg Val Gln Gly Arg Ala Asn Gly Pro His Ala Ala Glu Glu
                405                  410                  415
Gln Gly Glu Gly His Gln Asp Val Gly Gly Arg Gly His Pro Val Cys
            420                  425                  430
Phe Val Leu Ala Ala Ala Leu Cys His Leu Cys Ala Asp Gln Ile Arg
            435                  440                  445
Leu Gly His Leu Ala Gly Gly Val Arg Asp Pro Gln Glu Gly Asp Ala
        450                  455                  460
Gly Gly Pro Val Ala Gly Leu Leu Glu Gln Leu His Gln Pro His Thr
465                  470                  475                  480
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<211> 3688
<212> DNA
<213> Drosophila

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tgggtttttgg tttaagatgc ttgggcatgt ttatccacca ttacgagtgg ctatatacac 420
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SUBSTITUTE SHEET (RULE 26)

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<210> 47
<211> 1191
<212> DNA
<213> Drosophila

<400> 47

SUBSTITUTE SHEET (RULE 26)

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<211> 396
<212> PRT
<213> Drosophila

<400> 48

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            20                   25                   30
Ala Val Leu Phe Val Met Phe Ile Asn Lys Asn Arg Lys Ser Arg Met
            35                   40                   45
Asn Tyr Phe Ile Lys Gln Leu Ala Leu Ala Asp Leu Cys Val Gly Leu
    50                   55                   60
Leu Asn Val Leu Thr Asp Ile Ile Trp Arg Ile Thr Ile Ser Trp Arg
65                   70                   75                   80
Ala Gly Asn Leu Ala Cys Lys Ala Ile Arg Phe Ser Gln Val Cys Val
            85                   90                   95
Thr Tyr Ser Ser Thr Tyr Val Leu Val Ala Met Ser Ile Asp Arg Tyr
            100                  105                  110
Asp Ala Ile Thr His Pro Met Asn Phe Ser Lys Ser Trp Lys Arg Ala
            115                  120                  125
Arg His Leu Val Ala Gly Ala Trp Leu Ile Ser Ala Leu Phe Ser Leu
            130                  135                  140
Pro Ile Leu Val Leu Tyr Glu Glu Lys Leu Ile Gln Gly His Pro Gln
145                  150                  155                  160
Cys Trp Ile Glu Leu Gly Ser Pro Ile Ala Trp Gln Val Tyr Met Ser
            165                  170                  175
Leu Val Ser Ala Thr Leu Phe Ala Ile Pro Ala Leu Ile Ile Ser Ala
            180                  185                  190
Cys Tyr Ala Ile Ile Val Lys Thr Ile Trp Ala Lys Gly Ser Ile Phe
            195                  200                  205
Val Pro Thr Glu Arg Ala Gly Phe Gly Ala Ala Pro Ala Arg Arg Ala
            210                  215                  220
Ser Ser Arg Gly Ile Ile Pro Arg Ala Lys Val Lys Thr Val Lys Met
225                  230                  235                  240
Thr Leu Thr Ile Val Phe Val Phe Ile Ile Cys Trp Ser Pro Tyr Ile
            245                  250                  255
Ile Phe Asp Leu Leu Gln Val Phe Gly Gln Ile Pro His Ser Gln Thr
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SUBSTITUTE SHEET (RULE 26)

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          290                       295                      300
Thr Leu Ser Arg Phe Pro Pro Phe Lys Trp Phe Thr Cys Cys Cys Lys
305                       310                       315                      320
Ser Tyr Arg Asn Asn Ser Gln Gln Asn Arg Cys His Thr Val Gly Arg
              325                       330                      335
Arg Leu His Asn Ser Cys Asp Ser Met Arg Thr Leu Thr Thr Ser Leu
              340                       345                      350
Thr Val Ser Arg Arg Ser Thr Asn Lys Thr Asn Ala Arg Val Val Ile
              355                       360                      365
Cys Glu Arg Pro Thr Lys Val Val Thr Val Pro Ala Met Ser Glu Arg
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Arg Gly Val Ser Leu Lys Gly Asn Thr Asp Ile Leu
385                       390                      395
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<211> 5051
<212> DNA
<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

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73

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Lys Pro Gly Asn His Gln Val Ile Leu Arg Arg Asn Gly Gln Leu Val
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Glu Gln Asp Gly Val Val Val Arg Arg Asn Ile Ser Glu Asn Gly Asp
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Thr Val Glu Thr Phe Phe Lys Cys Asn Ala Thr Tyr Cys Arg Glu Leu
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74

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Ser Cys Ser Thr Ile Ile Asn Phe Gly Gly Ala Arg Gly Ser Ala Asp
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SUBSTITUTE SHEET (RULE 26)

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<211> 192
<212> PRT
<213> Drosophila

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            20                  25                  30
Asp Ile Ser Lys Ala Pro Arg Phe Ser Asn Gly Ser Tyr Leu Tyr Glu
        35                  40                  45
Gly Leu Leu Ile Pro Ala His Leu Thr Ala Glu Tyr Asp Tyr Lys Leu
    50                  55                  60
Leu Ala Asp Asp Ser Lys Glu Lys Val Ala Ser His Val Arg Gly Cys
65                  70                  75                  80
Ala Cys His Leu Arg Pro Cys Ile Arg Phe Cys Cys Pro Gln Tyr Gln
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Lys Met Gln Lys Ser Lys Cys Tyr Gly Asp Met Ser Glu Asp Glu Leu
            100                 105                 110
Asn Lys His Asp Pro Phe Val Asn Val Thr Leu Ser Asp Gly Ser Val
        115                 120                 125
Val Arg Arg His Phe Lys Glu Asp Leu Ile Val Gln Ser Asp Leu Ala
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Lys Pro Gly Cys Pro Arg Met Tyr Phe Leu Asn His Glu Leu Pro Gly
145                 150                 155                 160
Asn Glu Phe Thr Leu Phe Glu Asn Gly Ser Leu Leu Arg His Trp Asp
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<211> 3640
<212> DNA
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77

<213> Drosophila

<400> 55

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78

SUBSTITUTE SHEET (RULE 26)

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<211> 1089
<212> DNA
<213> Drosophila

<400> 56
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<211> 362
<212> PRT
<213> Drosophila

<400> 57
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            20                  25                  30
Lys Ala Pro Arg Phe Ser Asn Gly Ser Tyr Leu Tyr Glu Gly Leu Leu
        35                  40                  45
Ile Pro Ala His Leu Thr Ala Glu Tyr Asp Tyr Lys Leu Leu Ala Asp
    50                  55                  60
Asp Ser Lys Glu Lys Val Ala Ser His Val Arg Gly Cys Ala Cys His
65                  70                  75                  80
Leu Arg Pro Cys Ile Arg Phe Cys Cys Pro Gln Tyr Gln Lys Met Gln
                85                  90                  95
Lys Ser Lys Cys Tyr Gly Asp Met Ser Glu Asp Glu Leu Asn Lys His
            100                 105                 110
Asp Pro Phe Val Asn Val Thr Leu Ser Asp Gly Ser Val Val Arg Arg
        115                 120                 125
His Phe Lys Glu Asp Leu Ile Val Gln Ser Asp Leu Ala Lys Pro Gly
    130                 135                 140
Cys Pro Arg Met Tyr Phe Leu Asn His Glu Leu Pro Gly Asn Glu Phe
145                 150                 155                 160
Thr Leu Phe Glu Asn Gly Ser Leu Leu Arg His Trp Asp Lys Val Glu
                165                 170                 175
Leu Ser Lys Arg Glu Tyr Cys Val Gln His Leu Ser Phe Lys Asp Asp
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79

SUBSTITUTE SHEET (RULE 26)

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     210                215                220
Leu Thr Ile Ser Val Tyr Leu Tyr Val Glu Lys Leu Arg Asn Leu His
225                230                235                240
Gly Lys Cys Phe Ile Cys Tyr Leu Ala Ser Leu Phe Leu Gly Tyr Phe
             245                250                255
Phe Leu Val Leu Asn Val Trp Lys Tyr Ser Ser Gly Phe Cys Val Thr
         260                265                270
Ala Gly Phe Leu Gly Tyr Phe Ser Val Met Ala Ala Phe Phe Trp Leu
         275                280                285
Ser Val Ile Gly Ile His Leu Arg Ile Lys Phe Ser Leu Ala Ser Asn
     290                295                300
Cys Leu His Arg Leu Leu Pro Glu Asn Pro Phe Arg Ala Tyr Asn Leu
305                310                315                320
Tyr Ala Trp Gly Ile Pro Leu Ile Met Thr Ala Ile Thr Tyr Thr Ala
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<212> DNA
<213> Drosophila

<400> 58
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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

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<211> 1221
<212> PRT
<213> Drosophila

<400> 60

SUBSTITUTE SHEET (RULE 26)

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Ile Ala Gly Phe Phe Pro Tyr Gly Asp Gly Val Glu Asn Ser Tyr Thr
        35              40                  45
Gly Arg Gly Val Met Pro Ser Val Lys Leu Ala Leu Gly His Val Asn
    50              55                  60
Glu His Gly Lys Ile Leu Ala Asn Tyr Arg Leu His Met Trp Trp Asn
65                  70              75                      80
Asp Thr Gln Cys Asn Ala Ala Val Gly Val Lys Ser Phe Phe Asp Met
            85              90                  95
Met His Ser Gly Pro Asn Lys Val Met Leu Phe Gly Ala Ala Cys Thr
            100             105                 110
His Val Thr Asp Pro Ile Ala Lys Ala Ser Lys His Trp His Leu Thr
        115             120                 125
Gln Leu Ser Tyr Ala Asp Thr His Pro Met Phe Thr Lys Asp Ala Phe
    130             135                 140
Pro Asn Phe Phe Arg Val Val Pro Ser Glu Asn Ala Phe Asn Ala Pro
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Arg Leu Ala Leu Leu Lys Glu Phe Asn Trp Thr Arg Val Gly Thr Val
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Tyr Gln Asn Glu Pro Arg Tyr Ser Leu Pro His Asn His Met Val Ala
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Asp Leu Asp Ala Met Glu Val Glu Val Val Glu Thr Gln Ser Phe Val
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Asn Asp Val Ala Glu Ser Leu Lys Lys Leu Arg Glu Lys Asp Val Arg
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Ile Ile Leu Gly Asn Phe Asn Glu His Phe Ala Arg Lys Ala Phe Cys
225             230                 235                 240
Glu Ala Tyr Lys Leu Asp Met Tyr Gly Arg Ala Tyr Gln Trp Leu Ile
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Met Ala Thr Tyr Ser Thr Asp Trp Trp Asn Val Thr Gln Asp Ser Glu
            260             265                 270
Cys Ser Val Glu Glu Ile Ala Thr Ala Leu Glu Gly Ala Ile Leu Val
    275             280                 285
Asp Leu Leu Pro Leu Ser Thr Ser Gly Asp Ile Thr Val Ala Gly Ile
    290             295                 300
Thr Ala Asp Glu Tyr Leu Val Glu Tyr Asp Arg Leu Arg Gly Thr Glu
305             310                 315                 320
Tyr Ser Arg Phe His Gly Tyr Thr Tyr Asp Gly Ile Trp Ala Ala Ala
            325             330                 335
Leu Ala Ile Gln Tyr Val Ala Glu Lys Arg Glu Asp Leu Leu Thr His
            340             345                 350
Phe Asp Tyr Arg Val Lys Asp Trp Glu Ser Val Phe Leu Glu Ala Leu
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Arg Asn Thr Ser Phe Glu Gly Val Thr Gly Pro Val Arg Phe Tyr Asn
    370             375                 380
Asn Glu Arg Lys Ala Asn Ile Leu Ile Asn Gln Phe Gln Leu Gly Gln
385             390                 395                 400
Met Glu Lys Ile Gly Glu Tyr His Ser Gln Lys Ser His Leu Asp Leu
            405             410                 415
Ser Leu Gly Lys Pro Val Lys Trp Val Gly Lys Thr Pro Pro Lys Asp
            420             425                 430
Arg Thr Leu Ile Tyr Ile Glu His Ser Gln Val Asn Pro Thr Ile Tyr
            435             440                 445
Ile Val Ser Ala Ser Ala Ser Val Ile Gly Val Ile Ile Ala Thr Val
    450             455                 460
Phe Leu Ala Phe Asn Ile Lys Tyr Arg Asn Gln Arg Tyr Ile Lys Met
465             470                 475                 480
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84

SUBSTITUTE SHEET (RULE 26)

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Ser Ser Pro His Leu Asn Asn Leu Ile Ile Val Gly Cys Met Met Thr
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Tyr Leu Ser Ile Ile Phe Leu Gly Leu Asp Thr Thr Leu Ser Ser Val
            500                 505                 510
Ala Ala Phe Pro Tyr Ile Cys Thr Ala Arg Ala Trp Ile Leu Met Ala
        515                 520                 525
Gly Phe Ser Leu Ser Phe Gly Ala Met Phe Ser Lys Thr Trp Arg Val
    530                 535                 540
His Ser Ile Phe Thr Asp Leu Lys Leu Asn Lys Lys Val Ile Lys Asp
545                 550                 555                 560
Tyr Gln Leu Phe Met Val Val Gly Val Leu Leu Ala Ile Asp Ile Ala
                565                 570                 575
Ile Ile Thr Thr Trp Gln Ile Ala Asp Pro Phe Tyr Arg Glu Thr Lys
            580                 585                 590
Gln Leu Glu Pro Leu His His Glu Asn Ile Asp Asp Val Leu Val Ile
    595                 600                 605
Pro Glu Asn Glu Tyr Cys Gln Ser Glu His Met Thr Ile Phe Val Ser
    610                 615                 620
Ile Ile Tyr Ala Tyr Lys Gly Leu Leu Leu Val Phe Gly Ala Phe Leu
625                 630                 635                 640
Ala Trp Glu Thr Arg His Val Ser Ile Pro Ala Leu Asn Asp Ser Lys
            645                 650                 655
His Ile Gly Phe Ser Val Tyr Asn Val Phe Ile Thr Cys Leu Ala Gly
            660                 665                 670
Ala Ala Ile Ser Leu Val Leu Ser Asp Arg Lys Asp Leu Val Phe Val
        675                 680                 685
Leu Leu Ser Phe Phe Ile Ile Phe Cys Thr Thr Ala Thr Leu Cys Leu
    690                 695                 700
Val Phe Val Pro Lys Leu Val Glu Leu Lys Arg Asn Pro Gln Gly Val
705                 710                 715                 720
Val Asp Lys Arg Val Arg Ala Thr Leu Arg Pro Met Ser Lys Asn Gly
            725                 730                 735
Arg Arg Asp Ser Ser Val Cys Glu Leu Glu Gln Arg Leu Arg Asp Val
            740                 745                 750
Lys Asn Thr Asn Cys Arg Phe Arg Lys Ala Leu Met Glu Lys Glu Asn
    755                 760                 765
Glu Leu Gln Ala Leu Ile Arg Lys Leu Gly Pro Glu Ala Arg Lys Trp
    770                 775                 780
Ile Asp Gly Val Thr Cys Thr Gly Gly Ser Asn Val Gly Ser Glu Leu
785                 790                 795                 800
Glu Pro Ile Leu Asn Asp Asp Ile Val Arg Leu Ser Ala Pro Pro Val
            805                 810                 815
Arg Arg Glu Met Pro Ser Thr Thr Glu Val Thr Glu Met Thr Ser Val
        820                 825                 830
Asp Ser Val Thr Ser Thr His Val Glu Met Asp Asn Ser Phe Val Ser
        835                 840                 845
Val Gln Ser Thr Val Met Ala Pro Ser Leu Pro Pro Lys Lys Lys Lys
    850                 855                 860
Gln Ser Ile Val Glu His His Ser His Ala Pro Ala Pro Thr Met Met
865                 870                 875                 880
Gln Pro Ile Gln Gln Gln Leu Gln Gln His Leu Gln Gln His Gln Gln
            885                 890                 895
Met Gln Gln Gln His Leu Gln Gln Gln Gln His Gln Gln Met Gln Gln
            900                 905                 910
Gln Gln Gln Gln Gln Gln His His His Arg His Leu Glu Lys Arg Asn
            915                 920                 925
Ser Val Ser Ala Gln Thr Asp Asp Asn Ile Gly Ser Ile Thr Ser Thr
    930                 935                 940
Ala Gly Lys Arg Ser Gly Gly Asp Cys Ser Ser Met Arg Glu Arg Arg
945                 950                 955                 960
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85

SUBSTITUTE SHEET (RULE 26)

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Gln Ser Thr Ala Ser Arg His Tyr Asp Ser Gly Ser Gln Thr Pro Thr
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Ala Arg Pro Lys Tyr Ser Ser Ser His Arg Asn Ser Ser Thr Asn Ile
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Ser Thr Ser Gln Ser Glu Leu Ser Asn Met Cys Pro His Ser Lys Pro
            995                 1000                1005
Ser Thr Pro Ala Val Ile Lys Thr Pro Thr Ala Ser Asp His Arg Arg
        1010                1015                1020
Thr Ser Met Gly Ser Ala Leu Lys Ser Asn Phe Val Val Ser Gln Ser
1025                1030                1035                1040
Asp Leu Trp Asp Thr His Thr Leu Ser His Ala Lys Gln Arg Gln Ser
                1045                1050                1055
Pro Arg Asn Tyr Ala Ser Pro Gln Arg Cys Ala Glu His His Gly Gly
            1060                1065                1070
His Gly Met Thr Tyr Asp Pro Asn Thr Thr Ser Pro Ile Gln Arg Ser
            1075                1080                1085
Val Ser Glu Lys Asn Arg Asn Lys His Arg Pro Lys Pro Gln Lys Gly
            1090                1095                1100
Thr Val Cys Gln Ser Glu Thr Asp Ser Glu Arg Glu Arg Asp Pro Pro
1105                1110                1115                1120
Pro Asn Ser Gln Pro Cys Val Gln Pro Arg Lys Val Ser Arg Ser Ser
            1125                1130                1135
Asn Ile Gln His Ala Ala His His His Ser Ser Pro Asn Val Ala Pro
            1140                1145                1150
Asp Lys Gln Arg Ser Arg Gln Arg Gly Lys Gln Asp Ser Ser Ile Tyr
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Gly Ala Ser Ser Glu Thr Glu Leu Leu Glu Gly Glu Thr Ala Ile Leu
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Pro Ile Phe Arg Lys Leu Leu Thr Glu Lys Ser Pro Asn Tyr Arg Gly
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<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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tcaaaaatgg ttgtcagacg gagcttatgg agtggcagac actccgaggt ccaaaactaa 18900
attaagaaac ccaatcgggt gccaaaatcc aattttaagt agacgaaagt agctggaaat 18960
```

91

gccaatcgga tatattcggg cgggattagc attgtg   18996

<210> 62
<211> 2250
<212> DNA
<213> Drosophila

<400> 62
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gacacacatc gcggaacccg aactccatac ggctgtgccg acactcaatc ccgacctaag 120
cccaattttt tgttgcgtga agttgacgaa gtgtgttgta ctgctgcaag tgcaagtccc 180
cgattgctag tgctattccg ggatcacaaa cgagcatcct tcttcggcct cacgattgac 240
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tgctattcgg ccatccttct gtgcgccgtg gtcgggaacc tgctggtggt gctaacgctc 600
gtccagaatc gtcgcatgcg caccatcacg aacgtttttc tgctcaacct ggccatctcg 660
gacatcctgc tcggcgtatt ctgcatgccg gtgaccctgg tcggcactct gctaaggcat 720
ttcatattcg gcgagctgct ctgcaagctc atccagtttg ctcaggtccc tatccccgtg 780
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ggctatacct ccatcagttt cctccagctg ctggcctact catccagctg ctgcaatccg 2040
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cacacgatcc tcgagagtcc gcgactctga   2250

<210> 63
<211> 749
<212> PRT
<213> Drosophila

<400> 63
Met Leu Pro Arg Leu Cys Ala Asp Ala Cys Arg Gln Cys Phe Ala Lys
1   5   10   15
Ile Ala Arg Arg Asp Thr His Arg Gly Thr Arg Thr Pro Tyr Gly Cys
            20   25   30
Ala Asp Thr Gln Ser Arg Pro Lys Pro Asn Phe Leu Leu Arg Glu Val

SUBSTITUTE SHEET (RULE 26)

```
                35                      40                      45
Asp Glu Val Cys Cys Thr Ala Ala Ser Ala Ser Pro Arg Leu Leu Val
    50                      55                      60
Leu Phe Arg Asp His Lys Arg Ala Ser Phe Phe Gly Leu Thr Ile Asp
65                      70                      75                      80
Ala Phe Tyr His Tyr Leu Arg Gln Ala Leu Pro Leu Ala Lys Glu Ala
                85                      90                      95
Ala Ile His Leu Asn Ala Ser Asn Glu Ile Ser Ala Val Gly Asp Gly
                100                     105                     110
Val Thr Ile Thr Gly Thr Pro Gly Asp Leu Leu Asn Tyr Ser Gly Leu
                115                     120                     125
Glu Leu Asp Leu Gly Leu Asp Leu Asp Leu Asn Leu Asp Met Asp Leu
    130                     135                     140
Ala Thr Thr Pro Ser Ser Ser Thr Leu Ala Pro Ala Val Thr Val Arg
145                     150                     155                     160
Thr Pro Gly Asn Arg Ser Val Val Arg Val Ser Ala Asp Val Pro Ile
                165                     170                     175
Trp Val Val Pro Cys Tyr Ser Ala Ile Leu Leu Cys Ala Val Val Gly
                180                     185                     190
Asn Leu Leu Val Val Leu Thr Leu Val Gln Asn Arg Arg Met Arg Thr
                195                     200                     205
Ile Thr Asn Val Phe Leu Leu Asn Leu Ala Ile Ser Asp Ile Leu Leu
    210                     215                     220
Gly Val Phe Cys Met Pro Val Thr Leu Val Gly Thr Leu Leu Arg His
225                     230                     235                     240
Phe Ile Phe Gly Glu Leu Leu Cys Lys Leu Ile Gln Phe Ala Gln Val
                245                     250                     255
Pro Ile Pro Val Thr Glu Pro His Asn Arg Leu Ser Asn Gly His Glu
                260                     265                     270
Pro Ala Arg Pro Arg Ala Asp Ser Pro Ala Asp Arg Val Gly Gln His
    275                     280                     285
Ser Gly Ala Asp Lys Glu Asp Asp Thr Ser Leu Leu Arg Arg Met Tyr
    290                     295                     300
Arg Tyr Ala Gly Asn Gly Val Ala Leu His Gly Ala Arg Leu Pro Gly
305                     310                     315                     320
Gln Leu Tyr Gly Ser Ile His Gly Leu Gly Ser Ala Ala Ser Val Ala
                325                     330                     335
Val Ser Ser Trp Thr Leu Val Ala Ile Ser Cys Glu Arg Tyr Tyr Ala
                340                     345                     350
Ile Cys His Pro Leu Arg Ser Arg Thr Trp Gln Thr Ile Asn His Ala
                355                     360                     365
Asn Lys Ile Ile Ala Ile Ile Trp Leu Gly Ser Leu Val Cys Met Thr
    370                     375                     380
Pro Ile Ala Ala Phe Ser Gln Leu Met Pro Thr Ser Arg Pro Gly Leu
385                     390                     395                     400
Arg Lys Cys Arg Glu Gln Trp Pro Ala Asp Ser Leu Asn Tyr Glu Arg
                405                     410                     415
Ala Tyr Asn Leu Phe Leu Asp Leu Ala Leu Leu Val Leu Pro Leu Leu
                420                     425                     430
Ala Leu Ser Phe Thr Tyr Leu Phe Ile Thr Arg Thr Leu Tyr Val Ser
    435                     440                     445
Met Arg Asn Glu Arg Ala Met Asn Phe Gly Ser Ser Gly Pro Glu Val
    450                     455                     460
Thr Thr Ser Ser Ser Ala Ala Val Ala Glu Ala Gly Ser Gln Arg Arg
465                     470                     475                     480
Ala Asn Gly Ser His Cys Gln Ser Leu Asp Thr Ile Val Pro His Gln
                485                     490                     495
His Asn Pro His Gln Gln His His His His Ser Gln Tyr Tyr Tyr Asp
                500                     505                     510
Tyr Gly His Cys Gly Ser Lys Arg Arg Leu Ile Ser Gly Gly Gly Pro
```

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SUBSTITUTE SHEET (RULE 26)

```
             515                     520                     525
Cys Glu Gly Arg Arg His Leu Tyr Cys Met Arg Ser Ala Ser Val Lys
    530                     535                     540
Ser Leu Arg His Gln Gln Ile Asn Gly Gly Gly Gly Thr Leu Ser Gly
545                     550                     555                     560
Thr Gly Ala Gly Asn Gly Glu Cys Cys Ser Arg Val His Arg Met Arg
                565                     570                     575
Gln Gln Met Gln Leu Gln Gln Gln Gly Tyr Val Ser Asp Asn Glu Ser
                580                     585                     590
Arg Arg Lys Ser Leu Ser Gln Pro Ser Leu Arg Ile Thr Glu Ala Gly
                595                     600                     605
Leu Arg Arg Ser Asn Glu Thr Lys Ser Leu Glu Ser Lys Lys Arg Val
    610                     615                     620
Val Lys Met Leu Phe Val Leu Val Leu Glu Phe Phe Ile Cys Trp Thr
625                     630                     635                     640
Pro Leu Tyr Val Ile Asn Thr Met Thr Met Leu Leu Gly Pro Thr Val
                645                     650                     655
Tyr Glu Tyr Val Gly Tyr Thr Ser Ile Ser Phe Leu Gln Leu Leu Ala
                660                     665                     670
Tyr Ser Ser Ser Cys Cys Asn Pro Ile Thr Tyr Cys Phe Met Asn Ala
    675                     680                     685
Ser Phe Arg Arg Ala Phe Val Asp Thr Phe Lys Gly Met Arg Val Cys
    690                     695                     700
Glu Arg Leu Cys Ala Pro Cys Cys Phe Trp Arg Arg Arg Ser Lys Asn
705                     710                     715                     720
Glu Thr Asn Leu Ser Val Ala Gly Asn Ser Ile Ala Leu Ala Asn Ser
                725                     730                     735
Val Met Ser Ser His Thr Ile Leu Glu Ser Pro Arg Leu
                740                     745
```

```
<210> 64
<211> 4289
<212> DNA
<213> Drosophila

<400> 64
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tccattaaag aagccaccaa ctttaagata cacgcatata acaactcctg agaattgtga 120
aaactgatct actttgatga tcaactttca ttgctgctga ttgaataatt gagtaatgag 180
taattggtat gctgataaac aggaaaacca aaatgtcaac agttgataag gaacattaaa 240
acacaaatta agaggacggt aagtccttca ctcggacctt ttcagctgag caccgtaaag 300
tgctgaaggg attgccccca cacccagacc gcgcccactt ccacttccac tttaaaataa 360
tcatcatggc cctctttttt ggccaggctg cggtggcttt gggccttaat tgtcgactca 420
gttgctgtgc tgtgctgtgt actcgacaag gcgacgaacc gagagccttg cagctccata 480
atgacaggcg gatggactcg aacactcgga cccggacccg gacccgaacc cggacccagt 540
ccacagccag gacataagcg gcttgtgctc cactcaactg tcgcctttcg gagctgctcc 600
tagcttgcaa ttaaaatacc cacttgggcc ctataaattg tgaacgtagg aaggcaggcg 660
gaaaaaaaaa aaaatattcc agcactttgg tgtatggagt ggggtccact taattcccag 720
gtactcaccc aaaaggattc caactataaa gacatacagc gagagtgctt aagtttttact 780
ctgtttattt gcagcaacct taggaagttc aattgaaaca ccaatagact agcgtctgag 840
ttattttacg agtacgatca taatcacaag taggtaaaaa aaatccatat tcgccttact 900
taaaacaaaa aaaaaaacca cacgcagatc gcttatcata catatttaca ccgcatctcg 960
ttgatcctga atgggtcctt ggaggcgaat cctctacagc ttagagctga ggactgttga 1020
cggcggcggc ggcactattg gtggtcacca ccgcattgag aaactcgtgg cgtgagcgac 1080
tccgccaggt gcccataccc atggctaggc cgggattgag actaatgttg gtgttggcac 1140
tcgcataggc gcccgggcct gcgcccgcct ggctggcgga gagtcctcca ccagcagcac 1200
caccgacgcc tccgctggca cctgctccac gacgccaggg cagacccttg aaggtgtcga 1260
caaaggcgcg ccggaagctg gcgttcatga agcagtaggt gatcggattg cagcagctgg 1320
atgagtaggc cagcagctgg aggaaactga tggccgtgta gtcgacatac tcgtacacca 1380
```

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SUBSTITUTE SHEET (RULE 26)

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ccggtccgat cagcatgacc atcgtgttga tcacgtacag cggagtccag cagatgaaaa 1440
actccagcac caggacgaac agcatcttga ccacacgctt cttgctctcc agggtcttgg 1500
cctcgttgga cctggatagt ggattgtgga ttgtggagaa atgggaatag ggaataggat 1560
tggcagaccg gttatcggac acgaatccta cctgcgaagt gccgcatcgt ggacgcgaat 1620
gctgggcgag gaggtcttgg ccagcgtcac cgtggtcgtc gtggtggtgg tgatcacagt 1680
tggagccgtt ggtctcgttg tcaaggtggt cgttgccata ttggttgatc ctccgcctgc 1740
ggatccctct gaatttccat tattattgtt actattttct atgtgaaaaa aaaaaaacat 1800
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gttgccataa ctaatctaaa ctaatacata gacgtaaaat aattaaattt tcaatttggt 1920
tttaagagtc tcaaaaataa tatagcatat tatgttaagt ggatttgtac cttcttatcg 1980
agcatttcac caacaatcta tatctttaaa gtattatgcc atattacatg tcatgtaaca 2040
ttaaataact tatgagttat gatatttaga tgcaaaataa tacttgaatg cattcataaa 2100
tgctcttaaa gttgtttgca tattcatggc ttttaaggat tgaaaaagga ttagtttcgt 2160
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caaataaata tgataaactg atcaaatgaa agcataattt gcttgtatgt atgcgtgttt 3360
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gaaattgttg tgctagcaga tacatttgtg gtttgttaga tatacatatt tgcttataaa 3540
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ttttgattga cggcggtgtg tgatgctcta agccagaaat gctagcatgt gtgcgcttaa 4260
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```

```
<210> 65
<211> 1248
<212> DNA
<213> Drosophila
```

```
<400> 65
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gccatatcct gtgagcgcta ctacgcgata tgccatccac tgcgctcgcg atcctggcag 120
acaatcagtc acgcctacaa gatcatcggc ttcatctggc tgggcggcat cctctgcatg 180
acgcccatag cggtctttag tcaattgata cccaccagtc gaccgggcta ctgcaagtgc 240
```

```
cgtgagtttt ggcccgacca gggatacgag ctcttctaca acatcctgct ggacttcctg 300
ctgctcgtcc tgccgcttct cgtcctctgc gtggcctaca tcctcatcac gcgtaccctg 360
tacgtaggca tggccaagga cagcggacgc atcctgcagc aatcgctgcc tgtttccgct 420
acaacggccg gcggaagcgc accgaatccg ggcaccagca gcagtagtaa ctgcatcctg 480
gtcctgaccg ccaccgcagt ctataatggt tggcggagga tcaaccaata tggcaacgac 540
caccttgaca acgagaccaa cggctccaac tgtgatcacc accaccacga cgaccacggt 600
gacgctggcc aagacctcct cgcccagcat tcgcgtccac gatgcggcac ttcgcaggta 660
ggattcgtgt ccgataaccg gtctgccaat cctattccct attcccattt ctccacaatc 720
cacaatccac tatccaggtc caacgaggcc aagaccctgg agagcaagaa gcgtgtggtc 780
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gtgaccacca atagtgccgc cgccgccgtc aacagtcctc agctctaa            1248
```

<210> 66
<211> 415
<212> PRT
<213> Drosophila

<400> 66

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Met His Ser Asn Gly Thr Gly Gly Ala Ala Ser Val Ala Val Ser Ser
1               5                   10                  15
Trp Thr Leu Val Ala Ile Ser Cys Glu Arg Tyr Tyr Ala Ile Cys His
            20                  25                  30
Pro Leu Arg Ser Arg Ser Trp Gln Thr Ile Ser His Ala Tyr Lys Ile
            35                  40                  45
Ile Gly Phe Ile Trp Leu Gly Gly Ile Leu Cys Met Thr Pro Ile Ala
        50                  55                  60
Val Phe Ser Gln Leu Ile Pro Thr Ser Arg Pro Gly Tyr Cys Lys Cys
65                  70                  75                  80
Arg Glu Phe Trp Pro Asp Gln Gly Tyr Glu Leu Phe Tyr Asn Ile Leu
                85                  90                  95
Leu Asp Phe Leu Leu Leu Val Leu Pro Leu Leu Val Leu Cys Val Ala
            100                 105                 110
Tyr Ile Leu Ile Thr Arg Thr Leu Tyr Val Gly Met Ala Lys Asp Ser
            115                 120                 125
Gly Arg Ile Leu Gln Gln Ser Leu Pro Val Ser Ala Thr Thr Ala Gly
        130                 135                 140
Gly Ser Ala Pro Asn Pro Gly Thr Ser Ser Ser Ser Asn Cys Ile Leu
145                 150                 155                 160
Val Leu Thr Ala Thr Ala Val Tyr Asn Gly Trp Arg Arg Ile Asn Gln
            165                 170                 175
Tyr Gly Asn Asp His Leu Asp Asn Glu Thr Asn Gly Ser Asn Cys Asp
            180                 185                 190
His His His His Asp Asp His Gly Asp Ala Gly Gln Asp Leu Leu Ala
            195                 200                 205
Gln His Ser Arg Pro Arg Cys Gly Thr Ser Gln Val Gly Phe Val Ser
        210                 215                 220
Asp Asn Arg Ser Ala Asn Pro Ile Pro Tyr Ser His Phe Ser Thr Ile
225                 230                 235                 240
His Asn Pro Leu Ser Arg Ser Asn Glu Ala Lys Thr Leu Glu Ser Lys
            245                 250                 255
Lys Arg Val Val Lys Met Leu Phe Val Leu Val Leu Glu Phe Phe Ile
            260                 265                 270
Cys Trp Thr Pro Leu Tyr Val Ile Asn Thr Met Val Met Leu Ile Gly
        275                 280                 285
```

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SUBSTITUTE SHEET (RULE 26)

```
Pro Val Val Tyr Glu Tyr Val Asp Tyr Thr Ala Ile Ser Phe Leu Gln
    290                 295                 300
Leu Leu Ala Tyr Ser Ser Ser Cys Cys Asn Pro Ile Thr Tyr Cys Phe
305                 310                 315                 320
Met Asn Ala Ser Phe Arg Arg Ala Phe Val Asp Thr Phe Lys Gly Leu
                325                 330                 335
Pro Trp Arg Arg Gly Ala Gly Ala Ser Gly Gly Val Gly Gly Ala Ala
            340                 345                 350
Gly Gly Gly Leu Ser Ala Ser Gln Ala Gly Ala Gly Pro Gly Ala Tyr
        355                 360                 365
Ala Ser Ala Asn Thr Asn Ile Ser Leu Asn Pro Gly Leu Ala Met Gly
    370                 375                 380
Met Gly Thr Trp Arg Ser Arg Ser Arg His Glu Phe Leu Asn Ala Val
385                 390                 395                 400
Val Thr Thr Asn Ser Ala Ala Ala Ala Val Asn Ser Pro Gln Leu
                405                 410                 415
```

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<210> 67
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97

SUBSTITUTE SHEET (RULE 26)

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99

SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

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Ser Ala Val Gly Ser Gly Ser Ser Ile Ala Val Ser Val Glu Asp Val
65   70   75   80
Val Ala Gly Gln Ala Gln Asp Ile Gln Ala Ser Glu Gly Ser Thr Asp
                85   90   95
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100

SUBSTITUTE SHEET (RULE 26)

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<210> 71

SUBSTITUTE SHEET (RULE 26)

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<212> DNA
<213> Drosophila

<400> 71
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tccatgcaga tgtggccaat ataccactat gctggcagct ctgataagct agtgttactg 180
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cgcaaaatct taaacccaat tttccatggc atctcgcttg ttatcctgct ggtcatcgcc 480
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<210> 72
<211> 423
<212> PRT
<213> Drosophila

<400> 72
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Phe Thr Ser Tyr Gly Gly Glu Gln Asn Arg Pro Val Lys Phe Lys Phe
                20                  25                  30
Val Ile Gly Ile Pro Asn Cys Gly Ser Met Gln Met Trp Pro Ile Tyr
        35                  40                  45
His Tyr Ala Gly Ser Ser Asp Lys Leu Val Leu Leu Asp Asp Gly Arg
    50                  55                  60
Leu Arg His Tyr Thr Asn Ala Glu Asn Glu Ala Glu Glu Arg His Gly
65                  70                  75                  80
Ile Gln Ser Asp Tyr Glu Glu Asp Ile Ala Gly Ser Leu Glu Pro Leu
                85                  90                  95
Tyr His Asp Tyr Asp Lys Gly Leu Tyr Cys Ile Asp Lys Ala Thr Ser
                100                 105                 110
Ser Thr Gly Glu Glu Asn Val Leu Phe Ala Asn Ile Cys Leu Ala Arg
            115                 120                 125
Lys Glu Ile Lys Trp Ser Asp Ser Asn Phe Leu Leu Arg Lys Ile Leu
        130                 135                 140
Asn Pro Ile Phe His Gly Ile Ser Leu Val Ile Leu Leu Val Ile Ala
145                 150                 155                 160
Ile Ile Tyr Phe Ile Leu Pro Thr Leu Ser Arg Asp Leu Val Gly Asn
                165                 170                 175
Ile Val Thr Thr Ile Ala Met Cys Leu Met Val Ser Gln Ala Ala Asp
                180                 185                 190
Leu Val Arg Ile Phe Thr Glu Leu Thr Ser His Val Ser Phe Ile Val
            195                 200                 205
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SUBSTITUTE SHEET (RULE 26)

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Ala Asp Ile Ile Leu Cys Phe Ser Leu Leu Ala Ala Phe Phe Trp Leu
    210                 215                 220
Asn Ser Phe Gly Phe Tyr Ile Trp Lys Thr Phe Arg Ser Arg Asn Val
225                 230                 235                 240
Phe Leu Arg Val Thr Asp Gly Arg Lys Tyr Cys Tyr Tyr Ser Ala Tyr
            245                 250                 255
Ala Trp Gly Cys Thr Ala Thr Met Ala Ala Leu Ala Val Phe Ala His
            260                 265                 270
Phe Phe Leu Asp Ala Glu Ser Tyr Lys Gln Glu His Met Val Gly Glu
        275                 280                 285
Gln Glu Thr Ile Gly Trp Leu Gly Ile Cys Ile Phe Phe Ala Pro Ile
    290                 295                 300
Ala Cys Thr Ile Leu Val Asn Ile Phe Phe Tyr Val Thr Thr Arg Lys
305                 310                 315                 320
Leu Ile Asn Arg Arg Thr Val Tyr Gly Arg Ile Ala His Lys Leu Lys
            325                 330                 335
Ala Asn Phe Ile Met Phe Ser Leu Met Leu Leu Val Met Ser Ile Ala
            340                 345                 350
Trp Leu Phe Leu Ile Met Ser Trp Leu Gln Met Glu Gly Leu Leu Tyr
        355                 360                 365
Ala His Ile Val Val Asn Ala Leu Gln Thr Pro Leu Leu Leu Tyr Ile
    370                 375                 380
Cys Val Leu Arg Gln Arg His Val Thr Phe Leu Leu Lys Lys Thr Cys
385                 390                 395                 400
Cys Tyr Asn Glu Pro Pro Ser Ala Asn Asp Trp Gly Asp Glu Leu His
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Tyr Met Asn Gly Asn Asp Tyr
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<210> 73
<211> 5299
<212> DNA
<213> Drosophila

<400> 73
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tcaactgctg ctaactggca actggagatt tggcgattgc agctgcccat tgtcaacact 180
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104

SUBSTITUTE SHEET (RULE 26)

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<211> 1467
<212> DNA
<213> Drosophila

<400> 74
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<210> 75
<211> 488
<212> PRT
<213> Drosophila

<400> 75
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            20                  25                  30
Thr Pro Pro Ile Val Trp Leu Ser Gly Asn Leu Leu Phe Gln Leu Val
        35                  40                  45
Leu His Leu Ala Ala Phe Leu His Cys Pro Pro Lys Trp Phe Gly Leu
    50                  55                  60
Ile Ser Lys Cys Val Glu Cys Pro Thr Glu Ser Thr Pro Phe Ala Ile
65                  70                  75                  80
Leu Phe Asp Ile Leu Asp Gly Ile Phe Arg Lys Arg Met Arg Cys Thr
                85                  90                  95
Thr Asn Ile Tyr Leu Thr Ala Leu Ala Ile Thr Asp Ile Ala Tyr Leu
            100                 105                 110
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SUBSTITUTE SHEET (RULE 26)

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Thr Cys Gln Leu Ile Leu Ser Leu Gln His Tyr Asp Tyr Pro Lys Tyr
        115                 120                 125
His Phe Lys Leu Tyr Trp Gln Leu Tyr Gly Tyr Phe Val Trp Leu Cys
        130                 135                 140
Asp Ser Phe Gly Tyr Ile Ser Ile Tyr Ile Ala Val Cys Phe Thr Ile
145                 150                 155                 160
Glu Arg Phe Ile Ala Ile Arg Tyr Pro Leu Lys Arg Gln Thr Phe Cys
                165                 170                 175
Thr Glu Ser Leu Ala Lys Lys Val Ile Ala Ala Val Ala Ile Phe Cys
        180                 185                 190
Leu Leu Ser Thr Leu Ser Thr Ala Phe Glu His Thr Ile Thr Ile Gly
        195                 200                 205
Thr Arg Gln Ile Asp Asp Ala Tyr Gln Pro Cys Asn Gln Thr Val Ala
210                 215                 220
Asn Ile Ser Pro Met Pro Pro Pro Val Ala Val Thr Pro Pro Leu
225                 230                 235                 240
Ala Thr Pro Pro Leu Pro Thr Pro Ala Thr Ile Trp Gln Ser Pro Asp
                245                 250                 255
Ser Ala Met Glu Ser Thr Thr Ser Gly Ser Ser Asn Gln Leu Val Asp
        260                 265                 270
Trp Gly Ser Gly Ser Gly Asp Gly Glu Pro Glu Asn Ile Pro Arg His
        275                 280                 285
Arg Arg His Trp Gln Ser Ser Gly Phe Val Thr Leu Pro Thr Leu Arg
        290                 295                 300
Lys Thr Leu Glu Glu Gln Asp Gln Lys Val Ala Asp Ala Ala Gln Arg
305                 310                 315                 320
Ser Gly Val Thr Glu Ser Leu Leu Gln Leu Trp Arg Arg Lys Arg Ser
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Thr Glu Tyr Cys Gln Asn Val Thr Tyr Tyr Asn His Gly Leu Ser Glu
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Leu Gly Tyr Asp Glu Leu Tyr Ser Tyr Leu Trp Asn Leu Phe Thr Leu
        370                 375                 380
Leu Val Phe Val Val Phe Pro Leu Leu Leu Leu Ala Thr Phe Asn Ser
385                 390                 395                 400
Ile Leu Ile Leu Leu Val His Arg Ser Lys Asn Leu Arg Gly Asp Leu
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Thr Asn Ala Ser Ser Ile Arg Arg Thr Lys Tyr Arg Lys Thr Val Arg
        420                 425                 430
Glu Leu Ile Thr Gly Tyr Arg Tyr Arg Arg Arg His Ala Arg Asn Asn
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<211> 3946
<212> DNA
<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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108

SUBSTITUTE SHEET (RULE 26)

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<212> DNA
<213> Drosophila

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<211> 583
<212> PRT
<213> Drosophila

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Asn Ile Trp Arg Arg Val Arg Leu Val Thr Ser Gln Glu Ser Asp Arg
            35   40   45
Asn Ala Tyr Gln Val Leu Lys Pro Ser Ser Arg Asn Ala Thr Ser Thr
        50   55   60
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65   70   75   80
Thr Thr Thr Pro Ala Ala Pro Gln Thr Gln Arg Ser Ala Lys Gln Leu

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Asp Leu Asn Phe Pro Gly Gly Asn Val Ser Ser Ala Ala Arg Leu Glu
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            115                   120                   125
Ser Ser Thr Thr Ser Thr Thr Thr Pro Ala Thr Pro Arg Arg Ser Ser
            130                   135                   140
Gly Ala Lys Ala Arg Ala Ala Gly Thr Thr Gly Arg Val Thr Pro Gly
145                   150                   155                   160
Ser Ser Ser Asn Ser Thr Pro Pro Ser Ile Val Ser Thr His Leu Pro
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Phe Ala Gly Leu Arg Lys Glu Pro Trp Val Val Pro Val Leu Val Leu
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Ala Thr Leu Thr Met Leu Met Met Ala Ala Phe Glu Ile Phe Val Leu
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Phe Lys Ala Trp Arg Thr Ser Pro Ser Arg Arg His Leu Phe Leu Gly
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Gln Met Leu Leu Leu Gly Leu Phe Ala Cys Ala Ser Leu Gly Ala Ile
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Val Phe Leu Ile Ser Leu Asn Gly Gly Val Tyr Leu Pro Ala Pro Tyr
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Gln Gly Leu Leu Leu Leu Phe Ala Leu Leu Ile Gln Val Ala Ile Gly
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Gly Gln Trp Leu Leu Thr Gln Pro Pro Glu Val Tyr Thr Thr Ser Val
305                   310                   315                   320
Pro Val Met Gly Ser Gly Phe Leu Ser Thr Thr Val Ala Ser Gln Thr
                325                   330                   335
Asn Tyr Ser Ala Leu Phe Tyr Pro Thr Ser Tyr Thr Thr Leu Asp Gly
                340                   345                   350
Thr Pro Glu Ile Tyr Thr Arg Ile Ala Ala Val Ser Thr Val Leu Ile
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Pro Leu Cys Lys Thr Gln Phe Ser Glu Leu Leu Phe Ser Leu Ile Tyr
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Ile Val Phe Leu Ile Val Phe Ile Ala Val Leu Ala Ile Lys Ser Arg
385                   390                   395                   400
Gly Ile Arg Asp Asn Tyr Arg Glu Ala Thr Tyr Ile Gly Leu Ala Ile
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Gly Gly Ala Ile Pro Ile Trp Leu Gly Trp Met Leu Cys Gly Leu Ala
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Val Ala Glu Arg His Lys Asp Ala Cys Val Ala Phe Gly Leu Val Ala
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Thr Ser Ala Thr Val Phe Leu Val Met Phe Met Pro Lys Gly Arg Gln
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465                   470                   475                   480
Gln Phe Ser Ser Leu Ser Arg Ala Gly Ser Gly Tyr Ser Pro Ser Phe
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Phe His Phe Lys Pro Ile Lys Tyr Gly Val Met Ser Gly Cys Gly Leu
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Pro Asn Ser Ala Ser Asn Thr Gly Gln Gly Leu Ser Ser Lys His Cys
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Ser Ser Ala Asn Asn Gly Gly Gly Lys Ser Arg Ser Tyr Glu Leu Phe
    530                   535                   540
Pro Ser Lys Phe Val Thr Phe Ser Ala Arg Gly Gly Arg Thr Gln Leu
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Lys Leu Asp Thr Val Pro Phe Arg Pro His Ser Ser Ala Leu Val Ser
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SUBSTITUTE SHEET (RULE 26)

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<211> 3524
<212> DNA
<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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<211> 1356
<212> DNA
<213> Drosophila
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<210> 81
<211> 451
<212> PRT
<213> Drosophila
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1               5                   10                  15
Glu Ser Leu Tyr Thr Thr Glu Leu Asn His Arg Trp Ile Ser Gly Ser
            20                  25                  30
Ser Thr Ile Gln Pro Glu Glu Ser Leu Tyr Gly Thr Asp Leu Pro Thr
            35                  40                  45
Tyr Gln His Cys Ile Ala Thr Arg Asn Ser Phe Ala Asp Leu Phe Thr
        50                  55                  60
Val Val Leu Tyr Gly Phe Val Cys Ile Ile Gly Leu Phe Gly Asn Thr
65                  70                  75                  80
Leu Val Ile Tyr Val Val Leu Arg Phe Ser Lys Met Gln Thr Val Thr
                    85                  90                  95
Asn Ile Tyr Ile Leu Asn Leu Ala Val Ala Asp Glu Cys Phe Leu Ile
```

SUBSTITUTE SHEET (RULE 26)

```
                    100                    105                    110
Gly Ile Pro Phe Leu Leu Tyr Thr Met Arg Ile Cys Ser Trp Arg Phe
        115                    120                    125
Gly Glu Phe Met Cys Lys Ala Tyr Met Val Ser Thr Ser Ile Thr Ser
    130                    135                    140
Phe Thr Ser Ser Ile Phe Leu Leu Ile Met Ser Ala Asp Arg Tyr Ile
145                    150                    155                    160
Ala Val Cys His Pro Ile Ser Ser Pro Arg Tyr Arg Thr Leu His Ile
            165                    170                    175
Ala Lys Val Val Ser Ala Ile Ala Trp Ser Thr Ser Ala Val Leu Met
            180                    185                    190
Leu Pro Val Ile Leu Tyr Ala Ser Thr Val Glu Gln Glu Asp Gly Ile
    195                    200                    205
Asn Tyr Ser Cys Asn Ile Met Trp Pro Asp Ala Tyr Lys Lys His Ser
    210                    215                    220
Gly Thr Thr Phe Ile Leu Tyr Thr Phe Phe Leu Gly Phe Ala Thr Pro
225                    230                    235                    240
Leu Cys Phe Ile Leu Ser Phe Tyr Tyr Leu Val Ile Arg Lys Leu Arg
            245                    250                    255
Ser Val Gly Pro Lys Pro Gly Thr Lys Ser Lys Glu Lys Arg Arg Ala
            260                    265                    270
His Arg Lys Val Thr Arg Leu Val Leu Thr Val Ala Leu Ile His Ser
    275                    280                    285
Asn Pro Ala Gln Arg Asp Leu Ser Arg Leu Glu Ile Leu Ile Phe Leu
    290                    295                    300
Leu Leu Gly Ala Leu Val Tyr Ser Asn Ser Ala Val Asn Pro Ile Leu
305                    310                    315       .            320
Tyr Ala Phe Leu Ser Glu Asn Phe Arg Lys Ser Phe Phe Lys Ala Phe
            325                    330                    335
Thr Cys Met Asn Lys Gln Asp Ile Asn Ala Gln Leu Gln Leu Glu Pro
            340                    345                    350
Ser Val Phe Thr Lys Gln Gly Ser Lys Lys Arg Gly Gly Ser Lys Arg
            355                    360                    365
Leu Leu Thr Ser Asn Pro Gln Ile Pro Pro Leu Leu Pro Leu Asn Ala
    370                    375                    380
Gly Asn Asn Asn Ser Ser Thr Thr Thr Ser Ser Thr Thr Thr Ala Glu
385                    390                    395                    400
Lys Thr Gly Thr Thr Gly Thr Gln Lys Ser Cys Asn Ser Asn Gly Lys
            405                    410                    415
Val Thr Ala Pro Pro Glu Asn Leu Ile Ile Cys Leu Ser Glu Gln Gln
            420                    425                    430
Glu Ala Phe Cys Thr Thr Ala Arg Arg Gly Ser Gly Ala Val Gln Gln
            435                    440                    445
Thr Asp Leu
    450
```

<210> 82
<211> 7448
<212> DNA
<213> Drosophila

<400> 82
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gttgtcttga cggcccggca aaaagcaaca tccaaggaaa atgttgccat tttagatgcg 180
ccgcccgctg agcggaaaag tcgcgcggaa attactaaat cgatacgtgc tgcgtatcag 240
attttccatg ggttctgcat gcaaaaatac cttgaaatcc ttgcctgcag tcgcacacat 300
acacgtattg ccatctttgt acagacaagc ttgactaagt cgaactttac tatgttattc 360
tactaaaagg ttttaaagca aatgatctat actatactat actattaact tcaatagaat 420
```

```
tcctattttc tctggctagc aaacaaattt ggatcataaa aagattttca tggcatttat 480
gagatacgta gattgtgtgg ctcaaccttt tatctatatt atttccataa atttaagcac 540
caatggaaat gtttatctcc aaagcttagg aaaatttgga agtatatata ataaaaacct 600
tttatgtctg caaataagag atattacgtg tatactgagt ttcgcttgag tttcggagtt 660
aagaggcttc cctatagact gtttgaaaat cctataatgc cttggcattt ctaaaaggtc 720
aactgaaagc agtggaattg ctggtgggcg aggttcgtct cctaagtggc aaaatgatcc 780
agaatcggaa gcaaaccctg acgatgaaat aaactatacg agaaactgga gaacaattac 840
acatggactg tgggtgcaat tagggaccac acctttttcg ctgccgacgc gtctaaagtt 900
aatgaatatg ttaataatat gttatgcgcg tgcaaatttg ttcagggctt gaggggtttt 960
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catacccaaa tgccatgcgg ccattgttct atcaactgca cgatgtgcta atctctctaa 2220
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```

SUBSTITUTE SHEET (RULE 26)

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caaagtggcg aaatgtatta ccaataaatt tgccaaggga atggctacat tttgggaata 7440
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```

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SUBSTITUTE SHEET (RULE 26)

```
<210> 83
<211> 1896
<212> DNA
<213> Drosophila

<400> 83
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```

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<210> 84
<211> 631
<212> PRT
<213> Drosophila

<400> 84
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1               5                   10                  15
Leu Met Tyr Val Ala Ala Ser Ser Ser Ser Leu Arg Gly Leu Gly Leu
                20                  25                  30
Gly Ser Gly Val Gly Val Gly Gly Leu Pro Glu Asn Ile Ser Ile Val
            35                  40                  45
Tyr Glu Asp Ala Gly Asn Gly Thr Gly Gly Gly Gly Val Gly Gly Val
        50                  55                  60
Gly Gly Gly Tyr Pro Ser Gly Pro Asn Gly Thr Asp Ala Val Ala Leu
65                  70                  75                  80
Thr Glu Pro Gly Pro Thr Ala Pro Val Thr Thr Phe Asn Tyr Tyr Asn
                85                  90                  95
Glu Ser Ala Ala Ala Ala Glu Trp Ala His Phe Tyr Asp Leu Val Leu
            100                 105                 110
```

```
Ser Trp Gln Gly Ile Ile Leu Ile Ala Val Phe Ala Thr Phe Ile Val
        115             120             125
Val Thr Val Ile Gly Asn Thr Leu Val Ile Leu Ala Ile Leu Thr Thr
    130             135             140
Arg Arg Leu Arg Thr Ile Thr Asn Cys Phe Val Met Ser Leu Ala Val
145             150             155             160
Ala Asp Leu Leu Val Gly Ile Phe Val Met Pro Pro Ala Val Ala Val
            165             170             175
His Leu Ile Gly Ser Trp Gln Leu Gly Trp Val Leu Cys Asp Ile Trp
            180             185             190
Ile Ser Leu Asp Val Leu Leu Cys Thr Ala Ser Ile Leu Ser Leu Cys
            195             200             205
Ala Ile Ser Val Asp Arg Tyr Leu Ala Val Thr Arg Pro Leu Thr Tyr
    210             215             220
Ser Arg Lys Arg Arg Ser Lys Arg Leu Ala Leu Ile Met Ile Leu Ile
225             230             235             240
Val Trp Leu Leu Ala Leu Ala Ile Thr Cys Pro Pro Met Leu Gly Trp
            245             250             255
Tyr Glu Pro Gly Arg Arg Asp Leu Arg Glu Cys Arg Tyr Asn Gln Asn
            260             265             270
Glu Gly Tyr Val Ile Phe Ser Ala Met Gly Ser Phe Phe Ile Pro Met
            275             280             285
Ala Val Met Ile Tyr Val Tyr Ala Arg Ile Ser Cys Val Ile Ala Ser
    290             295             300
Arg His Asp Asn Met Thr Asp Ile Ser Val His Asn Lys Lys Phe Lys
305             310             315             320
Arg Tyr Thr Ala Ala Asp Val Glu Asn Glu Leu Ser Glu Gln Glu Gln
            325             330             335
His Ser Ser Val Gly Gln Arg Gln Arg Gln Ala Thr Ser Arg Thr Phe
            340             345             350
Ser Asn Gln Thr Ile Ala Lys Glu Leu Gln Asp Met Met Leu Ser Asp
            355             360             365
Ser Asp Asn Cys Ala Ala Met Gly Ala Gly Gly Ala Gly Gly Gly Gly
    370             375             380
Gly Gly Ala Ser Ser Ala Thr Gly Gly Thr His Cys Gln Ser Leu Leu
385             390             395             400
Ala Leu Pro Ser Gly Gly Val Gly Gly Ser Met Gly Cys Ala Lys Asn
            405             410             415
Gly Cys Tyr Glu Leu Thr Arg Pro Ser Ser Leu Lys Arg Ala Ser Thr
            420             425             430
Ala Ser Thr Thr Ile Thr Thr Met Thr Ser Gly Met Gly Pro Gly Ser
    435             440             445
Ser Leu Leu Asp Ala Gln Trp Gln Ser Gln Pro Pro Gly Gln Thr Gly
    450             455             460
Gln Val Gln Thr His Ser Leu Ser Gln Pro Pro Arg Thr His Ser Phe
465             470             475             480
Arg His Ser His Gly Glu Arg Asp Arg Glu Arg Leu Arg Ser His His
            485             490             495
His His Pro His Tyr His His Gln Ala Gly Val Thr Thr Thr Ser Thr
            500             505             510
Ser Gly Asn Thr Ser Ala Asn Thr Asn Ser Lys Ser Leu Ser Asn Arg
            515             520             525
Ile Thr Ser Leu Lys Lys Glu Asn Lys Thr Thr Gln Thr Leu Ser Ile
    530             535             540
Val Val Gly Gly Phe Ile Ala Cys Trp Leu Pro Phe Phe Ile Asn Tyr
545             550             555             560
Leu Ile Thr Pro Phe Leu Ala Glu His Gln Ala Ser Gln Met Leu Ala
            565             570             575
Lys Ala Leu Thr Trp Leu Gly Trp Phe Asn Ser Ala Ile Asn Pro Phe
            580             585             590
```

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SUBSTITUTE SHEET (RULE 26)

```
Ile Tyr Ala Phe Tyr Ser Val Asp Phe Arg Ala Ala Phe Trp Arg Leu
        595                 600             605
Thr Cys Lys Arg Phe Phe Ser Ala Gly Gln Lys Pro Gln Phe Pro Thr
    610                 615             620
Asn Thr Met Ser Ile Arg Arg
625                 630
```

```
<210> 85
<211> 3836
<212> DNA
<213> Drosophila
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```
<400> 85
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tatgcgtttg cgattcttat agttcaggta tttaaccttc ggatacttgc gcggtgtgct 180
ggtctggagg ctacgaactt gttcctccaa tctggccaaa ttctcccttg tgcgctggag 240
ttcggccttt tgttctcgaa taagagagct ctgctcctcg tacgccatct gaaggctcct 300
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118

SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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65                  70              75                  80
Val Cys Ser Val Arg Pro Cys Ile Arg Ile Cys Cys Pro Ala Lys Asn
            85                  90                  95
Phe Leu Ala Asn Gly Lys Cys Asp Asp Gly Leu Lys Glu Glu Leu Ala
            100                 105                 110
Arg Phe Lys Pro Tyr Ile Tyr Phe Thr Tyr Met Asp Leu Gln Ala Arg
        115                 120                 125
Val Pro Leu Thr Asp Met Ala Ile Ile Arg Asp Glu Phe Phe Asp Cys
    130                 135                 140
Asp Glu Met Ile Tyr Ile Ser Asp Phe Asn Tyr Phe Leu Glu Glu Val
145                 150                 155                 160
Ser Ile Gln Ile Phe Asn Lys Cys Gly Leu Ile Val Trp Phe Gln Asp
            165                 170                 175
Gly Lys Phe Trp Val Thr Val Asp Leu Phe Met Glu Lys Gln Asp Tyr
            180                 185                 190
Cys Leu Tyr Arg His Asn Phe Asp Ser Asp Phe Pro Lys Ser Met Trp
        195                 200                 205
Ile Ile Arg His Arg Cys Thr Ser His Ile Ser Pro Gly Ser Leu Glu
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Ile Leu Ile Ile Thr Met Ile Cys Phe Val Leu Thr Ile Ala Val Tyr
225                 230                 235                 240
Leu Tyr Ile Lys Lys Leu Arg Asn Val Thr Gly Lys Cys Ile Val Cys
            245                 250                 255
Cys Ile Val Ser Arg Phe Ile Gln Cys Leu Ile Met Ile Leu Asp His
            260                 265                 270
Leu Asn Leu Leu Asn Gly Ile Cys Ser Pro Ala Gly Tyr Ser Ser His
            275                 280                 285
Phe Phe Arg Met Ala Ser Asn Leu Trp Leu Ser Val Ile Ser Tyr His
    290                 295                 300
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305                 310                 315                 320
Phe Leu Arg Tyr Asn Ala Phe Val Trp Ser Thr Ala Ala Ile Met Thr
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Gly Ser Ile Tyr Ile Val Asn Gln Ile Trp Glu Asn Asp Pro Ser Lys
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            355                 360                 365
Trp His Pro Ser Val Trp Ile Tyr Ile Ser Gly Pro Ser Leu Ala Leu
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Ser Thr Phe Asn Val Ala Met Phe Ala Leu Thr Ala Ile Tyr Ile Arg
385                 390                 395                 400
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<400> 88

SUBSTITUTE SHEET (RULE 26)

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121

SUBSTITUTE SHEET (RULE 26)

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<211> 412
<212> PRT
<213> Drosophila

<400> 90

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            20                  25                  30
Ile Ile Gly Val Ile Ile Met Val Leu Gly Val Phe Gly Asn Ser Leu
        35                  40                  45
Ala Leu Phe Ile Leu Ala Arg Lys Lys Leu Asn Lys Asn Ser Lys Tyr
    50                  55                  60
Thr Leu Met Leu Arg Cys Leu Ala Thr Asn Asn Leu Val Ala Leu Leu
65                  70                  75                  80
Gly Met Leu Thr Thr Thr Leu Leu Lys Met Tyr Leu Ser Lys Glu Val
                85                  90                  95
Leu Gln Ser Phe Ile Arg Val Asp Cys Val Gly Leu Val Val Trp Arg
            100                 105                 110
Phe Phe Gly Leu Ser Ser Gly Cys Ile Ala Ala Val Met Ala Ala Glu
        115                 120                 125
Arg Trp Met Ala Leu Ala Arg Pro Phe Ile Tyr His Lys His Ile Thr
    130                 135                 140
Tyr Glu Leu Ile Arg Lys Ser Ile Asn Ser Ile Leu Met Ile Ala Val
145                 150                 155                 160
Val Ile Thr Phe Leu Pro Phe Val Gly Phe Gly Ala Tyr Ile Asp Glu
                165                 170                 175
Ser Asn Pro Asp Gln Leu Lys Cys Ile Arg Tyr Arg Asp Ala Pro Gly
            180                 185                 190
Val Trp Asn Lys Thr Tyr Ala Val Leu Phe Met Val Phe Gly Thr Leu
            195                 200                 205
Leu Cys Ile Val Ile Val Ala Cys Asn Leu Phe Val Ala His Thr Leu
    210                 215                 220
Leu Cys Val Ile Gly Arg Ser Arg Thr Ala Lys Arg His Met His Tyr
225                 230                 235                 240
Asp Leu Val Ser Arg Asp Lys Asn Ser Ala Ile Ser Ile Asp Pro Glu
                245                 250                 255
Ser Ser Ser Gly Thr Thr Leu Tyr Gln Thr Gln Leu Ser Thr Gly Ser
            260                 265                 270
```

SUBSTITUTE SHEET (RULE 26)

```
Gly Asn Ser His Arg Ser Val Gln Pro Ala Arg Gln Tyr Arg His Ser
        275             280                 285
Val Ser Val Thr Met Ala Ala Thr Asp Ser Ser Pro Val Glu Ile Lys
    290             295                 300
Phe Ala Lys Leu Met Ala Phe Leu Ser Ile Ser Phe Val Ile Cys Trp
305                 310                 315                 320
Met Pro Gln Met Ile Ala Ile Pro Leu Ala Ile Ala Pro Asn Arg Val
            325                 330                 335
Pro Ala Ser Asn Lys Phe Phe Ile Ile Ala Asp Val Leu Thr Ala Leu
            340                 345                 350
His Phe Thr Ser Asp Pro Tyr Val Tyr Val Leu Ser Arg Ser Lys Ser
        355                 360                 365
Ile Asn Trp Ser Leu Leu Gly Cys Ile Lys Arg Trp Arg Ser Gly Trp
    370                 375                 380
Arg Pro Gly Gly Leu Arg Arg Ser Gln Ser Asp Gln Ser Arg Met Arg
385                 390                 395                 400
Thr Thr Met Thr Glu Ala Asn Thr Leu Glu Phe Asn
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<210> 91
<211> 5340
<212> DNA
<213> Drosophila
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<400> 91
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tatttttgca atattctaag tactataacc taccaaaata actgtaaaag aaagtttcta 240
tgaacgtttg aaatcaaaat taggtccgat tttgcgtagt tttcgacaaa gtgtcaccgt 300
caaaagggct tcgactggca tatccctcaa agggttaaca tgcttttctt tggtcttctt 360
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124

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<210> 92

125

SUBSTITUTE SHEET (RULE 26)

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<212> DNA
<213> Drosophila

<400> 92
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<210> 93
<211> 1019
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SUBSTITUTE SHEET (RULE 26)

<212> PRT
<213> Drosophila

<400> 93

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            20                  25                  30
Thr Asp Trp Ser Leu Arg Arg Glu Arg Asp Lys Leu Cys Ser Phe Ile
            35                  40                  45
Phe Lys Arg Val Leu Thr His Thr Glu Cys Lys Arg Leu Leu Glu Ala
    50                  55                  60
Ala Lys Ile Tyr Gly Glu Ser Ser Asp Phe Asn Ser Trp Pro Val Asn
65                  70                  75                  80
Glu Gln Leu Gln Trp Tyr Arg Asn Phe Asp Val Asn Asn Thr Asn Leu
                85                  90                  95
Leu Leu Ala Val Arg Asn Gln Ser Ser Asp Gly Gly Ser Thr Met Ser
            100                 105                 110
Gly Ser Ser Ser Asp Ser Glu Ile Leu Gly Pro Val Leu Pro Pro Phe
        115                 120                 125
Ala Leu Trp Gln Thr Ile Leu Ile Ala Ile Cys Leu Ala Ile Cys Ile
    130                 135                 140
Ile Leu Thr Val Gly Gly Asn Ile Leu Val Leu Leu Ala Phe Ile Val
145                 150                 155                 160
Asp Arg Asn Ile Arg Gln Pro Ser Asn Tyr Phe Ile Ala Ser Leu Ala
            165                 170                 175
Ala Thr Asp Met Leu Ile Gly Thr Val Ser Met Pro Phe Tyr Thr Ile
            180                 185                 190
Tyr Val Leu Lys Gly Tyr Trp Asp Leu Gly Pro Met Leu Cys Asp Leu
        195                 200                 205
Trp Leu Ser Val Asp Tyr Thr Val Cys Leu Val Ser Gln Tyr Thr Val
    210                 215                 220
Leu Leu Ile Thr Ile Asp Arg Tyr Cys Ser Val Lys Ile Ala Ala Lys
225                 230                 235                 240
Tyr Arg Ser Trp Arg Thr Arg Thr Arg Val Ile Tyr Met Val Thr Ile
            245                 250                 255
Thr Trp Ile Ile Pro Ala Leu Leu Phe Phe Ile Ser Ile Phe Gly Trp
            260                 265                 270
Glu His Phe Thr Gly Lys Arg Asp Leu Leu Pro Gly Gln Cys Ala Val
    275                 280                 285
Gln Phe Leu Lys Asp Pro Ile Phe Asn Thr Ala Leu Ile Ile Gly Tyr
    290                 295                 300
Tyr Trp Thr Thr Leu Ile Val Leu Phe Val Leu Tyr Ala Gly Ile Tyr
305                 310                 315                 320
Lys Thr Ala Tyr Asp Met Gln Lys Arg Ser Glu Ala Lys Gln Arg Lys
            325                 330                 335
Met Gln Ser Met Val Ala Leu Ser Ala Gly Ala Met Ser Gly Met Ala
            340                 345                 350
Gly His Ala Ala Gly Ile Gly Val Ile Glu Glu Lys Ile Leu Lys Thr
        355                 360                 365
Lys Val Glu Leu Ala Gly Asp Gln Thr Asp Leu Asp Ser Ala Cys Thr
    370                 375                 380
Thr Val Ile Lys Arg Leu Ser Gly Ser Gly Gln Ala Asn Pro Leu Ala
385                 390                 395                 400
Val Ala Thr Glu Glu Val Glu Lys Met Thr Pro Glu Gln Arg Arg Ala
            405                 410                 415
Ser Ala Ala Lys Ile Gln Glu Glu Ala Lys Lys Arg Glu Ala Ala Val
            420                 425                 430
Asp Ala Glu Lys Ser Glu Arg Ser Ser Ser Pro Ala Phe Asp Ser Asp
        435                 440                 445
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127

SUBSTITUTE SHEET (RULE 26)

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Glu Glu Ser Ser Val Asn Gln Ala Gln Gln Leu Ile Thr Gln Gln Lys
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Leu Asn Asn Met Arg Lys Arg Ser Ser Ile Gly Leu Val Phe Gly Ala
465             470             475             480
Gln Ala Ala Leu Leu Ala Thr Arg Gly Lys Gly Asn Leu Gln Lys Ser
            485             490             495
Thr Thr Asn Ser Lys Ser Ile Glu Ala Met His Gln Tyr His His His
        500             505             510
Gln Gln His His His Asn Gln Ser Pro Leu Gln Arg Ala Gln Ser Lys
    515             520             525
Glu Glu Met Arg Ser Leu His His His Gln Asn Gln Gln Gln Pro His
    530             535             540
His Gln His His Gln Asn Gln Pro Asn Pro Pro Leu Asp Arg Pro Lys
545             550             555             560
Arg Thr Ser Cys Ser Thr Leu Ser Gln Ile Ala Glu His Asp Arg Leu
            565             570             575
Val Asp Leu Ser Ala Pro Pro Thr Leu Leu Asn Thr Ser Asp Pro Leu
            580             585             590
Ser Pro Val Asp Leu Ala Pro Ile Glu Val Pro Ser Asp Gln Val His
    595             600             605
Gln Gly Leu Val Gln Thr Ile Leu Pro Pro Pro Asp Ala Phe Gln Cys
    610             615             620
Pro Thr Pro Leu Ser Asp Asp Tyr Ser Asp Arg Pro Phe Gly Asn Ser
625             630             635             640
Ser Gly Asn Ser Glu Leu Ala Leu Thr Tyr Asp Leu Met Thr Asn Ser
            645             650             655
Glu Leu Arg Tyr Met Asp Glu Ser Ser Ala Met Leu Ala Ser Val Thr
            660             665             670
Ala Asn Ser Thr Thr Ser Pro Asn Asp Ser Val Gln Gly Lys Pro Pro
    675             680             685
Val Leu Pro Pro Pro Pro Pro Ala Arg Arg Asn Pro Pro Lys Ser Asn
    690             695             700
Leu Asn Gln Ser Leu Ser Gln Thr Pro Ser Gln Asn Gln Ser Pro Ser
705             710             715             720
Gln Ser Leu Ser Leu Asn Leu Asn Pro Asn His Asn Gln Ser Gln Ser
            725             730             735
Gln Ser Ile Glu Glu Ala Val Ala Ile Glu Lys Arg Leu Leu Val Ser
    740             745             750
Tyr Thr Gly Ile Glu Asp Phe Ala Lys Val Arg Arg Glu Ser Cys Ile
    755             760             765
Glu Ala Ile Cys Leu Leu Asp Val Pro Gly Lys Leu Ala Ala Asp Cys
    770             775             780
Pro His Arg Arg Ala Ser Ser Pro Met Glu Thr Ser Ser Lys Asp Ala
785             790             795             800
Ile Leu Tyr Ser Pro Met Pro Pro Met Pro Leu Ser Pro Lys Val Lys
            805             810             815
Thr Ser Thr Pro Gln Thr Gly Thr Pro Gln Ser Ala Ala Gly Val Thr
            820             825             830
Pro Pro Val Pro Leu Glu Arg Ile Glu Glu Arg Glu Thr Ser Asp Ser
    835             840             845
Asn Thr Asn Lys Met Pro Ser Thr Ser Gly Thr Thr Ser Ser Thr Gly
    850             855             860
Gly Val Gly Gly Gly Gly Glu Gln Asp Gly Val Gly Ala Thr Lys Lys
865             870             875             880
Asn Ala Gly Asp Asp Asp Ala Asn Arg Glu Glu Lys Ser Leu Ala Ala
            885             890             895
Ser Arg Asn Ser Ser Lys Arg Ala Phe Ile His Ser Ile Gly Lys His
            900             905             910
Phe Lys Ser Lys Lys Ala Leu Pro Leu Ile Leu Gly Val Gly Gly Arg
    915             920             925
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SUBSTITUTE SHEET (RULE 26)

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Gln Lys Ser Lys Ser Glu Asn Arg Ala Arg Lys Ala Phe Arg Thr Ile
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Ser Phe Ile Leu Gly Cys Phe Val Ala Cys Trp Thr Pro Tyr His Val
945                 950                 955                 960
Leu Ala Leu Val Glu Gly Phe Cys Arg His Pro Pro Cys Ile Asn Glu
                965                 970                 975
His Leu Tyr Met Phe Ser Tyr Phe Leu Cys Tyr Ala Asn Ser Pro Met
                980                 985                 990
Asn Pro Phe Cys Tyr Ala Leu Ala Asn Gln Gln Phe Lys Lys Thr Phe
        995                 1000                1005
Thr Arg Ile Leu Lys Gly Asp Leu His Met Thr
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<210> 94
<211> 4172
<212> DNA
<213> Drosophila

<400> 94
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SUBSTITUTE SHEET (RULE 26)

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<211> 1014
<212> DNA
<213> Drosophila

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<210> 96
<211> 337
<212> PRT
<213> Drosophila
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SUBSTITUTE SHEET (RULE 26)

<400> 96

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Glu Thr Gln Arg Thr Thr Ala Asn Ala Thr Ser Arg His Asn Gln Leu
        35                  40                  45
His Val Ala Arg Trp Asn Ala Thr Gly Asn Ala Thr Ile Ser Ala Thr
    50                  55                  60
Phe Glu Asp Val Pro Phe Asp Ala Asn Asn Tyr Trp Ala Leu Leu Ala
65                  70                  75                  80
Leu Val Leu Val Leu Gly Thr Ala Ala Gly Asn Ile Leu Val Cys Leu
                85                  90                  95
Ala Ile Ala Trp Glu Arg Arg Leu Gln Asn Val Thr Asn Tyr Phe Leu
            100                 105                 110
Met Ser Leu Ala Ile Thr Asp Leu Met Val Ala Val Leu Val Met Pro
        115                 120                 125
Leu Gly Ile Leu Thr Leu Val Lys Gly Glu Ser Phe Val Pro Phe Lys
        130                 135                 140
Val Arg Asn Arg Val Glu Glu Tyr Asn Asn Gln Ser Gln Arg Gln Lys
145                 150                 155                 160
Arg Gly Lys Asp Ile Gln Ala Arg Thr Ser Cys Asp Val Ala Asn Thr
                165                 170                 175
Arg His Glu Leu His Leu Met Lys Leu Leu Val Gly Met Ala Leu Ala
            180                 185                 190
Val Cys Arg Leu His Tyr Val Ser Asp Ile Ser Ile Lys Ala Gly Lys
        195                 200                 205
His Val Ala Thr Leu Met Thr Val Leu Phe Val Arg Phe Gly Ser His
    210                 215                 220
Tyr Lys His Lys His Lys His Lys His Glu His Gly His Gln Tyr Lys
225                 230                 235                 240
Gln Lys Gly Arg Arg Thr His Thr Gln Thr His Thr Trp Ser Asn Pro
            245                 250                 255
Trp Gln Ser Gly Gln Cys Ser Lys Lys Glu Asp Gln Gln Met Ala Ala
        260                 265                 270
Cys Tyr Ile Lys Cys Glu Lys Tyr Cys Ser Gly Ser Asp Arg Ser Ser
        275                 280                 285
Cys Cys Cys Ser Cys Thr Gly Thr Arg Pro Pro Thr Gly Gly Lys Lys
    290                 295                 300
Gly Arg Asn Arg Asp Leu Pro Ala Val Lys Gly Phe Ala Glu Gly Pro
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Asp
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<210> 97
<211> 9268
<212> DNA
<213> Drosophila

<400> 97
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tttttcccagc ggccatacgg attcatgttc gaccagattc tggattcaca aatcccgcgc 360
ccaaatctca gggcacacgc aacaacacag taaacacaag tatcactcac cgaatgtgtg 420
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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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136

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<210> 101
<211> 2089
<212> DNA
<213> Drosophila
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caaaagaaat aacaaataag tgccgcgcat taatgtcgaa taactttttct agtcgttggc 180
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aactcaataa agttttgccc acgtaaatgg gcgtgtgtca ataaccaagg caactagcaa 300
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```

<210> 102
<211> 504
<212> PRT
<213> Drosophila

<400> 102

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            20              25              30
Leu Gln Cys Leu Val Gln Glu His Ile Glu Ala Ser Thr Tyr Gly Asn
        35              40              45
Asp Ser Gly His Cys Leu Thr Gln Phe Asp Ser Ile Leu Cys Trp Pro
    50              55              60
Arg Thr Ala Arg Gly Thr Leu Ala Val Leu Gln Cys Met Asp Glu Leu
65              70              75              80
Gln Gly Ile His Tyr Asp Ser Ser Lys Asn Ala Thr Arg Phe Cys His
                85              90              95
Ala Asn Gly Thr Trp Glu Lys Tyr Thr Asn Tyr Asp Ala Cys Ala His
            100             105             110
Leu Pro Ala Pro Glu Ser Val Pro Glu Phe Glu Val Ile Val Glu Leu
        115             120             125
Pro Thr Ile Ile Tyr Tyr Ile Gly Tyr Thr Leu Ser Leu Val Ser Leu
    130             135             140
Ser Leu Ala Leu Ile Val Phe Ala Tyr Phe Lys Glu Leu Arg Cys Leu
145             150             155             160
Arg Asn Thr Ile His Ala Asn Leu Phe Phe Thr Tyr Ile Met Ser Ala
                165             170             175
Leu Phe Trp Ile Leu Leu Leu Ser Val Gln Ile Ser Ile Arg Ser Gly
            180             185             190
Val Gly Ser Cys Ile Ala Leu Ile Thr Leu Phe His Phe Phe Thr Leu
        195             200             205
Thr Asn Phe Phe Trp Met Leu Val Glu Gly Leu Tyr Leu Tyr Met Leu
    210             215             220
Val Val Lys Thr Phe Ser Gly Asp Asn Leu Arg Phe Asn Ile Tyr Ala
225             230             235             240
Ser Ile Gly Trp Gly Gly Pro Ala Leu Phe Val Val Thr Trp Ala Val
                245             250             255
Ala Lys Ser Leu Thr Val Thr Tyr Ser Thr Pro Glu Lys Tyr Glu Ile
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Asn Cys Pro Trp Met Gln Glu Thr His Val Asp Trp Ile Tyr Gln Gly
        275             280             285
```

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```
Pro Val Cys Ala Val Leu Ile Ile Asn Leu Thr Phe Leu Leu Arg Ile
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Met Trp Val Leu Ile Thr Lys Leu Arg Ser Ala Asn Thr Val Glu Thr
305             310             315                 320
Arg Gln Tyr Arg Lys Ala Ala Lys Ala Leu Leu Val Leu Ile Pro Leu
            325             330             335
Phe Gly Ile Thr Tyr Leu Val Val Leu Ala Gly Pro Ser Glu Ser Gly
            340             345             350
Leu Met Gly His Met Phe Ala Val Leu Arg Ala Val Leu Leu Ser Thr
        355             360             365
Gln Gly Phe Ser Val Ser Leu Phe Tyr Cys Phe Leu Asn Ser Glu Val
    370             375             380
Arg Asn Ala Leu Arg His His Ile Ser Thr Trp Arg Asp Thr Arg Thr
385             390             395                 400
Ile Gln Leu Asn Gln Asn Arg Arg Tyr Thr Thr Lys Ser Phe Ser Lys
            405             410             415
Gly Gly Gly Ser Pro Arg Ala Glu Ser Met Arg Pro Leu Thr Ser Tyr
            420             425             430
Tyr Gly Arg Gly Lys Arg Glu Ser Cys Val Ser Ser Ala Thr Thr Thr
        435             440             445
Thr Leu Val Gly Gln His Ala Pro Leu Ser Leu His Arg Gly Ser Asn
    450             455             460
Asn Ala Leu His Thr Met Pro Thr Leu Ala Ala Asn Ala Met Ser Ser
465             470             475                 480
Gly Ser Thr Leu Ser Val Met Pro Arg Ala Ile Ser Pro Leu Met Arg
            485             490             495
Gln Gly Leu Glu Glu Asn Ser Val
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<211> 3731
<212> DNA
<213> Drosophila
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acgagcgtct ccagcggtac gagttggact gaattaatgc cctttttcag aaagaataag 180
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cagaaacata agaaaataag taagaataaa aaggatatct aaagccaacc aaccatgcag 600
aataaacata acattaagaa ctgatgtagg gaaatgcacg gttttaagta gatcacttta 660
gttggcacga gtgtgttagt atatttagag aacgggtgca atttaacttt ggaattattt 720
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<211> 1167
<212> DNA '
<213> Drosophila
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<211> 388
<212> PRT
<213> Drosophila

<400> 105

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                20                  25                  30
Leu Pro Cys Phe Glu Glu Phe Lys Gly Val His Tyr Asp Thr Thr Asp
            35                  40                  45
Asn Ala Thr Arg Phe Cys Phe Pro Asn Gly Thr Trp Asp His Tyr Ser
        50                  55                  60
Asp Tyr Asp Arg Cys His Gln Asn Ser Gly Ser Ile Pro Val Val Pro
65                  70                  75                  80
Asp Phe Ser Pro Asn Val Glu Leu Pro Ala Ile Ile Tyr Ala Gly Gly
                85                  90                  95
Tyr Phe Leu Ser Phe Ala Thr Leu Val Val Ala Leu Ile Ile Phe Leu
            100                 105                 110
Ser Phe Lys Asp Leu Arg Cys Leu Arg Asn Thr Ile His Ala Asn Leu
        115                 120                 125
Phe Leu Thr Tyr Ile Thr Ser Ala Leu Leu Trp Ile Leu Thr Leu Phe
    130                 135                 140
Leu Gln Val Ile Thr Thr Glu Ser Ser Gln Ala Gly Cys Ile Thr Leu
145                 150                 155                 160
Val Ile Met Phe Gln Tyr Phe Tyr Leu Thr Asn Phe Phe Trp Met Phe
                165                 170                 175
Val Glu Gly Leu Tyr Leu Tyr Thr Leu Val Val Gln Thr Phe Ser Ser
            180                 185                 190
Asp Asn Ile Ser Phe Ile Ile Tyr Ala Leu Ile Gly Trp Gly Cys Pro
        195                 200                 205
Ala Val Cys Ile Leu Val Trp Ser Ile Ala Lys Ala Phe Ala Pro His
    210                 215                 220
Leu Glu Asn Glu His Phe Asn Gly Leu Glu Ile Asp Cys Ala Trp Met
225                 230                 235                 240
Arg Glu Ser His Ile Asp Trp Ile Phe Lys Val Pro Ala Ser Leu Ala
                245                 250                 255
Leu Leu Val Asn Leu Val Phe Leu Ile Arg Ile Met Trp Val Leu Ile
            260                 265                 270
Thr Lys Leu Arg Ser Ala His Thr Leu Glu Thr Arg Gln Tyr Tyr Lys
        275                 280                 285
Ala Ser Lys Ala Leu Leu Val Leu Ile Pro Leu Phe Gly Ile Thr Tyr
    290                 295                 300
Leu Leu Val Leu Thr Gly Pro Glu Gln Gly Ile Ser Arg Asn Leu Phe
305                 310                 315                 320
Glu Ala Ile Arg Ala Phe Leu Ile Ser Thr Gln Gly Phe Phe Val Ala
                325                 330                 335
Leu Phe Tyr Cys Phe Leu Asn Ser Glu Val Arg Gln Thr Leu Arg His
            340                 345                 350
Gly Phe Thr Arg Trp Arg Glu Ser Arg Asn Ile His Arg Asn Ser Ser
        355                 360                 365
Ile Lys Asn Arg Arg Trp Ala Asn Gln Ser Leu Arg Gly Asp Cys Thr
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SUBSTITUTE SHEET (RULE 26)

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His Leu Ala Phe
385


<210> 106
<211> 7564
<212> DNA
<213> Drosophila

<400> 106
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cgaactcaaa aaaaaaaaaa aaaaaaagga atccctcaaa aggagaacca agaaaaatgg 240
gatttatctc tggccaagct ccagccatac aaatctaatt tagaccacac gacggcttca 300
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143

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<213> Drosophila
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<211> 540
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145

SUBSTITUTE SHEET (RULE 26)

<212> PRT
<213> Drosophila

<400> 108

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Leu Val Val Cys Ile Leu Gly Thr Ile Ala Asn Thr Leu Asn Ile Ile
            35                  40                  45
Val Leu Thr Arg Arg Glu Met Arg Ser Pro Thr Asn Ala Ile Leu Thr
        50                  55                  60
Gly Leu Ala Val Ala Asp Leu Ala Val Met Leu Glu Tyr Ile Pro Tyr
65                  70                  75                  80
Thr Ile His Asp Tyr Ile Leu Thr Asp Ser Leu Pro Arg Glu Glu Lys
                85                  90                  95
Leu Ser Tyr Ser Trp Ala Cys Phe Ile Lys Phe His Ser Ile Phe Ala
            100                 105                 110
Gln Val Leu His Thr Ile Ser Ile Trp Leu Thr Val Thr Leu Ala Val
            115                 120                 125
Trp Arg Tyr Ile Ala Val Gly Tyr Pro Gln Lys Asn Arg Val Trp Cys
    130                 135                 140
Gly Met Arg Thr Thr Ile Ile Thr Ile Thr Thr Ala Tyr Val Val Cys
145                 150                 155                 160
Val Leu Val Val Ser Pro Ser Leu Tyr Leu Ile Thr Ala Ile Thr Glu
                165                 170                 175
Tyr Val Asp Gln Leu Asp Met Asn Gly Lys Val Ile Asn Ser Ile Pro
                180                 185                 190
Met Thr Gln Tyr Val Ile Asp Tyr Arg Asn Glu Leu Leu Ser Ala Arg
            195                 200                 205
Thr Ala Ala Leu Asn Ala Thr Pro Thr Ser Ala Pro Leu Asn Glu Thr
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Val Trp Leu Asn Ala Ser Thr Leu Leu Thr Ser Thr Thr Thr Ala Ala
225                 230                 235                 240
Pro Pro Thr Pro Ser Pro Val Val Arg Asn Val Thr Val Tyr Arg Leu
                245                 250                 255
Tyr His Ser Asp Leu Ala Leu His Asn Ala Ser Leu Gln Asn Ala Thr
                260                 265                 270
Phe Leu Ile Tyr Ser Val Val Ile Lys Leu Ile Pro Cys Ile Ala Leu
            275                 280                 285
Thr Ile Leu Ser Val Arg Leu Ile Leu Ala Leu Leu Glu Ala Lys Arg
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Arg Arg Lys Lys Leu Thr Ser Lys Pro Ala Thr Pro Gly Ala Ser Asn
305                 310                 315                 320
Gly Thr Lys Ser Pro Ala Asn Gly Lys Ala Ala Asp Arg Pro Arg Lys
                325                 330                 335
Asn Ser Lys Thr Leu Glu Lys Glu Lys Gln Thr Asp Arg Thr Thr Arg
            340                 345                 350
Met Leu Leu Ala Val Leu Leu Leu Phe Leu Ile Thr Glu Phe Pro Gln
            355                 360                 365
Gly Ile Met Gly Leu Leu Asn Ala Val Leu Gly Asp Val Phe Tyr Leu
            370                 375                 380
Gln Cys Tyr Leu Arg Leu Ser Asp Leu Met Asp Ile Leu Ala Leu Ile
385                 390                 395                 400
Asn Ser Ser Ile Asn Phe Ile Leu Tyr Cys Ser Met Ser Lys Gln Phe
                405                 410                 415
Arg Thr Thr Phe Thr Leu Leu Phe Arg Pro Lys Phe Leu Asp Lys Trp
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Leu Pro Val Ala Gln Asp Glu Met Ala Ala Ala Arg Ala Glu Arg Ser
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SUBSTITUTE SHEET (RULE 26)

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Ala Val Ala Pro Val Leu Glu Lys Gly Arg Gln Gln Pro Gln Val His
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Arg Arg Ser Arg Gly Arg Arg Thr Leu Leu Ser Arg Leu Leu Ser Val
465                 470             475             480
Leu Lys Arg Gly Arg Arg Arg Ser Ser Gly Glu Gly Gly Gly Val Gly
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Gly Gly Gly Ala Pro Leu Ala Gly Asn Asp Ala Val Glu Pro Ala Phe
            500             505             510
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<211> 5251
<212> DNA
<213> Drosophila

<400> 109
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SUBSTITUTE SHEET (RULE 26)

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gaaatatgtt ggaacttcga tggcttttac gatgatggtg tttctggttt ggcttatggg 4920
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cgcagaaaca gacgtcccat aaataaaaga gcatcctaca cagagaaaaa agaattaggc 5160
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```

```
<210> 110
<211> 2325
<212> DNA
<213> Drosophila

<400> 110
atgtccgcgt ttcgctactt ctcgatcacc gatttctcct tcgagggacc tctgctaccg 60
ctgcacgcgg ccaccacgag caaggatgcc aaggactcgg acagccccag ttccgagctg 120
aacatacct acaccgtctt cgaggtcctg gtggccatcg tcagcatcat cggcaacgtg 180
```

```
ctggtgatca tcgtcttccg ccgggaaaga aagttgcgac gccgcaccaa ctactacata 240
gtatccctgg ccatggccga tttgctagtg ggcgcattgg gtattccctt cgccatcctg 300
gcctccatgg gactacccag aaaccttcat gcctgcctct tcacagtctc cctgctcgtg 360
gtgctgtgta ccatctccat cttctgtctg gtggccgtgt ccgtggatcg atactgggcc 420
atcctatatc cgatggccta ctcaaggaat gtccgcaccc gcacggcgat attcatcatc 480
tccatgtgct gggtggccgg gacgatagtg ggcttcctgc cgcttttcgg ctggcacgcc 540
gatgtcaatc acaaccagga gtgtctcttc gtggaggtga tggactacaa ctacctcgtc 600
ttcctctatt ttgccaccat tatcactccg gctctgctga tgctggcctt ctacacgcac 660
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cgagaaatgt ggaacatagt ggaggcctcc agtggcgccg agctgggtga aaccagctac 1380
gagttccctt cccccgctcc gggttcccag cgcagcagtg aacgaaatag cagttccaca 1440
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cacaactaca gtttcagcca ggatgaggac gaagatgatg atgatctgga gtttgaggac 1560
gtattcgtgc cggccagctc tgttccaaat cccgttcagc ctggcataga tcccgtggaa 1620
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gagcaatccg gtatctttgt gatcgatagt gaggcgagtc ccggctcaaa tgggcacaag 1920
cctaagtatc gaaagggcac ggcattcact cggagttcgc tgaagaagag ccgatcctgc 1980
aactgtagct ccatcgctaa gggacgaggg gtccacgacg agcccagcag taatctctgc 2040
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aactttttta gtccgctgag atcggtgggc agtttcatgc agcattccaa cttgtttcac 2160
ttcctccagc ctcacgccgc ccgtcccacc tcatcgacgg cgtcgtccac ggcctccacg 2220
cccactccat caccaccgcc catgggccag gctcaggagg aatcggttcc agtgggtctg 2280
accacctcct cgccgtccct tctggcgacc agcgcggaga gttga         2325
```

```
<210> 111
<211> 774
<212> PRT
<213> Drosophila

<400> 111
Met Ser Ala Phe Arg Tyr Phe Ser Ile Thr Asp Phe Ser Phe Glu Gly
1               5                   10                  15
Pro Leu Leu Pro Leu His Ala Ala Thr Thr Ser Lys Asp Ala Lys Asp
            20                  25                  30
Ser Asp Ser Pro Ser Ser Glu Leu Asn Ile Pro Tyr Thr Val Phe Glu
        35                  40                  45
Val Leu Val Ala Ile Val Ser Ile Ile Gly Asn Val Leu Val Ile Ile
    50                  55                  60
Val Phe Arg Arg Glu Arg Lys Leu Arg Arg Arg Thr Asn Tyr Tyr Ile
65                  70                  75                  80
Val Ser Leu Ala Met Ala Asp Leu Leu Val Gly Ala Leu Gly Ile Pro
                85                  90                  95
Phe Ala Ile Leu Ala Ser Met Gly Leu Pro Arg Asn Leu His Ala Cys
            100                 105                 110
Leu Phe Thr Val Ser Leu Leu Val Val Leu Cys Thr Ile Ser Ile Phe
        115                 120                 125
Cys Leu Val Ala Val Ser Val Asp Arg Tyr Trp Ala Ile Leu Tyr Pro
```

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SUBSTITUTE SHEET (RULE 26)

```
        130                   135                   140
Met Ala Tyr Ser Arg Asn Val Arg Thr Arg Thr Ala Ile Phe Ile Ile
145                   150                   155                   160
Ser Met Cys Trp Val Ala Gly Thr Ile Val Gly Phe Leu Pro Leu Phe
                165                   170                   175
Gly Trp His Ala Asp Val Asn His Asn Gln Glu Cys Leu Phe Val Glu
                180                   185                   190
Val Met Asp Tyr Asn Tyr Leu Val Phe Leu Tyr Phe Ala Thr Ile Ile
            195                   200                   205
Thr Pro Ala Leu Leu Met Leu Ala Phe Tyr Thr His Ile Tyr Arg Val
        210                   215                   220
Ile Ile Lys Gln Val Arg Gln Ile Val Thr Met Asn Pro Ala Ser Asp
225                   230                   235                   240
Leu Ser Arg Arg Ser Ser Ala Ala Val Val Gln Val Thr Thr Pro Gly
                245                   250                   255
Arg Gly Gly His Thr Gly Thr Met Leu Arg Val Leu Gly Ala Ala Arg
                260                   265                   270
Lys Arg Asp Val Lys Ala Thr Gln Asn Leu Ser Ile Ile Val Leu Phe
            275                   280                   285
Phe Met Ile Cys Trp Ile Pro Leu Tyr Thr Ile Asn Cys Ile Lys Ala
        290                   295                   300
Phe Cys Pro Asp Cys Tyr Val His Pro Lys Leu Thr Leu Phe Cys Ile
305                   310                   315                   320
Ile Leu Ser His Leu Asn Ser Ala Val Asn Pro Val Leu Tyr Ala Tyr
                325                   330                   335
His Leu Lys Asp Phe Arg Ala Ala Leu Lys Asn Leu Leu Leu Lys Met
            340                   345                   350
Met Gly Val Asp Ile Asp Gln Gln Ala Glu Ala Ile His Arg Phe Ser
            355                   360                   365
Val Ala Ser Gln His Arg Leu Gln Ser Met Asp Ser Asn Met Arg Ser
        370                   375                   380
Thr Gln Pro Arg Leu Tyr Val Gly Glu Tyr Ser Pro Ile Trp Leu Arg
385                   390                   395                   400
Gln Gln Gln Glu Ala Leu Lys Asn Ser Gln Leu Leu Pro Lys Cys Gly
                405                   410                   415
Val Val Ser Pro Cys Phe Asn Asn Ile Asn Gln Thr Val Ala Ala Val
            420                   425                   430
Ala Ser Val Thr Thr Asp Leu Glu Arg Glu Met Trp Asn Ile Val Glu
            435                   440                   445
Ala Ser Ser Gly Ala Glu Leu Gly Glu Thr Ser Tyr Glu Phe Pro Ser
        450                   455                   460
Pro Ala Pro Gly Ser Gln Arg Ser Ser Glu Arg Asn Ser Ser Ser Thr
465                   470                   475                   480
Val Pro Pro Ala Pro Pro Ala Pro Ala Lys Pro Ser Val Pro Ser Ala
                485                   490                   495
Ser Tyr Asp Asn His Asn Tyr Ser Phe Ser Gln Asp Glu Asp Glu Asp
            500                   505                   510
Asp Asp Asp Leu Glu Phe Glu Asp Val Phe Val Pro Ala Ser Ser Val
        515                   520                   525
Pro Asn Pro Val Gln Pro Gly Ile Asp Pro Val Glu Leu Arg Arg Ser
        530                   535                   540
Leu Ala Leu Val Met Arg Glu Lys Leu Arg Ser Asp Asp Thr Asp Ser
545                   550                   555                   560
Arg Pro Met Gly Asn Asn Gln Asp Leu Pro Ile Asp Glu Gln Ser Arg
                565                   570                   575
Glu Arg Pro Leu Ser Thr Gln Thr Ser Pro Thr Asn Gly Pro Leu Pro
            580                   585                   590
Ala Leu Leu Arg Ala Lys Leu Leu Ala Gly Asn Ser Asn Ser Ala His
        595                   600                   605
Cys Leu Pro Gly Ser Thr Ala Ser Pro Ala Pro Gln Glu Gln Ser Gly
```

150

```
            610                    615                    620
Ile Phe Val Ile Asp Ser Glu Ala Ser Pro Gly Ser Asn Gly His Lys
625                     630                    635                    640
Pro Lys Tyr Arg Lys Gly Thr Ala Phe Thr Arg Ser Ser Leu Lys Lys
                645                    650                    655
Ser Arg Ser Cys Asn Cys Ser Ser Ile Ala Lys Gly Arg Gly Val His
                660                    665                    670
Asp Glu Pro Ser Ser Asn Leu Cys Arg Asp Gln Glu Ser Ser Val Leu
                675                    680                    685
Pro Gln His Pro Gln Pro Ala Asn His Pro Thr Glu Asn Phe Phe Ser
        690                    695                    700
Pro Leu Arg Ser Val Gly Ser Phe Met Gln His Ser Asn Leu Phe His
705                     710                    715                    720
Phe Leu Gln Pro His Ala Ala Arg Pro Thr Ser Ser Thr Ala Ser Ser
                725                    730                    735
Thr Ala Ser Thr Pro Thr Pro Ser Pro Pro Pro Met Gly Gln Ala Gln
                740                    745                    750
Glu Glu Ser Val Pro Val Gly Leu Thr Thr Ser Ser Pro Ser Leu Leu
        755                    760                    765
Ala Thr Ser Ala Glu Ser
770
```


```
<210> 112
<211> 4314
<212> DNA
<213> Drosophila
```

```
<400> 112
gagccaattc ttttttggct ttacgtgacg ttggcagaac aaatcgtttt tgttttagcc 60
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ctttaatgcg attgctggtt gctcattacg gccaatcctt actagtactt gcactttctg 180
tgaattcgtc tggggtttcc atttggctga ttgcattttc ataacaattt ggaggattac 240
taatgcgcca cgttgtccct gcatttgcat gaccttgaac cagtagccac ctcattagaa 300
tttcatttgt agtcaacaag gcgcagacga cagggccaca atcgataaaa acccaaatgt 360
attttatggc caaattacat ttttactaga atgaatccat agaaagatgc ggaaaataag 420
cgggcgcgga atatgctaag ctttatttgc agccatggga ataatcttaa tacagcaaat 480
tcatccttta aggtatctct agaagtaagt ttagtaagcg aactttgtcc gtcatttcca 540
ttgagttgaa tgctacattt tcgaaatctt attttaaatg cgattcaata caatatacag 600
aatctactat gtttaagatc gcaacatttt tttttacact ttcttaacta aacactttaa 660
aagcacatct gtgttacact ttggtatgca tgtgaaacat ttggttaact aaaacatata 720
tctacgcaat ttaaaaggcg atctattaaa tttcaagggg caagcttttc gtttttaaat 780
ttaattccta tatttaaatg gtgggcgttc actagtgatt gatttatgct taccattatc 840
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gaccaaagtt taattttaag agcgccagta tgctgaatag tatgagtcaa aagattgaat 960
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attaactttt aattgccaaa tgcaaatgaa tgcaaaagca gtttaaacaa aacgctttgg 1140
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gcatcaggaa gccgcacgag agagtgagtt cgagtttatc agttagttga cttggacacc 1260
gatcatggcg tactgagcgg cgactggcgg cttgttcgtc ggattctgga tgtggagtac 1320
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taggggcac ttgcctgcat tatcgacggt ttcggctgct ccgccgactc aatggagaag 1440
cgctgcgttt gactggaatt ggttagtgcc ctcctcaggc ggcgcgattc gatgttgttt 1500
cgcgaattca gcgaaccctt cgataccttc ttgccaaaca gaacggccta aaggagtggg 1560
aaatcggtaa ggtaattagt taaatagaaa aattcagaca ttcgaattat taataaatat 1620
attaataaat atatataaat atttataata cagataaatt tgaaatatag tattgcgcat 1680
actataaccc ccacttccgt tttactcacc ttgaatgcct ctcggaactt gtggctcata 1740
atgttatata acagcgggtt gatgcaggtg gacaagtagt agaggacacc ggagacatag 1800
gtcatcaccg tgtagacaaa ctcgtgctga tcccgcagtt tggccccccg tgcaggggcg 1860
```

151

SUBSTITUTE SHEET (RULE 26)

```
tagatggcaa tcagtcgctg ggcgtggaag ggggcccagc agaggaagaa gcacaccacc 1920
acggccacta aaggggaggg gggggcggta aaagtcagtg acgtgggggat gaaaatggaa 1980
tggcaatgga aatggggaag acacagcgag agtcacagat aaagagtcaa cgattatatt 2040
ttttggtaat cgcaattgtc atcataaatg gagagtgcca aaatgacaaa cgcagtaaat 2100
tggctgcaga cgggttgatt agcccagctt agggcatatg gtcaaacagt tggcatacac 2160
tgagcaaaag ttgaagtaaa gcttctaaaa tggttcttca ttgcatataa agaaagattt 2220
agatatcata tttcagaatt tttaatttgc aagacttttg tgagaagact aaaccttatt 2280
aaaaacggag tcttctactt ttgttttttgt caaaatttct tactaattta atcatctgaa 2340
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atacccccgt actattgctg gtatttttcg ccagtgtata tcgtgctata attacctagc 2460
atcctgagta ctcgccgggt gccatagtga ttgagccgac ctctcaccga gctaagttga 2520
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ccgataagta ggtacaacac taggataata gacatcggag ccaggaagaa tatgaacgtg 2760
gacagctgga atgagtgctt cactatgacc cgcactatgc cgcattgctc cactcccgaa 2820
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gccgatgtct ccgccaacag accacgtccg atgcagatgt actccccaaa cacgtacggg 3060
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cttacttgtt agcttataag taagaatatt gttctttgtt tatcttacta aagtatattg 4260
aaatgtaaac aaataataat aattacaatt caaatctaat ttagattaat taaa      4314
```

<210> 113
<211> 1287
<212> DNA
<213> Drosophila

<400> 113
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acctgcattg tgattaagaa gaaccgttca atgcacacgg ccacgaatta ctacctcttt 180
tcgctggcca tctcggattt cctgctcctg ttgtcgggcg ttccgcagga ggtgtcctac 240
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gcggagacat cggcgaatgc cacggtgcta acgattacgg ccttcacggt ggagcggtat 360
attgccattt gccatccgtt tctgggccag gccatgagta aactcagtcg cgccattcgc 420
atcatcgtcc tggtttggat tatggccata gttacggcca ttccgcaggc tgcccaattt 480
ggaatcgagc actattcggg agtggagcaa tgcggcatag tgcgggtcat agtgaagcac 540
tcattccagc tgtccacgtt catattcttc ctggctccga tgtctattat cctagtgttg 600
tacctactta tcggtgtgca cctgtatcga tccactttgg tggagggtcc tgcctcggtt 660
gccagacggc agcagctgaa gagtgtgccc agtgatacga tcctatatcg ctatggtgga 720
```

SUBSTITUTE SHEET (RULE 26)

```
tccggtaccg ctatgagttt caacggcgga ggaagtggag cagggacagc gggcttgatg 780
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cgagtactca ggatgctagt ggccgtggtg gtgtgcttct tcctctgctg ggcccccttc 900
cacgcccagc gactgattgc catctacgcc cctgcacggg gggccaaact gcgggatcag 960
cacgagtttg tctacacggt gatgacctat gtctccggtg tcctctacta cttgtccacc 1020
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gttctgtttg caagaaggt atcgaagggt tcgctgaatt cgcgaaacaa catcgaatcg 1140
cgccgcctga ggagggcact aaccaattcc agtcaaacgc agcgcttctc cattgagtcg 1200
gcggagcagc cgaaaccgtc gataatgcag gcaagtgccc cctataatca atggatagct 1260
gcggacaacg gctggaaaaa ctcctaa                                     1287
```

<210> 114
<211> 428
<212> PRT
<213> Drosophila

<400> 114

```
Met Ser Ala Gly Asn Met Ser His Asp Leu Gly Pro Pro Arg Asp Pro
1               5                   10                  15
Leu Ala Ile Val Ile Pro Val Thr Val Val Tyr Ser Leu Ile Phe Ile
            20                  25                  30
Thr Gly Val Val Gly Asn Ile Ser Thr Cys Ile Val Ile Lys Lys Asn
        35                  40                  45
Arg Ser Met His Thr Ala Thr Asn Tyr Tyr Leu Phe Ser Leu Ala Ile
    50                  55                  60
Ser Asp Phe Leu Leu Leu Leu Ser Gly Val Pro Gln Glu Val Ser Tyr
65                  70                  75                  80
Ile Trp Ser Lys Tyr Pro Tyr Val Phe Gly Glu Tyr Ile Cys Ile Gly
            85                  90                  95
Arg Gly Leu Leu Ala Glu Thr Ser Ala Asn Ala Thr Val Leu Thr Ile
            100                 105                 110
Thr Ala Phe Thr Val Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Leu
        115                 120                 125
Gly Gln Ala Met Ser Lys Leu Ser Arg Ala Ile Arg Ile Ile Val Leu
    130                 135                 140
Val Trp Ile Met Ala Ile Val Thr Ala Ile Pro Gln Ala Ala Gln Phe
145                 150                 155                 160
Gly Ile Glu His Tyr Ser Gly Val Glu Gln Cys Gly Ile Val Arg Val
            165                 170                 175
Ile Val Lys His Ser Phe Gln Leu Ser Thr Phe Ile Phe Phe Leu Ala
            180                 185                 190
Pro Met Ser Ile Ile Leu Val Leu Tyr Leu Leu Ile Gly Val His Leu
    195                 200                 205
Tyr Arg Ser Thr Leu Val Glu Gly Pro Ala Ser Val Ala Arg Arg Gln
    210                 215                 220
Gln Leu Lys Ser Val Pro Ser Asp Thr Ile Leu Tyr Arg Tyr Gly Gly
225                 230                 235                 240
Ser Gly Thr Ala Met Ser Phe Asn Gly Gly Gly Ser Gly Ala Gly Thr
            245                 250                 255
Ala Gly Leu Met Gly Gly Ser Gly Ala Gln Leu Ser Ser Val Arg Gly
            260                 265                 270
Arg Leu Asn His Tyr Gly Thr Arg Arg Val Leu Arg Met Leu Val Ala
    275                 280                 285
Val Val Val Cys Phe Phe Leu Cys Trp Ala Pro Phe His Ala Gln Arg
    290                 295                 300
Leu Ile Ala Ile Tyr Ala Pro Ala Arg Gly Ala Lys Leu Arg Asp Gln
305                 310                 315                 320
His Glu Phe Val Tyr Thr Val Met Thr Tyr Val Ser Gly Val Leu Tyr
            325                 330                 335
```

SUBSTITUTE SHEET (RULE 26)

```
Tyr Leu Ser Thr Cys Ile Asn Pro Leu Leu Tyr Asn Ile Met Ser His
             340                 345             350
Lys Phe Arg Glu Ala Phe Lys Ala Val Leu Phe Gly Lys Lys Val Ser
         355                 360             365
Lys Gly Ser Leu Asn Ser Arg Asn Asn Ile Glu Ser Arg Arg Leu Arg
     370                 375             380
Arg Ala Leu Thr Asn Ser Ser Gln Thr Gln Arg Phe Ser Ile Glu Ser
385                 390             395                 400
Ala Glu Gln Pro Lys Pro Ser Ile Met Gln Ala Ser Ala Pro Tyr Asn
             405             410             415
Gln Trp Ile Ala Ala Asp Asn Gly Trp Lys Asn Ser
         420             425
```

```
<210> 115
<211> 5927
<212> DNA
<213> Drosophila

<400> 115
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tgtctgtttg tccctaaagt aattaaaagt aagtaaagca aagtcacccc ctcgtcggtg 180
ggcgtggctg tccagtgatt tgccacccgc aacgatttt ttttccagta cttttccttt 240
tttcttttt ttgcgtttat gcaaatggcc gctgaccaaa agaattaatg cgtcccgaaa 300
gtgagttgaa ttggaatgag ccgcaattct cggagtccaa aaactgcggg cagcctgtca 360
gccgtctgtt ttcacttctt ttgcgggcgg gacgaaacat caacgaatgt caatgaattt 420
acaggggaat gctataaaaa gcccgaccaa acaaaaaatg taaagcccgt aattccccat 480
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His Asp Val Val Val Asp Tyr Asp Ala Lys Lys Asn Ile Thr Tyr Gly
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Met Cys Thr Phe Thr Thr Asn Asp Phe Leu Gly Pro Arg Thr Tyr Gln
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Gln Leu Ile Leu Leu Leu Lys Ser Leu Asp Val Ile Glu Thr Asn Thr
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SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

<400> 119

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<211> 540
<212> PRT
<213> Drosophila

<400> 120

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            35                  40                  45
Ile Gly Asn Thr Leu Val Ile Trp Val Val Ala Thr Thr Arg Gln Met
        50                  55                  60
Arg Thr Val Thr Asn Met Tyr Ile Ala Asn Leu Ala Phe Ala Asp Val
65                  70                  75                  80
Ile Ile Gly Leu Phe Cys Ile Pro Phe Gln Phe Gln Ala Ala Leu Leu
                85                  90                  95
Gln Ser Trp Asn Leu Pro Trp Phe Met Cys Ser Phe Cys Pro Phe Val
            100                 105                 110
Gln Ala Leu Ser Val Asn Val Ser Val Phe Thr Leu Thr Ala Ile Ala
            115                 120                 125
Ile Asp Arg His Arg Ala Ile Ile Asn Pro Leu Arg Ala Arg Pro Thr
        130                 135                 140
Lys Phe Val Ser Lys Phe Ile Ile Gly Gly Ile Trp Met Leu Ala Leu
145                 150                 155                 160
Leu Phe Ala Val Pro Phe Ala Ile Ala Phe Arg Val Glu Glu Leu Thr
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Glu Arg Phe Arg Glu Asn Asn Glu Thr Tyr Asn Val Thr Arg Pro Phe
            180                 185                 190
Cys Met Asn Lys Asn Leu Ser Asp Asp Gln Leu Gln Ser Phe Arg Tyr
            195                 200                 205
Thr Leu Val Phe Val Gln Tyr Leu Val Pro Phe Cys Val Ile Ser Phe
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Val Tyr Ile Gln Met Ala Val Arg Leu Trp Gly Thr Arg Ala Pro Gly
225                 230                 235                 240
Asn Ala Gln Asp Ser Arg Asp Ile Thr Leu Leu Lys Asn Lys Lys Lys
                245                 250                 255
Val Ile Lys Met Leu Ile Ile Val Val Ile Ile Phe Gly Leu Cys Trp
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Leu Pro Leu Gln Leu Tyr Asn Ile Leu Tyr Val Thr Ile Pro Glu Ile
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Asn Asp Tyr His Phe Ile Ser Ile Val Trp Phe Cys Cys Asp Trp Leu
        290                 295                 300
Ala Met Ser Asn Ser Cys Tyr Asn Pro Phe Ile Tyr Gly Ile Tyr Asn
305                 310                 315                 320
Glu Lys Phe Lys Arg Glu Phe Asn Lys Arg Phe Ala Ala Cys Phe Cys
            325                 330                 335
Lys Phe Lys Thr Ser Met Asp Ala His Glu Arg Thr Phe Ser Met His
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Thr Arg Ala Ser Ser Ile Arg Ser Thr Tyr Ala Asn Ser Ser Met Arg
        355                 360                 365
Ile Arg Ser Asn Leu Phe Gly Pro Ala Arg Gly Gly Val Asn Asn Gly
        370                 375                 380
```

SUBSTITUTE SHEET (RULE 26)

```
Lys Pro Gly Leu His Met Pro Arg Val His Gly Ser Gly Ala Asn Ser
385                 390             395             400
Gly Ile Tyr Asn Gly Ser Ser Gly Gln Asn Asn Asn Val Asn Gly Gln
            405                 410             415
His His Gln His Gln Ser Val Val Thr Phe Ala Ala Thr Pro Gly Val
        420                 425             430
Ser Ala Pro Gly Val Gly Val Ala Met Pro Pro Trp Arg Arg Asn Asn
        435             440             445
Phe Lys Pro Leu His Pro Asn Val Ile Glu Cys Glu Asp Asp Val Ala
    450             455             460
Leu Met Glu Leu Pro Ser Thr Thr Pro Pro Ser Glu Glu Leu Ala Ser
465             470             475                 480
Gly Ala Gly Val Gln Leu Ala Leu Leu Ser Arg Glu Ser Ser Ser Cys
            485             490                 495
Ile Cys Glu Gln Glu Phe Gly Ser Gln Thr Glu Cys Asp Gly Thr Cys
        500             505             510
Ile Leu Ser Glu Val Ser Arg Val His Leu Pro Gly Ser Gln Ala Lys
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Asp Lys Asp Ala Gly Lys Ser Leu Trp Gln Pro Leu
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```

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<211> 4391
<212> DNA
<213> Drosophila

<400> 121
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ttgcacaaaa gagtctatgt gcttagttga tgatatcagt cgatatctct ttaattggcc 240
aataactgct gaatatgtgg cagcacaata tagttacgaa agtaatcggc ttaagagccc 300
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<211> 2325
<212> DNA
<213> Drosophila
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SUBSTITUTE SHEET (RULE 26)

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<212> PRT
<213> Drosophila

<400> 123
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            20                  25                  30
Met Phe Cys Glu Pro Glu Glu Phe Gln His Asp Tyr Ile Thr Arg Asn
        35                  40                  45
His Asp Gln Thr Pro His Gln Asn Lys Trp Lys Arg Ala Arg Ile Gly
    50                  55                  60
Glu Arg Ala Thr Leu His Asp Val Cys Leu Leu Arg Asn Gly Met Pro
65                  70                  75                  80
Val Thr Arg Glu Cys Arg Val Lys Asp Asn Arg Ala Asn Trp Glu Ser
                85                  90                  95
Thr Glu His Trp Asp Pro Val Val Cys Leu Arg Arg Phe Arg Glu His
            100                 105                 110
Thr Ile Ser Gly Asp Leu Asn Ser Leu His Asp Asp Val Leu Glu Gly
        115                 120                 125
Arg Arg Arg Thr Asn Asp Thr Gln Gly Arg Arg Glu Met Thr Gly Ile
    130                 135                 140
Met Arg Asn Met Phe Arg Gln Arg Gly Gly Asn Leu Leu Pro Ala Asp
145                 150                 155                 160
Val His Met Thr Gly Gln Met Phe Gly Ala Leu Met Gln Gln Asp Lys
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Asp Ala Thr Val Ser Val Asp Leu Val Ser Val Cys Lys Glu Ile Met
            180                 185                 190
Ser Cys Asp Ser Lys Val Leu Arg Leu Ser Ala Gln Leu Asn Ala Thr
```

```
                195                    200                    205
Asn Ser Leu Leu Ser Gln Phe Glu Ser Tyr Met Asp Ala Leu Pro Glu
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225                    230                    235                    240
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                245                    250                    255
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                260                    265                    270
Phe Ala Asn Pro Glu Cys Asp Arg Ile Thr Gly Leu Ala Ile Phe Ser
                275                    280                    285
Ala Pro Gly Asp Gln Arg Lys Thr Ser Ala Ser Gly Phe Trp Tyr Arg
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Phe Ile Arg Phe Ser Glu Asp Leu Ala Lys Val Lys Glu Glu Ser Asn
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Ser Arg Gly Ala Thr Tyr Leu Ile Phe Lys Val Tyr Ala His Asp Ala
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Leu Phe Val Glu Thr Ser Leu Gln Arg Thr Arg Lys Pro Arg Ser Lys
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Val Ile Ser Ile Ser Ile Pro Gly Leu Arg Ser Asn Tyr Leu Ser Leu
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Pro Leu Pro Phe Leu Leu Arg Asn Glu Asn Leu Arg Asn Pro Asp Ser
385                    390                    395                    400
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Trp Ser Thr Glu Gly Val Ser Thr Glu Ser Ser Ser Asp Leu Leu Lys
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Asp Ala Ile Ile Glu Cys His Thr Asn His Leu Thr Gln Phe Ala Phe
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Ile Thr Pro Ile Asn Glu Lys Val Leu Asp Ile Ile Ser Ile Val Gly
465                    470                    475                    480
Cys Ser Leu Ser Leu Leu Gly Ile Leu Gly Ile Phe Leu Thr Ala Ala
                485                    490                    495
Leu Phe Lys Ser Trp Arg Ser Gln Ala Ser Thr Lys Val Leu Leu His
                500                    505                    510
Leu Cys Leu Ala Met Cys Leu Gln Met Met Leu Phe Val Phe Leu Asn
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Thr Asp Asp Val Ser Glu Ala Leu Val Val Asn Gly Asn Thr Val Arg
    530                    535                    540
Cys Val Ala Leu Gly Ala Ala Met Gln Tyr Ser Ile Leu Val Leu Phe
545                    550                    555                    560
Ser Trp Met Leu Ile Ile Ala Phe Leu Gln Phe Gln Arg Tyr Val Thr
                565                    570                    575
Val Ile Gly Ile Glu Arg Pro Pro Arg Tyr Ile Leu Lys Ala Ala Ile
                580                    585                    590
Val Ala Trp Leu Leu Pro Leu Val Pro Thr Leu Leu Val Ala Leu Ile
    595                    600                    605
Asp Pro Asp Ser Tyr Val Pro Ser Ala Ala Gln Leu Ser Thr Asp Thr
    610                    615                    620
Gly Ile Cys Tyr Pro Ser Gly Tyr Gly Leu Ile Phe Gly Val Val Leu
625                    630                    635                    640
Pro Val Thr Leu Ile Thr Val Cys Asn Leu Val Ile Phe Val Tyr Val
                645                    650                    655
Phe Tyr Ser Ile Ser His Ser Leu Ser Gln Ser Ile His Lys Asn Glu
                660                    665                    670
Lys Lys Met Val Val Lys Gln Ile Arg Leu Ser Ile Met Leu Phe Phe
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             675                    680                    685
Leu Leu Gly Leu Thr Trp Ile Phe Gly Ile Phe Ala Phe Met Gln Ala
    690                    695                    700
Gly Val Ala Phe Ser Tyr Leu Phe Cys Ile Thr Ala Thr Met Gln Gly
705                    710                    715  .               720
Phe Val Met Phe Ile Tyr Phe Val Leu Leu Asp Ser Thr Asn Arg Arg
                   725                    730                    735
Leu Trp Val Gly Leu Ile Cys Pro Thr Lys Met Glu Leu Asp Val Gln
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Lys Arg Thr Thr Glu Leu Gln Ser Met Thr Thr Ser Ser Thr Asn Tyr
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Asn Ser Arg Ser His Gln
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<211> 7986
<212> DNA
<213> Drosophila

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caatacgaga atgggcgaat ataagtttgc tcgaacggct ggtccgttcc gagctgaaat 540
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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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<212> DNA
<213> Drosophila

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<212> PRT
<213> Drosophila

<400> 126

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        35                  40                  45
Met Ala Thr Gly Ala Gly Ala Gly Lys Leu Gly Val Pro Ser Met Asn
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Ser Tyr Leu Val Ser Met Ala Trp Pro Lys Ser Leu Ala Val Ala Val
65                  70                  75                  80
Phe Leu Val Ile Ile Leu Val Thr Val Val Gly Asn Thr Leu Val Ile
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Leu Ala Val Leu Thr Thr Arg Arg Leu Arg Thr Val Thr Asn Cys Phe
            100                 105                 110
Val Met Asn Leu Ala Ile Thr Asp Trp Leu Val Gly Thr Cys Val Met
        115                 120                 125
Pro Pro Ser Val Val Leu Tyr Ile Thr Gly Thr Trp Arg Phe Gly Trp
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Ile Leu Cys Asp Ile Trp Ile Ser Leu Asp Ile Leu Leu Cys Ser Gly
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Ser Ile Leu Ser Leu Cys Ala Ile Ser Leu Asp Arg Tyr Leu Ala Val
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Thr Gln Pro Leu Thr Tyr Ser Lys Lys Arg Arg Ser Lys Arg Leu Ala
            180                 185                 190
Leu Leu Met Ile Leu Val Val Trp Ile Thr Ala Leu Ser Ile Thr Cys
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Pro Pro Tyr Leu Gly Trp Tyr Glu Val Gly Arg His Gln Ala Glu Phe
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Val Asp Cys Arg Tyr Asn Gln Asn Lys Gly Tyr Val Val Phe Ser Ala
225                 230                 235                 240
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Pro Thr Phe Tyr Glu Leu Val Glu Val Ser Arg Leu Ser Ser Leu Ile
    370                     375                     380
His Cys Ser Ala Ile Ser Cys Lys Tyr Gly Gly Pro Cys Met His Ser
385                     390                     395                 400
Thr Pro Ser Gly Met His Tyr Val Gly Thr Glu Ala Ser Phe Ser Asp
            405                     410                     415
Thr Cys Leu Gly Gly Asn Lys Leu Glu Ala Glu Ala Lys Gln Lys Gln
            420                     425                     430
Gln Gln Gln Arg Ser Ser Phe Asp His His His Pro His Ala His His
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His Gly Ser His Gly Gln Gln Ser His His Asn His His His Arg Met
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Pro Met Arg Val Ser Thr Thr Lys Arg Asp Ser Lys Thr Ala Lys Thr
465                     470                     475                 480
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            485                     490                     495
Val Tyr Tyr Leu Leu Ile Pro Phe Leu Pro Arg Pro Ala Val Leu Glu
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<212> DNA
<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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<210> 128
<211> 1503
<212> DNA
<213> Drosophila
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gactcctatg cgtacgagga gctaatcatt cctgctcatc tcacgggtct atatacattt 180
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SUBSTITUTE SHEET (RULE 26)

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<211> 172
<212> PRT
<213> Drosophila

<400> 129
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            20                  25                  30
Ile Ser His Ile Pro Lys Leu Asn Asp Ser Tyr Ala Tyr Glu Glu Leu
        35                  40                  45
Ile Ile Pro Ala His Leu Thr Gly Leu Tyr Thr Phe Arg Gln Leu Ala
    50                  55                  60
Asp Gly Ser Gln Glu Pro Val Lys Ser His Leu Arg Ala Cys Ile Cys
65                  70                  75                  80
Lys Leu Lys Pro Cys Ile Arg Phe Cys Cys Pro Arg Asn Lys Met Met
                85                  90                  95
Pro Asn Ser Arg Cys Ser Asp Gly Leu Thr Glu Asn Leu Lys Arg Ile
            100                 105                 110
Asn Pro Tyr Leu Lys Ile Thr Leu Glu Asp Gly Thr Ile Gly Lys Tyr
        115                 120                 125
Tyr Leu Leu Thr Asp Met Ile Val Leu Arg Tyr Glu Phe Arg Tyr Cys
    130                 135                 140
Glu Lys Val Val Ser Val Gln Glu Asp Gln Tyr Lys Leu Tyr Glu Val
145                 150                 155                 160
Lys Ile Ser Ile Phe Leu Lys Tyr Leu Ser Ile Ile
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```

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<211> 6552
<212> DNA
<213> Drosophila

<400> 130
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tcatttgatt cattgtgtct gttcgtgtgt gttggcgtgt tactctgtta agttggatgc 180
aattctgtcg ccgatggttg tggttttgtg tccatggccc atcaatgggg atgctccatc 240
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gagggcgccg acctcgaggc ccgctagcta ctgtatccaa ttgaactgtg atttagctaa 360
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atttctttac actcgcttac ctaatcgtac tgtgggaatc ggaaggaagg ttctgtgtgc 480
```

```
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172

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<211> 1392
<212> DNA
<213> Drosophila

<400> 131
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173

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<211> 444
<212> PRT
<213> Drosophila

<400> 132
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            20                  25                  30
His Lys Asn Ser Arg Arg Val Cys Leu Thr Ile Leu Leu Val Trp Ala
        35                  40                  45
Ile Ser Ala Ala Ile Gly Ser Pro Ile Val Leu Gly Leu Asn Asn Thr
    50                  55                  60
Pro Asn Arg Glu Pro Asp Val Cys Ala Phe Tyr Asn Ala Asp Phe Ile
65                  70                  75                  80
Leu Tyr Ser Ser Leu Ser Ser Phe Tyr Ile Pro Cys Ile Ile Met Val
                85                  90                  95
Phe Leu Tyr Trp Asn Ile Phe Lys Ala Leu Arg Ser Arg Ala Arg Lys
            100                 105                 110
Gln Arg Ala Ala Arg Lys Pro His Leu Ser Glu Leu Thr Gly Gly Ser
        115                 120                 125
Val Ile Glu Asn Ile Ala Gln Thr Arg Arg Leu Ala Glu Thr Ala Leu
    130                 135                 140
Asp Ser Ser Arg His Ala Ser Arg Ile Leu Pro Asp Glu Ala Ala Thr
145                 150                 155                 160
Asn Thr Ala Ser Gly Ser Asn Glu Glu Glu Asp Glu Asn Ala Ile Ser
                165                 170                 175
Pro Asp Ile Asp Asp Cys His Val Ile Val Asn Asp Lys Ser Thr Glu
            180                 185                 190
Phe Met Leu Ala Thr Val Val Glu Glu Thr Gly Asn Ser Val Val Ala
        195                 200                 205
Gln Ile Thr Thr Gln Pro Gln Leu Val Val Ala Asp Pro Asn Gly Asn
    210                 215                 220
His Asp Ser Gly Tyr Ala Ala Ser Asn Val Asp Asp Val Leu Ala Gly
225                 230                 235                 240
Val Ala Pro Ala Ser Ala Ser Ala Ala Thr Ser Ala Ala Pro Arg Ser
                245                 250                 255
Ser Gly Ser Pro Pro Asp Ser Pro Leu Pro Ser Gly Ala Thr Leu Gln
            260                 265                 270
Arg Ser Ser Val Ser Ser Gln Arg Arg Pro Thr Gly Asp Asp Ser Pro
        275                 280                 285
Lys Arg Gly Glu Pro Ala Leu Ser Val Ala Met Lys Pro Leu Ser Phe
    290                 295                 300
```

SUBSTITUTE SHEET (RULE 26)

```
Val Arg Tyr Gly Val Gln Glu Ala Met Thr Leu Ala Arg Asn Asp Ser
305             310             315             320
Thr Leu Ser Thr Thr Ser Lys Thr Ser Ser Arg Lys Asp Lys Lys Asn
            325             330             335
Ser Gln Ala Ser Arg Phe Thr Ile Tyr Lys Val His Lys Ala Ser Lys
            340             345             350
Lys Lys Arg Glu Lys Ser Ser Ala Lys Lys Glu Arg Lys Ala Thr Lys
        355             360             365
Thr Leu Ala Ile Val Leu Gly Val Phe Leu Phe Cys Trp Leu Pro Phe
    370             375             380
Phe Ser Cys Asn Ile Met Asp Ala Met Cys Ala Lys Phe Lys Lys Asp
385             390             395             400
Cys Arg Pro Gly Leu Thr Ala Tyr Met Met Thr Thr Trp Leu Gly Tyr
            405             410             415
Ile Asn Ser Phe Val Asn Pro Val Ile Tyr Thr Ile Phe Asn Pro Glu
            420             425             430
Phe Arg Lys Ala Phe Lys Lys Ile Met His Met Gly
    435             440
```

```
<210> 133
<211> 2970
<212> DNA
<213> Drosophila
```

```
<400> 133
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agcaatggtc agcgctacac tttcctgttc aagggcatgg aggatctcca tctggacgaa  180
cgcatcatgc agttcctgtc catctcgaat gccattatgg cctgccgcag cgacgcaccc  240
ggcaatggct gctatcgtgc ccaccactat tcggttatac cattgggacc gcaatccgga  300
ctgattagct gggtggacgg ggtcacacca gtctttgcgc tctacaagaa gtggcaacag  360
agacggtccc aagttgctgg gaatgcggga gcaggtgctg tggcaaatgt cccgcgacgt  420
ttcacagact tgttctacaa caaactctcg cccctgttgg ccaagcacaa tatgcaggtg  480
agcgatccac gacgccaatg gccaatatcc gtcctgctcc aggtgctcga cgaattgtca  540
caggaaacac ccaatgatct gcttgcccgc gaactgtggt gccaggcggg aaatgccgcc  600
gagtggcggc aatcggtgcg tcgctttgtc cgctgcatgt cggtcatgtc gatgattggc  660
tatgtcattg gcctgggcga tcgtcatttg acaacgtgc ttatcaacct gggaagcggc  720
gacatcgtgc atatcgacta caacgtgtgc ttcgagaagg ccgcaccct gcgcatcccc  780
gagaaggtgc ccttccgtct tacccagaat ctagtgcagg ccatgggcat cacaggaatc  840
gaggtaagac tattgctcat cctataccaa tcaattatct caacaaatcg ctgctggggg  900
tgtttaagaa acggtgctcc taaagataat gtccacttt attgctatat ctccatttaa  960
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accagatgat agggcagtgc cagtcccaca cagaagtcgg agacggccag cgacaggatg 1920
aacagattgg agatgaccga tcgcaggtgg cggcaggtgc gcaccgccac aatggtcaga 1980
atattgccgc ccaggataag gacaaacaag aaggcattga tggctagcca cagcagatgg 2040
```

SUBSTITUTE SHEET (RULE 26)

```
ccggcaccga aactggtcgc ctggagggtt atttccgttg gcgtttccgt ggcgttctgg 2100
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agtggttggc tatctggcaa ccgtgggagc tggagttgtg ctgacttttg gccaggactt 2280
cggctcggct cggatcggat tcagattcaa ttgggtttcg gctcggaccg tgggcgtcgt 2340
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```

```
<210> 134
<211> 1116
<212> DNA
<213> Drosophila
```

```
<400> 134
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ctccaggcga ccagtttcgg tgccggccat ctgctgtggc tagccatcaa tgccttcttg 180
tttgtcctta tcctgggcgg caatattctg accattgtgg cggtgcgcac ctgccgccac 240
ctgcgatcgg tcatctccaa tctgttcatc ctgtcgctgg ccgtctccga cttctgtgtg 300
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ctgatctcga ttgcggtgga tcggtatata gcagtcgtct atgctctgca ctatagaaga 480
tacatgaccc gtcgagtggc atatagcatc atcatattca attggtgctt gggtgcattg 540
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catccagact ggaagagcgt ccagattgtg gtcttcatca tgggctgctt cacgctctgt 840
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atgatctaca agacgacgtt ctctctggcc attgccaact ctgctctcaa tccgattatc 960
tactcgtgga gaaactctgg ctttcggcga gcctttgtcc aaacattatg ctgccgaacg 1020
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tcatctcagg agatcaaacc gaaggccact cagtga                            1116
```

```
<210> 135
<211> 371
<212> PRT
<213> Drosophila
```

```
<400> 135
Met Ala Phe Thr Ser Ser Ser Ser Pro Ala Trp Asp Tyr Arg Ser Ser
1               5                   10                  15
Pro Glu Ala Leu Gly Val Val Pro Phe Leu Trp Gln His Gln Asn Ala
            20                  25                  30
Thr Glu Thr Pro Thr Glu Ile Thr Leu Gln Ala Thr Ser Phe Gly Ala
        35                  40                  45
Gly His Leu Leu Trp Leu Ala Ile Asn Ala Phe Leu Phe Val Leu Ile
    50                  55                  60
Leu Gly Gly Asn Ile Leu Thr Ile Val Ala Val Arg Thr Cys Arg His
65                  70                  75                  80
Leu Arg Ser Val Ile Ser Asn Leu Phe Ile Leu Ser Leu Ala Val Ser
```

SUBSTITUTE SHEET (RULE 26)

```
                85                    90                    95
Asp Phe Cys Val Gly Leu Ala Leu Pro Tyr His Leu Val Phe Tyr Met
            100                 105                 110
Gly Ser Asp Ile Gly Ala Met Arg Gly Pro Cys Leu Leu Arg Phe Phe
            115                 120                 125
Leu Leu Ile Cys Ala Cys Cys Val Ser Met Leu Thr Leu Ile Ser Ile
            130                 135                 140
Ala Val Asp Arg Tyr Ile Ala Val Val Tyr Ala Leu His Tyr Arg Arg
145                 150                 155                 160
Tyr Met Thr Arg Arg Val Ala Tyr Ser Ile Ile Ile Phe Asn Trp Cys
                165                 170                 175
Leu Gly Ala Leu Val Ala Leu Leu Pro Val Phe Trp Asn Arg Trp Pro
            180                 185                 190
Asp Ala Gln Ala Cys Glu Phe Asp Glu Val Leu Ala Pro Gly Tyr Ile
            195                 200                 205
Ala Gly Val Ile Thr Pro Gly Phe Val Ile Ile Trp Ile Cys Met Phe
            210                 215                 220
Leu Val Tyr Trp Arg Ile Met Arg Glu Ala Ser Lys Gln Ala Leu Arg
225                 230                 235                 240
Leu Arg Gln Ser Val Val Tyr Asn Thr Asp Glu Ala Thr Thr Met Arg
                245                 250                 255
Asn Leu Leu Leu His Pro Asp Trp Lys Ser Val Gln Ile Val Val Phe
            260                 265                 270
Ile Met Gly Cys Phe Thr Leu Cys Trp Leu Pro Tyr Phe Cys Val Ala
            275                 280                 285
Ile Ala Gln Leu Phe Ser Ile Cys Gln Ser Ser Ser Met Ile Tyr Lys
            290                 295                 300
Thr Thr Phe Ser Leu Ala Ile Ala Asn Ser Ala Leu Asn Pro Ile Ile
305                 310                 315                 320
Tyr Ser Trp Lys Asn Ser Gly Phe Arg Arg Ala Phe Val Gln Thr Leu
                325                 330                 335
Cys Cys Arg Thr Ala Arg Gln Cys Glu Asp Gln Leu Pro Ala Asp Ser
                340                 345                 350
Lys His Arg Met Glu Ala Thr Ser Ser Ser Gln Glu Ile Lys Pro Lys
                355                 360                 365
Ala Thr Gln
            370
```

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<210> 136
<211> 7659
<212> DNA
<213> Drosophila

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tgatatccaa ctggacatga ccagtttccg gaggaatgca ctccagttac acaactggca 180
caaacatttg tttgctgttt tctgaccaaa aacaagccac acttatgctg gcactttttt 240
gttgacagaa atatgcaagc agacacaagt aaatatttat ttgattattt attttaaaga 300
aatgtgcaag ctcaccgaat aaatattata ttttaaaatc aataagtaga aacctaaaca 360
aatacaagct ggtgaagcga ttgctctgca aattccacat atttaaacta ttaatttaca 420
aaaataaatg tggcggtcaa tttccagctg aacagttctc aacaattaat gaaaataatt 480
gccactgata ataatagttt tttttattat tcgattacat actttaaata tttttttagt 540
ttcccaatta gaaaacttttt ttttaacaaa atatttaata ttccgtaaca gtatttatgc 600
ttaattacca gatgacagtt tttatttctt ttgactatac ttacattatt ttgaaaaaat 660
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aaactcaatt aagttacaca cgcaacccac atcttctgtg taaaaaaaaa tcaatgtatt 780
cgaccataaa taattccgct gcaatcagtg caacagtatt cagtcctgga actttaatag 840
cgccaagctg ttggaaaacc aattaaattc cctttcaaat ggagcgtaaa acgcaaaata 900
```

177

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cttacgtatg atgggggcgc cacacactcg cacacgcatt tatgagctcg gcaaaaccca 960
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```

```
<210> 137
<211> 1365
<212> DNA
<213> Drosophila
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SUBSTITUTE SHEET (RULE 26)

<400> 137

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gcggagagcg gaccggactt cgatgcactt cgggccgcct gcgaaacgcg gctaaatgcc 180
agcggtcaac tggcgggctc cggaggacca ggcgcagaag caggaaccca ctgtgccggc 240
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<210> 138
<211> 444
<212> PRT
<213> Drosophila

<400> 138

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            20                  25                  30
Ser Gly Pro Asp Phe Asp Ala Leu Arg Ala Ala Cys Glu Thr Arg Leu
        35                  40                  45
Asn Ala Ser Gly Gln Leu Ala Gly Ser Gly Gly Pro Gly Ala Glu Ala
    50                  55                  60
Gly Thr His Cys Ala Gly Thr Phe Asp Gly Trp Leu Cys Trp Pro Asp
65                  70                  75                  80
Thr Ala Val Gly Thr Ser Ala Tyr Glu Leu Cys Pro Asp Phe Ile Thr
                85                  90                  95
Gly Phe Asp Pro Ala Arg Tyr Ala His Lys Glu Cys Gly Leu Asp Gly
            100                 105                 110
Glu Trp Phe Lys His Pro Leu Thr Asn Lys Thr Trp Ser Asn Tyr Thr
        115                 120                 125
Thr Cys Val Asn Leu Glu Asp Leu Asn Trp Arg His Thr Val Asn Leu
    130                 135                 140
Ile Ser Glu Val Gly Tyr Gly Thr Ser Leu Leu Ala Ile Leu Leu Ser
145                 150                 155                 160
Leu Ala Ile Leu Gly Tyr Phe Asn Asn Ser Ile Arg Ile Phe Val Phe
                165                 170                 175
Arg Leu Asn Arg Ser Leu Lys Cys Ala Arg Ile Thr Leu His Met Asn
            180                 185                 190
Leu Phe Ala Ser Phe Ala Ala Asn Asn Ser Leu Trp Leu Val Trp Tyr
        195                 200                 205
Leu Leu Val Met Pro Asn Ser Glu Leu Leu His Gln Ser Pro Met Arg
    210                 215                 220
```

180

SUBSTITUTE SHEET (RULE 26)

```
Cys Val Ala Leu His Ile Thr Leu His Tyr Phe Leu Leu Ser Asn Tyr
225             230             235             240
Ser Trp Met Leu Cys Glu Gly Phe Tyr Leu His Thr Val Leu Val Ala
            245             250             255
Ala Phe Ile Ser Glu Lys Arg Leu Val Lys Trp Leu Ile Ala Phe Gly
            260             265             270
Trp Gly Ser Pro Ala Ile Val Ile Phe Val Tyr Ser Met Ala Arg Gly
        275             280             285
Leu Gly Gly Thr Pro Glu Asp Asn Arg His Cys Trp Met Asn Gln Thr
    290             295             300
Asn Tyr Gln Asn Ile Leu Met Val Pro Val Cys Ile Ser Met Phe Leu
305             310             315             320
Asn Leu Leu Phe Leu Cys Asn Ile Val Arg Val Val Leu Leu Lys Leu
            325             330             335
Asn Ala Pro Ala Ser Ile Gln Gly Ser Cys Gly Pro Ser Arg Thr Val
            340             345             350
Leu Gln Ala Phe Arg Ala Thr Leu Leu Leu Val Pro Leu Leu Gly Leu
        355             360             365
Gln Tyr Ile Leu Thr Pro Phe Arg Pro Ala Pro Lys His Pro Trp Glu
    370             375             380
Asn Thr Tyr Glu Ile Ile Ser Ala Phe Thr Ala Ser Phe Gln Val Ser
385             390             395             400
Lys Met Phe Ser Phe Arg Phe Cys Ser Arg Phe Val Phe Phe Ser Phe
            405             410             415
Phe Phe Phe Ala Phe Phe Phe Pro Ala Phe Val Leu His Ala Leu Ile
        420             425             430
Lys Ser Leu Tyr Asp Ser Glu Leu Ala Lys Lys Leu
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```

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<211> 4185
<212> DNA
<213> Drosophila

<400> 139
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gtaagcccac caaatcgaag cgttcagggg cggccaaaag gaaaatgaat cattctaccg 240
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```

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<210> 140
<211> 1584
<212> DNA
<213> Drosophila

<400> 140
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```

```
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```

<210> 141
<211> 322
<212> PRT
<213> Drosophila

<400> 141

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            20                  25                  30
Asn Leu Leu Ile Ile Ala Thr Tyr Ala Asn Phe Lys Gly Pro Thr Glu
        35                  40                  45
Val Ile Asn Tyr Tyr Leu Leu Ser Leu Ala Ile Ala Asp Leu Leu Cys
    50                  55                  60
Gly Leu Leu Val Val Pro Phe Ser Val Tyr Pro Ala Leu Thr Gly Glu
65                  70                  75                  80
Trp Met Tyr Gly Asp Ile Val Cys Arg Phe Thr Gly Tyr Leu Glu Val
                85                  90                  95
Thr Leu Trp Ala Val Ser Val Tyr Thr Phe Met Trp Ile Ser Val Asp
            100                 105                 110
Arg Tyr Leu Ala Val Arg Lys Pro Leu Arg Tyr Glu Thr Val Gln Thr
            115                 120                 125
Lys Thr Arg Cys Gln Cys Trp Met Val Phe Thr Trp Ile Ser Ala Ala
        130                 135                 140
Leu Leu Cys Cys Pro Pro Ile Leu Gly Tyr Ser Met Pro Ile Glu Asn
145                 150                 155                 160
Asn Met Thr His Ile Cys Met Leu Asp Trp Gly Asn Met Ala Ala Tyr
                165                 170                 175
Ser Ala Thr Leu Ala Ile Leu Val Leu Gly Pro Ser Leu Ile Ser Ile
            180                 185                 190
Val His Asn Tyr Gly Tyr Ile Phe Val Met Met Arg Lys Ile Arg Ser
            195                 200                 205
Gly Glu Pro Ile His Asp Lys Glu Tyr Ala Thr Ala Leu Ala Glu Asn
        210                 215                 220
Leu Ser Asn Pro Ser His Met Met Ser Phe Ala Leu Val Phe Ala Phe
225                 230                 235                 240
Trp Val Ser Trp Leu Pro Trp Ile Leu Leu Arg Leu Tyr Glu Val Val
                245                 250                 255
Thr Gly Asp Val Ile Gln Ser Thr Leu Ile Asn Phe Ala Val Val Trp
```

SUBSTITUTE SHEET (RULE 26)

```
          260                    265                    270
Ile Gly Ile Leu Asn Ser Phe Trp Lys Ile Leu Ile Met Thr Ser Met
          275                    280                    285
Ser Pro Gln Phe Arg Ile Ala Leu Arg Val Phe Cys Leu Thr Ile Cys
          290                    295                    300
Cys Lys Thr Lys Gly Arg Leu Gln Ala Glu Leu Ile Gly Leu Asp Pro
305                    310                    315                    320
Asp Asp
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<210> 142
<211> 4900
<212> DNA
<213> Drosophila

<400> 142
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SUBSTITUTE SHEET (RULE 26)

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gaattcgccg tcatccatgt agagtttgtc tccggttcac attcatgata atccacatcc 2820
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```

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<211> 1245
<212> DNA
<213> Drosophila

<400> 143
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ctatggcagg agtaccagat gaagaacatg acccctcagg tggatgagtg ccagggctat 180
tgccaggggg aaatatacaa ctggttgcga gcctacaaca gcatccatg atacgtttcg 240
ctgatgattt gcattttcgg gacaatagca aacatcttga acataatggt cctgaccaga 300
aaggaaatgg ccaagacgcc cataaataat atacttaagt ggctggcggt ggccgatatg 360
tttgtgatgc tggaatatat accctataca tcgtatcagt atatatatat ggggccaggt 420
gaaaaagatt tgagctacac ctgggcggtt tgtctgctgg ttcacatgca cttcacccag 480
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cgtgagacgt acgacgtgga caaggtcaac tcggaggcca tgtatcatgt ttatttcgac 720
aaggactcgg tgctctacag attcaacttc tggatacatt ccgtgctcat caaacttctg 780
ccgtgcggca tattaattgt gatcagtgca gtacttatgc acgttttgtg cgaggcatcg 840
```

SUBSTITUTE SHEET (RULE 26)

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cttttgctgg ttgcggtact ggttttgttt ctgatcacgg agtttccgca gggattactt 1020
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gagctgatgg atctgctggc actgatcaac gccgccgtcg gattcgtgct gtacggtctg 1140
atgtcgaaac agttccggac caccttccga tcgctgttca tgaagcggca ctttggcagc 1200
accgaaatga ccagattgac ccgcgtaacc acgacttgcg tctag         1245
```

<210> 144
<211> 414
<212> PRT
<213> Drosophila

<400> 144

```
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1               5                   10                  15
Arg Val Pro Phe Asn Asp Thr Val Leu Lys Asp Tyr His Leu Thr Ser
            20                  25                  30
Thr Asp Ile Glu Lys Phe Val Lys Leu Trp Gln Glu Tyr Gln Met Lys
            35                  40                  45
Asn Met Thr Pro Gln Val Asp Glu Cys Gln Gly Tyr Cys Gln Gly Glu
        50                  55                  60
Ile Tyr Asn Trp Leu Arg Ala Tyr Asn Ser Ile His Gly Tyr Val Ser
65                  70                  75                  80
Leu Met Ile Cys Ile Phe Gly Thr Ile Ala Asn Ile Leu Asn Ile Met
                85                  90                  95
Val Leu Thr Arg Lys Glu Met Ala Lys Thr Pro Ile Asn Asn Ile Leu
            100                 105                 110
Lys Trp Leu Ala Val Ala Asp Met Phe Val Met Leu Glu Tyr Ile Pro
            115                 120                 125
Tyr Thr Ser Tyr Gln Tyr Ile Tyr Met Gly Pro Gly Glu Lys Asp Leu
            130                 135                 140
Ser Tyr Thr Trp Ala Val Cys Leu Leu Val His Met His Phe Thr Gln
145                 150                 155                 160
Ile Leu His Thr Ile Ser Ile Gly Leu Thr Val Thr Leu Ala Val Trp
                165                 170                 175
Arg Tyr Val Ala Ile Arg His Pro Asn Gly Gly Cys Ala Asn Phe Leu
            180                 185                 190
Leu Ala His Ser Arg Glu Ala Ile Leu Leu Pro Phe Ile Leu Ser Pro
            195                 200                 205
Ile Leu Cys Leu Pro Thr Tyr Phe Val Phe Gln Val Arg Glu Thr Tyr
            210                 215                 220
Asp Val Asp Lys Val Asn Ser Glu Ala Met Tyr His Val Tyr Phe Asp
225                 230                 235                 240
Lys Asp Ser Val Leu Tyr Arg Phe Asn Trp Ile His Ser Val Leu
                245                 250                 255
Ile Lys Leu Leu Pro Cys Gly Ile Leu Ile Val Ile Ser Ala Val Leu
            260                 265                 270
Met His Val Leu Cys Glu Ala Ser Arg Arg Arg Leu Lys Leu Arg Asp
            275                 280                 285
Tyr Asn Asn Pro Ala Lys Tyr Ala Ile Gln Leu Asn Leu Asn Glu Thr
        290                 295                 300
Lys Ser Lys Lys Pro Pro Arg Cys Asp Arg Arg Asn Asp Arg Thr Thr
305                 310                 315                 320
Leu Leu Leu Val Ala Val Leu Val Leu Phe Leu Ile Thr Glu Phe Pro
                325                 330                 335
Gln Gly Leu Leu Gly Leu Leu Ser Gly Val Met Glu Lys Cys Phe Phe
            340                 345                 350
Ala His Cys Tyr Pro Pro Phe Gly Glu Leu Met Asp Leu Leu Ala Leu
            355                 360                 365
```

SUBSTITUTE SHEET (RULE 26)

```
Ile Asn Ala Ala Val Gly Phe Val Leu Tyr Gly Leu Met Ser Lys Gln
    370                 375             380
Phe Arg Thr Thr Phe Arg Ser Leu Phe Met Lys Arg His Phe Gly Ser
385                 390                 395                 400
Thr Glu Met Thr Arg Leu Thr Arg Val Thr Thr Thr Cys Val
                405             410
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<210> 145
<211> 4116
<212> DNA
<213> Drosophila

<400> 145

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gcaaaaaata acataatcct gtcaagtcat gcagacaggg cgatttacat tataatttta 180
aatggcaatg gattagtcat catcagtacc tgcttatctg gttttcctga ttttttaaatc 240
aaatctgtga ctgtatctct tacctttcct cttgtacctc gttattataa aatgcgaaaa 300
ccctctgcca aaggacacta taaaacgaat tttttaaaag acgccaaaca aaatggcact 360
ttttgttgag aagaaaatat gccgataaga acgttttact tgtaagacgc tgcagaaaga 420
ttaggaacga aaactatcga caatgtttac ttgtataatc tgagctttct aaaacacaaa 480
aatagtgtac ttttaccata cgcttaattt cgaaattaat ccgggatata cagttgggga 540
tccagatttt aaattcgtga acacagctgc tggagtaggg catttcctga tcgatctgtt 600
agttttcgga ctttttacttt ggttgttgta aacaatatcc gcaagtttct cgcaaagtgg 660
gttgcgttgt gccgtgcctc agtagagcac tacacactac cttcgattga gttcgctggg 720
atttggattt cgttcacagt ccaagtttgg accgtgctag gagaagataa tgatccgatc 780
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SUBSTITUTE SHEET (RULE 26)

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```

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<210> 146
<211> 1709
<212> DNA
<213> Drosophila

<400> 146
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agctacggct tagatggccc atttgtgcac aactggacgg tgattccccg tcacttcgta 180
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188

<210> 147
<211> 492
<212> PRT
<213> Drosophila

<400> 147
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His Cys Ser Trp Gly Phe His Glu Glu Thr His Tyr Pro Cys Ala Phe
            20   25   30
Ile Asp Thr Ala Asn Ile Thr Gly Ser Tyr Gly Leu Asp Gly Pro Phe
        35   40   45
Val His Asn Trp Thr Val Ile Pro Arg His Phe Val Ala Val Tyr Asp
    50   55   60
Phe Val Ile Glu Asn Gly Ile Arg Ile Pro Ala Ser Arg His Leu Arg
65   70   75   80
Ala Cys Val Cys Lys Thr Lys Pro Cys Val Arg Ile Cys Cys Leu Arg
                85   90   95
Gly Glu Ile Tyr Asp Leu Glu Lys Arg Gln Cys Leu Val Pro Val Ala
            100   105   110
Gly Val Ser Ser Leu Pro Ser His Ser His Met Glu Val Glu Leu Gly
        115   120   125
Asn Gly Ser Leu Arg Leu Val Lys Leu Gln Pro Arg Phe Ser Ile His
    130   135   140
Val Glu Thr Pro Cys Glu His Met Lys Ala Val Thr Lys Gly Ser Glu
145   150   155   160
Tyr Val His Trp Thr Leu His Glu Asn Gly Thr Ile Ser His Arg Gly
                165   170   175
His Ile Phe Ser Lys His Tyr Cys Phe Thr Pro Leu Leu His Gly Asn
            180   185   190
Ser Thr Trp Glu Trp Gln Pro Leu Ala Cys Ala Pro Glu Lys Leu Tyr
        195   200   205
Phe Val Leu Gly Val Arg Glu Trp Thr Tyr Ala Ile Cys Leu Leu Ile
    210   215   220
Ala Ile Leu Ser Met Phe Ile Val Leu Met Val Tyr Leu Met Cys Ser
225   230   235   240
Glu Met Arg Asn Ser Phe Tyr Gly Val Ala Ile Lys Ala Tyr Ala Ile
                245   250   255
Cys Met Ile Leu Gly Tyr Ala Leu Leu Ala Tyr Leu Thr Leu His Asn
            260   265   270
Pro Ala Asn Leu Ser Asn Ala Ala Cys Arg Ile Leu Pro Ser Leu Ala
        275   280   285
Leu Met Asn Leu Val Leu Ser Phe Tyr Ile Leu Ser Phe Ile Ala Phe
    290   295   300
Lys Leu Tyr Leu Ser Phe Tyr Gly Val Val Phe Thr Lys Leu Met Phe
305   310   315   320
Trp Leu Ile Phe Thr Pro Ile Val Leu Val Ala Val Gly Trp Ser Phe
                325   330   335
Phe Val Gly Phe Ser Tyr Tyr Gly Ser Arg Leu Ile Phe Gly Gly Asp
            340   345   350
Thr Cys Trp Phe Asp Pro Arg Asn Trp Ser Val Met Ile Tyr Phe Tyr
        355   360   365
Ala Pro Val Phe Val Ala Cys Ala Ile Ser Gly Phe Phe Tyr Val Leu
    370   375   380
Ser Gln Ile Tyr Ile Arg Asp Gln Pro Asp Ile Glu Thr Glu Lys Ser
385   390   395   400
Phe Glu Ser Ile Glu Lys Asn Arg Phe Lys Ser Phe Trp Lys Tyr Phe
                405   410   415
Gly Tyr Thr Ala Val Val Trp Val Val Cys Ile Cys Ser Phe Ala Phe
            420   425   430

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SUBSTITUTE SHEET (RULE 26)

```
Asn Tyr Tyr Trp Glu Asn Arg Ser His Leu Asn Tyr Ala Val Ser Phe
        435             440             445
Cys Met Ala Phe His Gly Phe Ala Ala Leu Tyr Ala Leu Ile Gly Lys
    450             455             460
Asn Gln Gln Ile Gln Asn Phe Leu Arg Arg Ile Asp Asn Gly Glu Asp
465             470             475             480
Thr Cys Glu Asn Ser Val Pro Leu Ser Ser Phe Gly
            485             490
```

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<210> 148
<211> 3772
<212> DNA
<213> Drosophila
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<400> 148
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tatccgtcgt tgtaaagcta ccttatccac tacgattact acactatcct acaaaaaact 180
atgctggtta aaagactata cacctagctc catatactat atatatatat acaatatcga 240
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ctttagcact cttagtttaa tgtttaaagt tagtttcgct gttaagttta caccgtagtc 480
gaggcgtctt gagtagttct tttgtacatt aagcttacac ttagctctac attagatata 540
ccatgtcgaa cctacgagtc tacgaacata cgaacatata tatgtgcgtt gaaagcgttg 600
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SUBSTITUTE SHEET (RULE 26)

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<212> DNA
<213> Drosophila

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<211> 521
<212> PRT
<213> Drosophila

<400> 150
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SUBSTITUTE SHEET (RULE 26)

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Pro Tyr Pro Gly Val Phe Val Gly Asp Leu Ser Gln Leu Asn Arg Phe
        35                  40              45
Lys Arg His Ala Phe Ser Ala Val Val Gly Thr Leu Phe Val Leu Ala
    50                  55              60
Phe Cys Gly Asn Leu Ser Thr Leu Tyr Val Asn Ser Arg Arg Lys Leu
65                  70              75                  80
Arg Pro Phe Phe Arg Ala Cys Leu Ile Ser Leu Ala Cys Ser Asp Leu
            85                  90              95
Val Ser Ser Ile Phe Cys Thr Val Ser Tyr Met Ala Gln Phe Gln Ala
            100             105             110
Gln Tyr Leu Gln Leu Trp Thr Ile Gly Gly Phe Met Cys Lys Phe Val
    115             120             125
Pro Phe Ile Thr Thr Thr Ser Val Leu Ser Gly Ser Leu Thr Leu Val
    130             135             140
Ala Ile Ala Leu Asp Arg Tyr Leu Ala Val Met Arg Pro Val Leu Gly
145             150             155             160
Phe Trp Ser Pro Asp Lys Arg Phe Ser Thr Leu Ser Met Leu Leu Ile
            165             170             175
Trp Ala Cys Ser Ile Gly Ser Ser Gly Pro Leu Leu Gly Ile Tyr Asp
        180             185             190
Tyr Arg Lys Ile Tyr Leu Leu Asp Val Glu Asp Ser Ser Glu Glu Ser
        195             200             205
Glu Glu Val Val Thr Ala Val Pro Glu Glu Leu Val Val Thr Glu Leu
    210             215             220
Glu Met Val His Met Cys Leu Ala Gly Asp His Asp Val Gly Leu Tyr
225             230             235             240
Tyr Val Ile Leu Phe Thr Leu Ile Phe Leu Pro Cys Ile Val Ser Phe
            245             250             255
Leu Trp Leu Asn Ala Val Ile Ala Arg Gln Leu Trp Leu Arg Arg His
            260             265             270         .
Tyr His Gln Glu Gln Gln Glu Gln His Gln Glu Pro Lys Glu Gly Gln
        275             280             285
Phe Lys Thr Met Ala Asn Gly Gly Asp Leu Leu Met Pro Ser Thr Leu
    290             295             300
Val Ser Ala Met Gly Val Ala Val Pro Phe Ala Leu Asp Asn Thr Pro
305             310             315             320
Leu Pro Pro Lys Ser Thr Val Asn Ala Pro Gly Lys Lys Thr Thr Ala
            325             330             335
Ala Ala Leu Ala Arg Glu Ala Arg His Arg Lys Met Val Val Val Val
            340             345             350
Leu Leu Met Met Ala Val Phe Ile Cys Leu Arg Leu Pro Ala Trp Val
        355             360             365
Phe Leu Ile Met Arg Leu Tyr Gly Ser Tyr Ser Glu Pro Ile Asp Trp
    370             375             380
Leu Leu Tyr Phe Ser Phe Gly Ile Leu Asn Leu Phe Ser Cys Ala Leu
385             390             395             400
Asn Pro Ile Phe Tyr Thr Phe Leu Thr Gln Thr Ile Arg Thr Leu Thr
            405             410             415
Leu Val Lys His Lys Ile Gln Gly Phe Leu Gly Cys Pro Pro Gly Lys
        420             425             430
Val Pro Asp Gly Met Pro Thr Asp Gln Met Asp Lys Ser Gly Cys Cys
        435             440             445
Cys Gly Leu Arg Pro Pro Thr Phe Thr Trp Arg Cys His Pro Ser Arg
    450             455             460
Asp Arg Ala Ala Ala Thr Val Ile Arg Asp Val Asp Gln Pro Asp Pro
465             470             475             480
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SUBSTITUTE SHEET (RULE 26)

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Pro Ser Asp Gln Val Gln Pro Asp Pro Ser Ser Leu Arg Arg Phe Leu
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Ser Tyr Lys Gln Glu Val Phe Thr Ile Tyr Lys Gln Cys Gly Asp Ser
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Ser Ser Ala Ser Ile Glu Ser Ser Ala
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<211> 8599
<212> DNA
<213> Drosophila

<400> 151
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193

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194

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<210> 152
<211> 2121
<212> DNA
<213> Drosophila

<400> 152
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gcggtgctca tcctggtcct cacactgggc gtcatcgggg ccaactgcct ggtcatcttc 180
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gccgcccacc accccatcc gcacccacat cccaccgccg cccagcagct gcagatgcac 780
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SUBSTITUTE SHEET (RULE 26)

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```

<210> 153
<211> 706
<212> PRT
<213> Drosophila

<400> 153

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            20                  25                  30
Ile Gly Ile Ala Glu Thr Ile Glu Ala Val Leu Ile Leu Val Leu Thr
            35                  40                  45
Leu Gly Val Ile Gly Ala Asn Cys Leu Val Ile Phe Val Ile Asn Asn
        50                  55                  60
Arg Arg Tyr Ala Ala Tyr Ile His Gln Gln Pro Arg Tyr Leu Leu Thr
65                  70                  75                  80
Ser Leu Ala Leu Asn Asp Leu Thr Ile Gly Leu Leu Ile Thr Pro Phe
                85                  90                  95
Gly Leu Met Pro Ala Leu Phe His Cys Trp Pro Tyr Gly Glu Ile Phe
            100                 105                 110
Cys Gln Ile Gln Ala Leu Leu Arg Gly Ala Leu Ser Gln Gln Ser Ala
            115                 120                 125
Val Ile Leu Val Cys Met Ala Val Asp Arg Tyr Met Cys Ala Leu His
        130                 135                 140
Pro Arg Arg Tyr Tyr Gln His Ser Ser Lys Lys Gly Cys Val Ala Ile
145                 150                 155                 160
Leu Ser Leu Thr Trp Ile Ile Ser Leu Thr Val Phe Gly Phe Leu Val
                165                 170                 175
Leu Pro Lys Gly Tyr Tyr Phe Asn Asn Thr Gly Leu Met Ala Cys Glu
            180                 185                 190
Pro Phe Tyr Ser Lys Pro Ser Tyr Arg Ile Leu Ser Thr Cys Ala Leu
            195                 200                 205
Tyr Phe Pro Thr Thr Met Val Leu Met Tyr Cys Tyr Gly Ser Ser Phe
        210                 215                 220
His Met Ser Arg Phe Arg Leu Asn Asp Pro Thr Met Pro Leu Thr Ala
225                 230                 235                 240
```

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SUBSTITUTE SHEET (RULE 26)

```
Ala Ala His His Pro His Pro His Pro His Pro Thr Ala Ala Gln Gln
                245         250                 255
Leu Gln Met His Gln His Gln Gln His His Gln Gln Ala Gly Met His
            260             265             270
Ser His Leu Tyr His Gly His Ser His His Pro Ser His Pro Ser His
            275             280             285
Pro Asn His Pro Asn His His Gly His Pro His His His Gly Pro Pro
    290             295             300
Val Met Gly His Leu Ser Met Ala Met Ser Met Gly Leu Ala Gly Met
305             310             315                 320
Pro Asn Met Thr Asn Lys Ile Thr Lys Lys Val Ser Gln Leu Asn Arg
            325             330             335
Ile Val Pro Ile Gln Glu Lys Asn Ser Ser Gly Ser Thr Ser Arg Ser
            340             345             350
Met Ala Ala Ile Ser Leu Gly Phe Ile Val Met Val Thr Pro Trp Thr
            355             360             365
Ile Gln Glu Ile Val Thr Ala Cys Thr Gly Ser Lys Ala Ser Val Leu
    370             375             380
Tyr Lys Gly Leu Leu Cys Asp Arg Phe Leu Pro Pro Phe Leu Asp Phe
385             390             395             400
Leu Val Thr Trp Thr Ala Leu Ser Asn Ser Leu Trp Asn Pro Phe Met
            405             410             415
Tyr Trp Leu Leu Asn Ser Asp Phe Arg Arg Met Ser Arg Gln Leu Met
            420             425             430
Pro Asn Lys Cys Phe Pro His Glu Asp Thr Pro Glu His Lys Ser Gly
            435             440             445
Cys Cys His Ile Asn Ala Asn Asp Phe Glu Ile Thr Thr Leu Pro Ile
    450             455             460
Pro Pro Glu Pro Pro Ser Ser Arg Pro Pro Gly Gly Ala Gly Gly Gly
465             470             475             480
Gly Gly Gly Pro Ser Ser Gly Gly Pro Ser Ser Gly Gly Gly Val Ala
            485             490             495
Ser Ser Ile Gly Gly Ser Val Leu Gly Ile Cys Gly Arg Ser Arg Thr
            500             505             510
Asn Ser Leu Ser Arg Ser Ala Ser Gln Tyr Ile Arg Gly Thr Met Gly
            515             520             525
Gly Gly Val His Asn His Gln Ala Thr Glu Thr Phe Ser Thr Thr Arg
    530             535             540
Pro Asp Ile Glu Gly Leu Ser Glu Lys Tyr Trp Gly Glu Ile Leu Glu
545             550             555             560
Arg Thr Val Ser Ser Gly Asn Leu Asn Ala Met Gln Lys His Leu Pro
            565             570             575
Pro His Leu Pro Tyr Ala His His Leu Val His Gln Ile His Gln Pro
            580             585             590
Gln Gln His His Gln Gln Gln Thr Thr Ser Phe Ser Lys Ala Ser Asp
            595             600             605
Leu Gln Leu Asn Leu Asn Leu Ser Gln Ala Ala Thr Ala Ala Glu Leu
            610             615             620
Gly Lys Phe Ser Asn Ser Glu Pro Lys Leu Cys Glu His Leu Phe His
625             630             635             640
Asp Tyr Ala Glu Asp Val Ile Leu Ala Lys Asn Gln Leu Leu Ala Arg
            645             650             655
Gln Ala Lys Cys Ser His His Pro Leu His Gln Gln Ala Lys Thr Arg
            660             665             670
Leu His Ser His Thr Gly Ser Leu Arg Phe Ser Arg Ile Arg Ala Ala
            675             680             685
Cys His Ser Pro Pro Pro Glu Lys Ser Ala Phe Pro Met Ala Glu Tyr
    690             695             700
Arg Lys
705
```

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SUBSTITUTE SHEET (RULE 26)

<210> 154
<211> 3332
<212> DNA
<213> Drosophila

<400> 154
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ttagtattgc ggactcatcc catccaactg ttgactcatt tcaaattcta tttaattata 180
tttctggtcc tggcacgaac aataaattga gtttatatgt attacgcccc ttcttgtggt 240
ctcactttat gaaaaagtta attgcgtgta gttgttggct ttgctagatg gatttttatt 300
gtgccgcttt actgtctgct tttttcttca ttttccactc gcctttcatt tttcatccgc 360
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gagcagaatt tcatatagtt gattgcattg tctgcaggaa gatgttcgca cgatgatgca 480
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tgaaatgctg atagcatgcg ctcaatattg tcagtaaata atacgcgctt gttagagcca 600
actgcatacc aactaaactg aacacagtga gaataaacat aacagaaagt tgaatttgct 660
taatatataa tttcataaat ttgtcacacc aaaattcgga tttaaattaa aagtataatt 720
atattaataa cattatttaa tataattata attatatata aaaatatatt tttatatgta 780
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SUBSTITUTE SHEET (RULE 26)

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atatggcaga gctttgcaaa aacgggtaaa cttaatccca tttttatatg atcgaatctc 3300
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<210> 155
<211> 1332
<212> DNA
<213> Drosophila

<400> 155
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accaatatcg cgaccaacgg ctgtgcccat tcgggcatcc tgttatttgt gctgacagct 180
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<210> 156
<211> 393
<212> PRT
<213> Drosophila

<400> 156
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1               5                   10                  15
Gly Lys Ala Ile Met Glu Gly His Ser Thr Pro Asn Gly Ala Ala Ala
            20                  25                  30
Ser His Arg Asn Asn Ser Thr Arg Thr Asn Ile Ala Thr Asn Gly Cys
        35                  40                  45
Ala His Ser Gly Ile Leu Leu Phe Val Leu Thr Ala Met Thr Leu Thr
    50                  55                  60
Ser Leu Ile Thr Pro Thr Glu Gln Leu Ala Val Ala Pro Asn Gly Thr
65                  70                  75                  80
Thr Leu His Gln Leu Glu Ser Val Glu Ser Glu Ser Tyr Pro Ser Ile
                85                  90                  95
Asn Gly Thr Gln Asn Glu Thr Met Val Thr Ser Val Arg Pro His Leu
            100                 105                 110
Asp His Arg Asn Arg Pro Thr Gln Gln Asn Gly Ser His Tyr Leu Glu
        115                 120                 125
Tyr Asp Asp Asp Gly Pro Asp Cys Ser Tyr Ser Tyr Asn Phe Ile Leu
    130                 135                 140
Lys Leu Ile Thr Met Ile Leu Tyr Ala Leu Val Cys Ile Ile Gly Leu
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SUBSTITUTE SHEET (RULE 26)

```
145              150              155              160
Phe Gly Asn Thr Leu Val Ile Tyr Val Val Met Arg Phe Ser Lys Met
             165                  170              175
Gln Thr Val Thr Asn Ile Tyr Ile Leu Asn Leu Ala Ile Ala Asp Glu
             180                  185              190
Cys Phe Leu Ile Gly Ile Pro Phe Leu Leu Tyr Thr Met Gln Val Gly
         195              200              205
Asn Trp Pro Phe Gly Asn Tyr Met Cys Lys Ala Tyr Met Val Ser Thr
    210              215                  220
Ser Ile Thr Ser Phe Thr Ser Ser Ile Phe Leu Leu Ile Met Ser Ala
225              230                  235              240
Asp Arg Tyr Ile Ala Val Cys His Pro Ile Ser Ser Pro Arg Tyr Arg
             245                  250              255
Thr Pro Phe Val Ser Lys Leu Val Ser Ala Phe Ala Trp Met Thr Ser
         260              265              270
Val Leu Leu Met Leu Pro Val Ile Leu Phe Ala Ser Thr Val Gln Ser
         275              280              285
Ser Asn Gly Asn Val Ser Cys Asn Ile Glu Trp Pro Asp Thr Gln Asn
         290              295              300
Ser His Thr Asp Ser Thr Phe Ile Leu Tyr Ser Leu Val Leu Gly Phe
305              310              315                  320
Ala Thr Pro Leu Thr Phe Ile Leu Val Phe Tyr Cys Leu Val Ile Arg
             325                  330              335
Lys Leu His Thr Val Gly Pro Lys His Lys Ser Lys Glu Lys Lys Arg
             340              345              350
Ser His Arg Lys Val Thr Lys Leu Val Leu Thr Val Ile Ile Tyr Asp
         355              360                  365
Ile Ser Ile Ser Cys Gly Thr Asn Tyr Tyr Leu Thr Thr Leu Val Phe
         370              375                  380
Ser Leu Ile Asn Ile Ile Ile Thr Leu
385              390
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<211> 5453
<212> DNA
<213> Drosophila

<400> 157
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tgatgtttgc actccggtgc agcgggacta taaataagcc gggtatttat tagggggcaat 540
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200

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<211> 1902
<212> DNA
<213> Drosophila

<400> 158
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<212> PRT
<213> Drosophila

<400> 159
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SUBSTITUTE SHEET (RULE 26)

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Pro Ser Ala Pro Thr Ala Gly Thr Phe Glu Ser Lys Ser Met Leu Glu
            35                  40                  45
Pro Thr Ser Ser His Ser Leu Ala Thr Gly Arg Val Pro Leu Leu His
            50                  55                  60
Asp Phe Asp Ala Ser Thr Thr Glu Ser Pro Gly Thr Tyr Val Leu Asp
65                  70                  75                  80
Gly Val Ala Arg Val Ala Gln Leu Ala Leu Glu Pro Thr Val Met Asp
                85                  90                  95
Ala Leu Pro Asp Ser Asp Thr Glu Gln Val Leu Gly Leu Tyr Cys Asn
                100                 105                 110
Trp Thr Trp Asp Thr Leu Leu Cys Trp Pro Pro Thr Pro Ala Gly Val
            115                 120                 125
Leu Ala Arg Met Asn Cys Pro Gly Gly Phe His Gly Val Asp Thr Arg
            130                 135                 140
Lys Phe Ala Ile Arg Lys Cys Glu Leu Asp Gly Arg Trp Gly Ser Arg
145                 150                 155                 160
Pro Asn Ala Thr Glu Val Asn Pro Pro Gly Trp Thr Asp Tyr Gly Pro
                165                 170                 175
Cys Tyr Lys Pro Glu Ile Ile Arg Leu Met Gln Gln Met Gly Ser Lys
                180                 185                 190
Asp Phe Asp Ala Tyr Ile Asp Ile Ala Arg Arg Thr Arg Thr Leu Glu
                195                 200                 205
Ile Val Gly Leu Cys Leu Ser Leu Phe Ala Leu Ile Val Ser Leu Leu
            210                 215                 220
Ile Phe Cys Thr Phe Arg Ser Leu Arg Asn Asn Arg Thr Lys Ile His
225                 230                 235                 240
Lys Asn Leu Phe Val Ala Met Val Leu Gln Val Ile Ile Arg Leu Thr
                245                 250                 255
Leu Tyr Leu Asp Gln Phe Arg Arg Gly Asn Lys Glu Ala Ala Thr Asn
                260                 265                 270
Thr Ser Leu Ser Val Ile Glu Asn Thr Pro Tyr Leu Cys Glu Ala Ser
            275                 280                 285
Tyr Val Leu Leu Glu Tyr Ala Arg Thr Ala Met Phe Met Trp Met Phe
            290                 295                 300
Ile Glu Gly Leu Tyr Leu His Asn Met Val Thr Val Ala Val Phe Gln
305                 310                 315                 320
Gly Ser Phe Pro Leu Lys Phe Phe Ser Arg Leu Gly Trp Cys Val Pro
            325                 330                 335
Ile Leu Met Thr Thr Val Trp Ala Arg Cys Thr Val Met Tyr Met Asp
            340                 345                 350
Thr Ser Leu Gly Glu Cys Leu Trp Asn Tyr Asn Leu Thr Pro Tyr Tyr
            355                 360                 365
Trp Ile Leu Glu Gly Pro Arg Leu Ala Val Ile Leu Leu Asn Phe Cys
370                 375                 380
Phe Leu Val Asn Ile Ile Arg Val Leu Val Met Lys Leu Arg Gln Ser
385                 390                 395                 400
Gln Ala Ser Asp Ile Glu Gln Thr Arg Lys Ala Val Arg Ala Ala Ile
                405                 410                 415
Val Leu Leu Pro Leu Leu Gly Ile Thr Asn Leu Leu His Gln Leu Ala
                420                 425                 430
Pro Leu Lys Thr Ala Thr Asn Phe Ala Val Trp Ser Tyr Gly Thr His
            435                 440                 445
Phe Leu Thr Ser Phe Gln Gly Phe Phe Ile Ala Leu Ile Tyr Cys Phe
            450                 455                 460
Leu Asn Gly Glu Val Arg Ala Val Leu Leu Lys Ser Leu Ala Thr Gln
465                 470                 475                 480
Leu Ser Val Arg Gly His Pro Glu Trp Ala Pro Lys Arg Ala Ser Met
                485                 490                 495
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203

SUBSTITUTE SHEET (RULE 26)

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Tyr Ser Gly Ala Tyr Asn Thr Ala Pro Asp Thr Asp Ala Val Gln Pro
        500                     505             510
Ala Gly Asp Pro Ser Ala Thr Gly Lys Arg Ile Ser Pro Pro Asn Lys
        515                     520             525
Arg Leu Asn Gly Arg Lys Pro Ser Ser Ala Ser Ile Val Met Ile His
        530                     535             540
Glu Pro Gln Gln Arg Gln Arg Leu Met Pro Arg Leu Gln Asn Lys Ala
545                     550             555                 560
Arg Glu Lys Gly Lys Asp Arg Val Glu Lys Thr Asp Ala Glu Ala Glu
                565             570                 575
Pro Asp Pro Thr Ile Ser His Ile His Ser Lys Glu Ala Gly Ser Ala
            580             585                 590
Arg Ser Arg Thr Arg Gly Ser Lys Trp Ile Met Gly Ile Cys Phe Arg
        595                 600                 605
Gly Gln Lys Val Leu Arg Val Pro Ser Ala Ser Ser Val Pro Pro Glu
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Ser Val Val Phe Glu Leu Ser Glu Gln
625                 630
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<211> 4385
<212> DNA
<213> Drosophila

<400> 160
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SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila
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gccaatggca agacgattgc ctcagtgcca ttgagtcaat acattctgga ctacaatcgg 600
caggatgagg tgaccatgca ggtcatgtcg agtacaacgc cagatgtttc ctgggcgata 660
ccaataacca catcctcgtc gttgggtgag cgcaatgtga ctgtctataa gctgtatcac 720
agcgcactgg cgctgcgtga tcggcagttc aggaatgcga ccttccttat atacagtgtc 780
```

205

SUBSTITUTE SHEET (RULE 26)

```
ctgatcaagc tgataccctg cttcgcactg accattctgt ctgtgcggct catcggtgct 840
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ccaattgtca atggaaaggt ggtgattccg acgcaaccca agagctgtaa actgctggag 960
aaggagaagc agaccgatcg caccacgagg atgcttctgg cggtactgct gctcttcctg 1020
gtcaccgagt ttccacaggg cattatgggt ctgctgaatg tgctcctggg cgatgccttc 1080
tttctgcaat gttacctaaa gctgagtgac cttatggaca tcttggcgct tattaattcg 1140
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ctcttccgtc cgcgctggct ggacaaatgg ctgccgctgt cgcagcacga cggcgaaggg 1260
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```

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<211> 462
<212> PRT
<213> Drosophila

<400> 162
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Asp Phe His Thr Asn Tyr Lys Tyr Phe His Gly Tyr Phe Ser Leu Ile
            20                  25                  30
Val Cys Ile Leu Gly Thr Ile Ala Asn Thr Leu Asn Ile Ile Val Leu
        35                  40                  45
Thr Arg Arg Glu Met Arg Ser Pro Thr Asn Ala Ile Leu Thr Gly Leu
    50                  55                  60
Ala Val Ala Asp Leu Ala Val Met Leu Glu Tyr Ile Pro Tyr Thr Val
65                  70                  75                  80
His Asp Tyr Ile Leu Ser Val Arg Leu Pro Arg Glu Glu Gln Leu Ser
                85                  90                  95
Tyr Ser Trp Ala Cys Phe Ile Lys Phe His Ser Val Phe Pro Gln Val
            100                 105                 110
Leu His Thr Ile Ser Ile Trp Leu Thr Val Thr Leu Ala Val Trp Arg
        115                 120                 125
Tyr Ile Ala Val Ser Tyr Pro Gln Arg Asn Arg Ile Trp Cys Gly Met
    130                 135                 140
Arg Thr Thr Leu Ile Thr Ile Ala Thr Ala Tyr Val Val Cys Val Leu
145                 150                 155                 160
Val Val Ser Pro Trp Leu Tyr Leu Val Thr Ala Ile Ala Lys Phe Leu
                165                 170                 175
Glu Thr Leu Asp Ala Asn Gly Lys Thr Ile Ala Ser Val Pro Leu Ser
            180                 185                 190
Gln Tyr Ile Leu Asp Tyr Asn Arg Gln Asp Glu Val Thr Met Gln Val
        195                 200                 205
Met Ser Thr Thr Pro Asp Val Ser Trp Ala Ile Pro Ile Thr Thr
    210                 215                 220
Ser Ser Ser Leu Gly Glu Arg Asn Val Thr Val Tyr Lys Leu Tyr His
225                 230                 235                 240
Ser Ala Leu Ala Leu Arg Asp Arg Gln Phe Arg Asn Ala Thr Phe Leu
                245                 250                 255
Ile Tyr Ser Val Leu Ile Lys Leu Ile Pro Cys Phe Ala Leu Thr Ile
            260                 265                 270
Leu Ser Val Arg Leu Ile Gly Ala Leu Leu Glu Ala Lys Arg Arg Arg
        275                 280                 285
Lys Ile Leu Ala Cys His Ala Ala Asn Asp Met Gln Pro Ile Val Asn
    290                 295                 300
Gly Lys Val Val Ile Pro Thr Gln Pro Lys Ser Cys Lys Leu Leu Glu
305                 310                 315                 320
Lys Glu Lys Gln Thr Asp Arg Thr Thr Arg Met Leu Leu Ala Val Leu
                325                 330                 335
```

206

SUBSTITUTE SHEET (RULE 26)

```
Leu Leu Phe Leu Val Thr Glu Phe Pro Gln Gly Ile Met Gly Leu Leu
            340                 345                 350
Asn Val Leu Leu Gly Asp Ala Phe Phe Leu Gln Cys Tyr Leu Lys Leu
            355                 360                 365
Ser Asp Leu Met Asp Ile Leu Ala Leu Ile Asn Ser Ser Ile Asn Phe
    370                 375                 380
Ile Leu Tyr Cys Ser Met Ser Arg Gln Phe Arg Ser Thr Phe Ala Leu
385                 390                 395                 400
Leu Phe Arg Pro Arg Trp Leu Asp Lys Trp Leu Pro Leu Ser Gln His
            405                 410                 415
Asp Gly Glu Gly Arg Val Gly Gly Ser Gly Gly Leu Gly Gly Tyr Gly
            420                 425                 430
Gly Tyr Gly Arg Gln Arg Leu Leu His Thr Asp Ala Val Ser Lys Ser
            435                 440                 445
Met Ala Ile Asp Leu Gly Leu Thr Thr Gln Val Thr Asn Val
    450                 455                 460
```

```
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<211> 4214
<212> DNA
<213> Drosophila

<400> 163
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gtaaatagcg ggcatcaatt gtgcatagtt tgaaggtaag ttgcccaata aatggcgcaa 180
agctcgtaac cgcgaattat atatgtatgt acatatacga taaaaataaa gtgtggcctt 240
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cagcctttg tttaaatttg agcagaaagt caagactgca aatggccaga aagacgaagg 1920
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tccagttgaa gtagacaaaa ttactcaacc tatgtttctg caagccacat gcgagagctt 2040
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gtagtagatg attaactggc catagtggct tttacgggca tctctcacag atccaagtag 2160
```

207

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```

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<211> 1859
<212> DNA
<213> Drosophila

<400> 164
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cccgtaaaag ccactatggc cagttaatca tctactactt gctgtccatg atcgttggtt 1080
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```
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<210> 165
<211> 513
<212> PRT
<213> Drosophila

<400> 165

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             20                  25                  30
His Thr Val Asn Ile Thr Asp Gly Leu Arg Met Lys Asp Gly Ser Tyr
         35                  40                  45
Ser Tyr Ala Gly Val Val Val Pro Pro His Leu Met Ala Glu Tyr Ser
     50                  55                  60
Phe Lys Val Ile Asp Gly Val Glu Tyr Arg Ala Lys Lys His Leu Arg
 65                  70                  75                  80
Gly Cys Val Cys Leu Leu Lys Pro Cys Ile Ser Phe Cys Cys Pro Glu
                 85                  90                  95
Asn Leu Val Phe Asp Ala Lys His Trp Asn Cys Thr Met Pro His Gln
                100                 105                 110
Val Arg Glu Ser Thr His Val Glu Leu Thr Tyr Ala Asn Arg Thr Val
             115                 120                 125
Asp Gln Val Arg Ile Arg Asp Arg Phe Val Val Arg Thr Glu Leu Gly
         130                 135                 140
Cys Arg Asn Lys Phe Val Asp Lys Lys His Asp Asn Phe Trp Gln Trp
145                 150                 155                 160
Asp Leu Phe Glu Asn Gly Thr Leu Arg Arg Asp Asn Arg Leu Trp Ser
                165                 170                 175
Thr Asp Glu Tyr Cys Phe Ser Pro Leu Glu His Asn Pro Glu Gln Trp
             180                 185                 190
Glu Leu Thr Pro Leu Asn Cys Glu Arg Phe Gln Thr Gly Tyr Arg Val
             195                 200                 205
Trp Ile Tyr Ala Ile Cys Ser Ile Ile Ala Ile Ile Ile Asn Ile Phe
         210                 215                 220
Ile Leu Ser Leu Leu Gly Ser Val Arg Asp Ala Arg Lys Ser His Tyr
225                 230                 235                 240
Gly Gln Leu Ile Ile Tyr Tyr Leu Leu Ser Met Ile Val Gly Tyr Ser
                 245                 250                 255
Leu Leu Val Tyr Leu Ala Leu Lys Asn Pro Met Lys Leu Ser His Val
             260                 265                 270
Ala Cys Arg Asn Ile Gly Phe Leu Ala Tyr Phe Cys Ile Met Leu Ser
         275                 280                 285
Phe Val Phe Leu Ala Ile Cys Ser Leu Asp Phe Leu Leu Lys Phe Lys
         290                 295                 300
Gln Lys Ala Val Arg Ser Ser Val Arg Arg Leu Ser Leu Ala Leu Ala
305                 310                 315                 320
```

SUBSTITUTE SHEET (RULE 26)

```
Val Leu Ala Val Ile Gly Leu Arg Phe Leu Val Ser Leu Ala Gln Asp
              325             330             335
Ser Lys Leu Pro Lys His Phe Lys Pro Gly Met Gly Glu Asp Tyr Cys
              340             345             350
Trp Phe Asp Val Arg Thr Trp Gly Ile Leu Ile Tyr Tyr Tyr Gly Pro
              355             360             365
Ile Ala Leu Leu Leu Ile Phe Ser Ile Val Cys Cys Leu Lys Ala Tyr
          370             375             380
Phe Ser Ile Tyr Glu Leu Pro Pro Asp Thr Gln Tyr Ile Leu Gly Thr
385             390             395             400
Gln Leu Lys Ile Val Lys Thr His Phe Tyr Ala Phe Ser Ala Tyr Ile
              405             410             415
Val Gly Val Phe Ala Val Trp Ile Arg Glu Ile Val Val Tyr Ile Met
              420             425             430
Ala Arg Val Arg Glu His Phe Phe Ile Ile Asp Phe Trp Ser Gly Ile
              435             440             445
Cys Ile Leu Gly Leu Ala Ile Ala Gly Phe Ile Leu Leu Leu Gly Lys
          450             455             460
Asn Leu His Val Lys Ser Trp Trp Ala Ile Asn Val Glu Ser Ser Gln
465             470             475             480
Thr Asp Leu Ser Ile Ile Asn Ala Arg Val Tyr Lys Phe Asp Glu Lys
              485             490             495
Gly Asp Leu Lys Ser Ser Asp Ser Pro Tyr Lys Pro Thr Val Thr Ser
              500             505             510
Leu
```

<210> 166
<211> 5208
<212> DNA
<213> Drosophila

<400> 166

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210

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SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

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<213> Drosophila

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Ile Asp Asp Pro Asn Val Pro Cys Asn Phe Tyr Asp Thr Val Asn Leu
        50   55   60
Thr Gly His Arg Leu Phe Pro Asn Gly Ser Tyr Asp Tyr Tyr Gly Thr
65   70   75   80
Ile Val Pro Ala Glu Leu Val Gly Thr Tyr Asp Tyr Ile His Ser Ser

SUBSTITUTE SHEET (RULE 26)

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Asn Ser Glu Val Asp Gly Cys Ile Ile Asp His Ser Asp Asn Arg Thr
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Trp Pro Asp Pro Pro Met Leu Asn Ile Thr Phe Arg Asn Glu Ser Thr
145             150             155             160
Ile Leu Val Asn Met Phe Thr Gln Phe Ala Ile Gln Ser Phe Arg Pro
            165             170             175
Cys Pro Lys Met Phe Ser Leu Gln Pro Glu Thr Asn Asn Trp Asp Asp
            180             185             190
Tyr Leu Leu Phe Glu Asn Gly Ser Met Leu Arg Val Asp Asp Lys Leu
            195             200             205
Leu Ile Arg Lys Asn Glu Phe Cys Met Val Pro Thr Tyr Val Asn Glu
            210             215             220
Ser Asp Met Phe Tyr Thr Ile His Pro Ala Asn Cys Asp Met Gln Asp
225             230             235             240
Asp His Ser Thr Val Lys Ile Ile Asn Ser Tyr Ala Val Tyr Leu Leu
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Ile Pro Glu Leu Arg Asn Gln His Gly Lys Ser Leu Val Cys Tyr Leu
            260             265             270
Ile Gly Leu Ser Val Gly Tyr Ser Ser Leu Cys Tyr Val Gln Leu Tyr
            275             280             285
Gln Val Asp Ala Thr Gly Val Thr Cys Lys Val Phe Gly Tyr Thr Ala
            290             295             300
Tyr Phe Phe Phe Met Gly Ala Tyr Met Trp Leu Ser Val Ile Ser Phe
305             310             315             320
Asp Leu Trp His Asn Phe Arg Gly Thr Arg Gly Ile Asn Arg Phe Gln
            325             330             335
Glu Lys Lys Arg Phe Leu Phe Tyr Ser Leu Tyr Ser Trp Gly Ile Ala
            340             345             350
Leu Val Phe Leu Ala Phe Thr Tyr Cys Ala Gln Gln Leu Thr Asn Leu
            355             360             365
Pro Ala Asn Leu Lys Pro Gly Ile Gly Asp Gly Val Tyr Cys Trp Leu
            370             375             380
Asp Met Ser Asn Trp Ala Ala Met Ile Tyr Phe Tyr Gly Pro Ile Leu
385             390             395             400
Ala Ile Val Val Ala Asn Thr Ile Met Phe Ile Met Thr Ala Ile Lys
            405             410             415
Ile His Gly Val Gln Arg Glu Met Ala Arg Ile Ile Ala Ser Glu Asn
            420             425             430
Ser Thr Lys Asn Leu Arg Thr Glu Lys Asp Lys Phe Gly Leu Phe Leu
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Arg Leu Phe Leu Ile Met Gly Ile Thr Trp Leu Thr Glu Leu Ile Ser
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Tyr Phe Val Gly Ser Asp Lys Gly Trp Ser Lys Leu Phe Tyr Ile Ser
465             470             475             480
Asp Leu Ala Asn Ala Met Gln Gly Phe Leu Ile Phe Met Leu Phe Val
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Met Lys Lys Lys Val Lys His Leu Ile Thr Asn Arg Thr Ile Arg Val
            500             505             510
Arg Ser Leu Arg Gln Thr Glu Ser Val Thr Met Gly Pro Thr Ser Phe
            515             520             525
Ser Met Lys Gln Arg Phe Met Asp Ala Ser Asn Gln Ile Arg Lys Leu
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Val Val Ile Arg Asn Ala Phe Ala Asn Gly Ser Thr Ser Asp Leu Pro
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<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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<212> PRT
<213> Drosophila

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Ala	Pro	His	Val	Phe	Cys	Ile	Phe	Tyr	Lys	Asn	Phe	Gly	Asn	Asn	Gln

SUBSTITUTE SHEET (RULE 26)

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                        500                        505                        510
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<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

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<213> Drosophila

SUBSTITUTE SHEET (RULE 26)

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Lys Met Trp Gln Tyr Trp Pro Phe Ile Ser Pro His Gly Leu Ser Val
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SUBSTITUTE SHEET (RULE 26)

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<212> DNA
<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

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<212> PRT
<213> Drosophila

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            20                  25                  30
Lys Trp Asn Tyr Ala Pro Pro Pro Ser Asn Thr Pro Tyr Asp Pro Ala
        35                  40                  45
Gln Ala Lys Gly Ala Ala Lys Lys Lys Arg Leu Met Lys Gln Leu
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SUBSTITUTE SHEET (RULE 26)

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Lys His Arg Pro Lys Glu Gln Arg Ser Arg Gln Arg Gln Arg Gln Lys
65                      70                    75                    80
His Arg Gln Arg Ile Lys Arg Arg Pro Arg Arg Arg Gly Ser Ser Ser
                  85                    90                    95
Ser Lys Ala Gly Asn Asn Asn Asn Asn Asn Arg Asn Ile Ala Phe Leu
                  100                   105                   110
Asn Gly Asn Thr Gln Lys Lys Tyr Cys Trp Gln Glu Phe Arg Thr Leu
                  115                   120                   125
Pro Lys Gly Met Arg Thr Asp Glu Gly Ala Gly Ala Trp Arg Asp Met
            130                   135                   140
Thr Ser Asp Gly Ala Val Thr Phe Trp Ile Phe Leu Leu Cys Leu Ile
145                   150                   155                   160
Ala Ser Pro His Leu Gln Gly Gly Val Ala Gly Arg Pro Asp Glu Leu
                  165                   170                   175
His Ile Gly Gly Ile Phe Pro Ile Ala Gly Lys Gly Gly Trp Gln Gly
                  180                   185                   190
Gly Gln Ala Cys Met Pro Ala Ala Arg Leu Ala Leu Asp Asp Val Asn
            195                   200                   205
Lys Gln Pro Asn Leu Leu Pro Gly Phe Lys Leu Ile Leu His Ser Asn
            210                   215                   220
Asp Ser Glu Cys Glu Pro Gly Leu Gly Ala Ser Val Met Tyr Asn Leu
225                   230                   235                   240
Leu Tyr Asn Lys Pro Gln Lys Leu Met Leu Leu Ala Gly Cys Ser Thr
                  245                   250                   255
Val Cys Thr Thr Val Ala Glu Ala Ala Lys Met Trp Asn Leu Ile Val
            260                   265                   270
Leu Cys Tyr Gly Ala Ser Ser Pro Ala Leu Ser Asp Arg Lys Arg Phe
            275                   280                   285
Pro Thr Leu Phe Arg Thr His Pro Ser Ala Thr Val His Asn Pro Thr
      290                   295                   300
Arg Ile Lys Leu Met Lys Lys Phe Gly Trp Ser Arg Val Ala Ile Leu
305                   310                   315                   320
Gln Gln Ala Glu Glu Val Phe Ile Ser Thr Val Glu Asp Leu Glu Asn
                  325                   330                   335
Arg Cys Met Glu Ala Gly Val Glu Ile Val Thr Arg Gln Ser Phe Leu
            340                   345                   350
Ser Asp Pro Thr Asp Ala Val Arg Asn Leu Arg Arg Gln Asp Ala Arg
            355                   360                   365
Ile Ile Val Gly Leu Phe Tyr Val Val Ala Ala Arg Arg Val Leu Cys
      370                   375                   380
Glu Met Tyr Lys Gln Gln Leu Tyr Gly Arg Ala His Val Trp Phe Phe
385                   390                   395                   400
Ile Gly Trp Tyr Glu Asp Asn Trp Tyr Glu Val Asn Leu Lys Ala Glu
                  405                   410                   415
Gly Ile Thr Cys Thr Val Glu Gln Met Arg Ile Ala Ala Glu Gly His
                  420                   425                   430
Leu Thr Thr Glu Ala Leu Met Trp Asn Gln Asn Asn Gln Thr Thr Ile
            435                   440                   445
Ser Gly Met Thr Ala Glu Glu Phe Arg Leu Val Leu Leu Leu Tyr Pro
      450                   455                         460
Leu Leu Lys Phe Leu Leu Gln Cys Ala Phe Phe Leu Arg Arg His Arg
465                   470                   475                   480
Leu Asn Gln Ala Leu Ile Glu Glu Gly Tyr Asp Ile Asn His Asp Arg
                  485                   490                   495
Tyr Pro Glu Gly Tyr Gln Glu Ala Pro Leu Ala Tyr Asp Ala Val Trp
            500                   505                   510
Ser Val Ala Leu Ala Phe Asn Lys Thr Met Glu Arg Leu Thr Thr Gly
            515                   520                   525
Lys Lys Ser Leu Arg Asp Phe Thr Tyr Thr Asp Lys Glu Ile Ala Asp
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SUBSTITUTE SHEET (RULE 26)

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          530                     535                     540
Glu Ile Tyr Ala Ala Met Asn Ser Thr Gln Phe Leu Gly Val Ser Gly
545                     550                     555                     560
Val Val Ala Phe Ser Ser Gln Gly Asp Arg Ile Ala Leu Thr Gln Ile
                565                     570                     575
Glu Gln Met Ile Asp Gly Lys Tyr Glu Lys Leu Gly Tyr Tyr Asp Thr
                580                     585                     590
Gln Leu Asp Asn Leu Ser Trp Leu Asn Thr Glu Gln Trp Ile Gly Gly
            595                     600                     605
Lys Lys Thr Lys His Val Thr Thr Glu Pro Asn Lys Asn Gly Asn Pro
        610                     615                     620
Ser Lys Asp Asp Val Asn Thr Arg Gly Ser Leu Thr Ser Leu Ser Glu
625                     630                     635                     640
Lys Asn Asp Glu Ser Lys Asn Pro Ser Ser Ser Ala Ser Leu Gln Gln
                645                     650                     655
Ala Pro Lys Val Ala Pro Lys Pro Lys Lys Leu Ser Ile Ser Asp Ala
                660                     665                     670
Gly Lys Asp Thr Val Thr Gln Lys Val Lys Glu Asn Glu Glu Pro Gly
            675                     680                     685
Phe Ser Lys Gln Phe Glu Lys Glu Ser Ile Gly Val Arg Ala Asn Arg
        690                     695                     700
Asn Ser Ser Ala Thr Lys Lys Glu Asn Glu Lys Leu Leu Val Lys Thr
705                     710                     715                     720
Val Pro Gly Lys Ser Leu Ile Lys Glu Ser Asn Asp Glu Asn Val Glu
                725                     730                     735
Pro Ser Arg Arg Thr Lys Ser Gln Pro Val Gly Lys Lys Val Tyr Glu
            740                     745                     750
Glu Ser Ser Thr Arg Arg Val Arg Glu Pro Phe Asp Ser Phe Asp Arg
            755                     760                     765
Glu Lys Tyr Leu Ser Asp Met Ile Asp Tyr Asp Arg Ser Ser Glu Asp
        770                     775                     780
Val Pro Glu Lys Lys Leu Ser Trp Glu Pro Asp Ser Thr Leu Arg Arg
785                     790                     795                     800
Arg Phe Val Ser Asn Asn Glu Tyr His Ser Ser Leu Glu Gly Glu Glu
                805                     810                     815
Glu Glu Ile Asp Leu Asp Ser Val Gly Ser Ser Thr Met Arg Gly Ser
            820                     825                     830
Tyr Arg Met Pro Gln Asn Ala Glu Asp Glu Arg Pro Val Ile Leu Ala
        835                     840                     845
Glu Ile Ile Asn Met Gly Lys Leu Lys Glu Leu Lys Glu Gln Arg Glu
        850                     855                     860
Ser Thr Asn Val Phe Arg Asn Asn Arg Arg Asp Asp Lys Thr Ile Asp
865                     870                     875                     880
Glu Val Lys Gly Ser Lys Ile Thr Gly Thr Ser Lys Gln His Val Glu
                885                     890                     895
Glu Val Lys Tyr Asn Glu Thr Ala Ser Asn Glu Asp Asp Asp Asn Ala
            900                     905                     910
Gln Val Lys His Ile Gly Thr Ile Thr Lys Ile Phe Ser Ile Ala Gln
        915                     920                     925
Arg Met Lys Glu Lys Lys Ser Ser Lys Glu Ser Glu Glu Asp Glu Asn
    930                     935                     940
Lys Asp Glu Asn Lys Asp Val Lys Lys Asp Glu Asn Lys Asp Asp Glu
945                     950                     955                     960
Gln Lys Leu Pro Pro Glu Pro Glu Ile Glu Leu Glu Ala Lys Lys Ala
                965                     970                     975
Trp Thr Phe Pro Ile Ala Glu Thr Ser Pro Asp Ile Pro Gly Glu Asn
            980                     985                     990
Gln Ile Leu Gln Glu Tyr Gln Lys Val Lys Ile Gly Lys Arg Asn Arg
        995                     1000                    1005
Lys Tyr Arg Cys Ile Gly Ile Asn Thr Asp Ile Ser Arg Lys Ser Lys
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Ile Lys Thr Phe Ile Ser Lys Ser Ala Gly Asp Asp Leu Val Val Tyr
1025                1030                1035                1040
His Asp Gly Gly Arg Leu Arg Asp Ile Gly Gln Thr Thr Glu Asn Leu
               1045                1050                1055
Lys Asn Gln Arg Lys Asn His Lys His Lys Thr Glu Pro Asp Asp Ile
           1060                1065                1070
Pro Val Asp Ile Gly His Ser Asp Asp Arg Val Arg Glu Ile Gly Val
           1075                1080                1085
Asn Thr Lys Lys Leu Pro Lys Ile Ile Ile Pro Pro Ile Ala Glu Met
           1090                1095                1100
His Val His Lys Asn Gly Lys Leu Arg Asp Ile Gly Thr Ser Thr Asp
1105                1110                1115                1120
Lys Pro Phe Trp Pro Ile Asp Asp Gly Thr Asp Val Ile Tyr Met His
               1125                1130                1135
Pro Ile Lys Thr Asp Arg Lys Lys Leu Asn Lys Leu Ile Val Asp Pro
           1140                1145                1150
Pro Pro Asp Asn Gly Pro Tyr Lys Met Pro Thr Lys Glu Asp Arg Arg
           1155                1160                1165
Thr Tyr Tyr Lys Gly Cys Glu Tyr His Phe Pro Gly Arg Thr Glu Trp
       1170                1175                1180
Arg Arg Leu Phe Phe Asn Lys Ile His Gly Lys Tyr Lys Leu Arg Arg
1185                1190                1195                1200
Pro Ser His Trp Leu Tyr Thr Leu Val Phe Ser Val Leu Tyr Ile Leu
               1205                1210                1215
Phe Val Ile Ile Phe Ser Met Ala Trp Phe Asp Phe Ile Lys Asp Asp
               1220                1225                1230
Ala Ser Arg Lys Val Pro Met Ile Lys Met Ala Gln Pro Phe Ile Ser
           1235                1240                1245
Phe Thr Pro Ile Gly Pro Arg Thr Asn Pro Lys Ala Val Ser Phe Asp
       1250                1255                1260
Pro Arg Asn Ser Thr Glu Val Met Glu Lys Tyr Ala Gly Ile Met Ala
1265                1270                1275                1280
Leu Leu Glu Lys Tyr Gly Asp Tyr Gly His Asn Pro Arg Phe Gly Thr
           1285                1290                1295
Cys Thr Ala Asn Glu Lys Phe Gly Tyr Pro Ser Gly Glu Pro Cys Val
           1300                1305                1310
Phe Leu Lys Val Asn Arg Ile Ile Gly Phe Lys Thr Glu Pro Tyr Ile
       1315                1320                1325
Asn Ser Asp Glu Leu Val Lys Ala Lys Ile Asp Glu Val Glu Phe Thr
       1330                1335                1340
Ala Leu Lys Arg Leu Leu Glu Asn Thr Thr Thr Glu Glu Gly His Leu
1345                1350                1355                1360
Asn Arg Thr Trp Ile Thr Cys Arg Ser Asp Lys Asp Lys Asn Val Leu
           1365                1370                1375
Ile Glu Phe His Pro Glu Pro Ala Ile Arg Thr Glu Tyr Thr Asp Ile
           1380                1385                1390
Glu Glu Lys Ile Glu Tyr Ile Ala Asn Glu Gly Lys Lys Ser Phe Phe
       1395                1400                1405
Gly Pro Asn Asp Val Asn Arg Ile Val Ala Leu Lys Ile Lys Asn Leu
       1410                1415                1420
Lys Ala Asn Glu Arg Val His Ile Asn Cys Lys Ile Val Ile Gln Ser
1425                1430                1435                1440
Ser His Pro Val Cys Asn Thr Ile Met Leu Phe Gly Val Ile Ile Cys
           1445                1450                1455
Leu Ile Ser Val Ile Leu Leu Gly Ile Asp Gly Arg Phe Val Ser Pro
           1460                1465                1470
Glu Glu Tyr Pro Lys Ile Phe Asp Pro Leu Gln Arg Tyr Leu Glu Thr
       1475                1480                1485
Phe Pro Leu Glu Asp Pro Val Ser Thr Thr Asp Asp Ile Lys Ile Arg
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SUBSTITUTE SHEET (RULE 26)

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         1490                    1495                    1500
Pro Glu Leu Glu His Cys Glu Ser Gln Arg Asn Ser Met Trp Leu Gly
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Leu Val Tyr Gly Phe Lys Gly Leu Ile Leu Val Phe Gly Leu Phe Leu
                1525                1530                1535
Ala Tyr Glu Thr Arg Ser Ile Lys Val Lys Gln Ile Asn Asp Ser Arg
                1540                1545                1550
Tyr Val Gly Met Ser Ile Tyr Asn Val Val Val Leu Cys Leu Ile Thr
            1555                1560                1565
Ala Pro Val Gly Met Val Ile Ala Ser Gln Gln Asp Ala.Ser Phe Ala
        1570                1575                1580
Phe Val Ala Leu Ala Val Ile Phe Cys Cys Phe Leu Ser Met Leu Leu
1585                1590                1595                1600
Ile Phe Val Pro Lys Val Ile Glu Val Ile Arg His Pro Lys Asp Lys
                1605                1610                1615
Ala Glu Ser Lys Tyr Asn Pro Asp Ser Ala Ile Ser Lys Glu Asp Glu
            1620                1625                1630
Glu Arg Tyr Gln Lys Leu Val Thr Glu Asn Glu Glu Leu Gln Arg Leu
        1635                1640                1645
Ile Thr Gln Lys Glu Glu Lys Ile Arg Val Leu Arg Gln Arg Leu Val
    1650                1655                1660
Glu Arg Gly Asp Ala Lys Gly Thr Glu Leu Asn Gly Ala Thr Gly Val
1665                1670                1675                1680
Ala Ser Ala Ala Val Ala Thr Thr Ser Gln Pro Ala Ser Leu Ile Asn
            1685                1690                1695
Ser Ser Ala His Ala Thr Pro Ala Ala Thr Leu Ala Ile Thr Gln Gly
                1700                1705                1710
Glu
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<211> 4463
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<213> Drosophila

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SUBSTITUTE SHEET (RULE 26)

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<211> 1938
<212> DNA
<213> Drosophila

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232

SUBSTITUTE SHEET (RULE 26)

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<213> Drosophila

<400> 180

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Tyr Val Arg Val Ile Gly Val Asn His Pro Arg His Tyr Ile Leu Met
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SUBSTITUTE SHEET (RULE 26)

645

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<211> 6938
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<213> Drosophila

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235

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```
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tcttggaagc agtagaatgt cttcattacc gccaaatcct tttgatatcc ttttttcccaa 6840
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<210> 182
<211> 2010
<212> DNA
<213> Drosophila

<400> 182

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aaggcatatt tgggttccta ttggcgggag ttgggtgcgg cctggaacag cacggacggc 360
acccaggagt ggggcgctcc atttcgcgac tgcaacctgt tgacgcgtcg ctggctctgg 420
ccatttcgca tatccttcag cgagcacagg atcaaagttg tggcggctgc cttcattgcc 480
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```

<210> 183
<211> 669
<212> PRT
<213> Drosophila

<400> 183

```
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            20                  25                  30
Gly Lys Phe Pro Asn Ala Asn Thr Pro Ile Ala Ile Asp Glu Pro Thr
```

```
          35                      40    =              45
Arg Ala Glu Val Ser Arg Arg Ala Asn Gly Ile Ala Ser Tyr Ala Leu
    50                      55              60
Asn Glu Asp Asp Asn Leu Leu Ala Phe Ala Ile Ala Ala Pro Ser Ile
65                      70              75              80
His Thr Val Val Val Lys Phe Arg Asp Asn Val Thr Ile Pro Pro Asp
                85                      90              95
Gln Val His Asn Lys Ala Tyr Leu Gly Ser Tyr Trp Arg Glu Leu Gly
            100                 105             110
Ala Ala Trp Asn Ser Thr Asp Gly Thr Gln Glu Trp Gly Ala Pro Phe
            115                 120             125
Arg Asp Cys Asn Leu Leu Thr Arg Arg Trp Leu Trp Pro Phe Arg Ile
    130                 135             140
Ser Phe Ser Glu His Arg Ile Lys Val Val Ala Ala Ala Phe Ile Ala
145                 150             155             160
Ala Asp Glu Asp Val Cys Asn Asp Gly Leu Glu Glu Val Phe Gly Arg
            165                 170             175
Arg His Gly Cys Asp Arg Asn Thr Thr Phe Cys Leu Leu Thr Glu Asn
            180                 185             190
Lys Pro Ala Ala Thr Arg Asp Val Tyr Thr Cys Leu Cys Arg Glu Ser
    195                 200             205
Tyr Tyr Leu Pro Asn Ser Thr Leu Gln Gly Phe Arg Gly Asp Arg Val
    210                 215             220
Glu Leu Ser Glu Gly Tyr Asp Asn Tyr Ser Cys Ile Pro Cys Pro Gly
225                 230             235             240
Gly Cys Thr Asn Cys Asp Ser Asn Gly Val Cys Leu Thr Phe Gln Glu
            245         .           250             255
Glu Glu Val Leu Asn Val Asp Ala Cys Leu Arg Leu Leu Val Ala Ile
            260                 265             270
Val Leu Gly Ala Cys Ile Leu Cys Cys Ile Val Leu Gly Val Ile Val
            275                 280             285
Phe Arg Gln Arg Lys Cys Lys Ala Ile Ala Ser Gly Met Trp Thr Val
    290                 295             300
Leu Glu Thr Ile Leu Leu Gly Ile Val Leu Leu Tyr Ala Ser Val Ala
305                 310             315             320
Val His Phe Phe Pro Ala Ser Thr Glu Arg Cys Leu Leu Glu Pro Trp
            325                 330             335
Leu Arg Glu Leu Gly Phe Ile Thr Cys Tyr Gly Ala Ile Ile Leu Lys
            340                 345             350
Leu Tyr Arg His Leu Val Asp Phe Arg Thr Arg Lys Ala His Arg Trp
.           355                 360             365
Val Leu Arg Asp Val Asp Leu Leu Lys Tyr Leu Gly Thr Met Val Phe
    370                 375             380
Ala Val Ile Cys Tyr Met Ala Ala Phe Thr Ala Ser Ser Leu Asp Leu
385 .               390                 395             400
Leu Glu Ser Ala Gln Leu Glu Ser Leu Arg Glu Ala Asp Thr Asn Thr
            405                 410             415
Cys His Pro Leu Lys Trp Glu Leu Val Thr Gln Thr Ser Glu Met Leu
            420                 425     .           430             .
Ile Leu Cys Phe Gly Leu His Leu Ser Ile Ala Ser Arg Asn Ala Asn
            435 .               440             445
Thr Gln Phe Arg Glu Arg Gln Phe Leu Val Thr Ala Leu Thr Leu Glu
    450                 455             460
Phe Leu Val Ser Ser Ser Phe Tyr Phe Leu Arg Phe Val Tyr Leu Pro
465                 470             475             480
Glu Met Ser Pro Ser Ala Ile Leu Leu Ala Leu Phe Ile Arg Ser Gln
            485                 490             495
Leu Thr Asn Ser Phe Ala Leu Gly Leu Ile Phe Val Pro Lys Leu Trp
            500                 505             510
Tyr Gln His Lys Gln Gly Thr Ser His Asp Ala Gly Gln Arg Leu Gly
```

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SUBSTITUTE SHEET (RULE 26)

```
             515                    520                    525
Gly Gly Tyr Ala Gly Leu Cys Leu Gly Asp Pro Asp Ile Gly Glu Leu
         530                    535                    540
Thr Ile Ser Glu Met Ser Pro Glu Asp Ile Arg Ala Glu Leu Lys Arg
545                    550                    555                    560
Leu Tyr Thr Gln Leu Glu Ile Met Lys Asn Lys Thr Leu Arg Gln Asp
                 565                    570                    575
Asn Pro His Ile Ser Lys Arg Arg Gly Gly Arg Lys Ala Gly His Arg
             580                    585                    590
Arg Phe Ser Leu Gln Lys Lys Gly Ser Lys Asp Lys Ala Leu Ser Ala
         595                    600                    605
Lys His Arg Ser Asn Lys His His Gln Asp Ile Glu Ile Thr Glu Ala
     610                    615                    620
Glu Pro Ser Arg Thr Pro Glu Asp Ser Val Cys Ser Ala Glu Gly Pro
625                    630                    635                    640
Thr Asp Thr Tyr Ala Glu Ile Ser Gly Val Ser His Ser Met Leu Ser
                 645                    650                    655
His Ser Met Val Ser His Ser Val Val Ser His Ser Lys
             660                    665
```

```
<210> 184
<211> 4243
<212> DNA
<213> Drosophila

<400> 184
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ttggtttttga ccaatcgcca gggtcctaca tatatggttt tgactatata ttctcgctat 180
gtttagttga ttatacgatt taggggttta ctttaggtat tttgagcatt ttcaattcat 240
gcgattgtcg ttgaaataac aattgggttt tagctttgct ttagctgccg tgactttgt 300
ttgtatctct ataaatttat caatattctc cgattctaat tgcgttgggg gtgtggttgt 360
ttattcgcag gacttctcac gtagttgtct ataatttgcg gtctcttaat tggcacagtt 420
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gttgcagtga ttgccatttt gaataattta tttgtggtta tttcttttcg tgagcaaaat 540
gctttacggc ttacagattt tcgattggcg tacgtacata catattacat attcatatac 600
atttatcgaa atgagtttac aacctgtgct taatttagtc gtacaaaaat actcagtatt 660
tacaacaaga tataaacgac ataaaatcat aaataaataa gttatcctat acaaagtccc 720
gatctgtgct ccaaggaacc cggcaaactc gaattgagat taaatgtttt aaaaacgaaa 780
acaaaaatga aaaaatgtga agaaatgaa atggcacgct ccacagattg aataatgtca 840
acattacgag taaatcagcc gacgcatttg ccggcatatt aattttacaa attaatggaa 900
cactttaatt gcattaaatt gattccaccc atccggctgg catcgattga ttcgattcgc 960
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attgtccgcc caggcgggat ccgcccgccg ccagccgctg ctgctgctgg gcgatggggg 1260
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tttgtctgtg tagcacataa agatgagata tatatacccca taaattccag atgcatgagt 1920
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SUBSTITUTE SHEET (RULE 26)

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gaaggtaaaa tgtctaatga atgccaagtg gcggcgagtt ggctgttgcc agaaccaaac 4200
cgatgccaat ttatatgcaa ctcgcgcttg gccaaagttt ttc          4243
```

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<211> 1224
<212> DNA
<213> Drosophila

<400> 185
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atatctgtgg atagatacta tgctattgtt aagcccctca agtatccgat tagcatgacg 180
aaacgcgtgg tcggcattat gctgctaaac acatggatat cgccggcact gctctccttc 240
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cggcaggaga agcagctgat gatgcggcac ggcaatgcca tgctgatgca ccgaccatcc 480
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gaggtcgagc aggagcacac ccccactaag gacaagcact taatcaaaat gaagcgggag 600
cacaaggccg cacgcacgct gggcatcatc atgggcacct tcatcctctg ctggctgcct 660
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SUBSTITUTE SHEET (RULE 26)

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tcgacggcct cgagtcatgt gtaa                                       1224
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<210> 186
<211> 407
<212> PRT
<213> Drosophila

<400> 186

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Pro Phe Leu Cys Asp Leu Trp Asn Ser Leu Asp Val Tyr Phe Ser Thr
            20                  25                  30
Ala Ser Ile Leu His Leu Cys Cys Ile Ser Val Asp Arg Tyr Tyr Ala
        35                  40                  45
Ile Val Lys Pro Leu Lys Tyr Pro Ile Ser Met Thr Lys Arg Val Val
    50                  55                  60
Gly Ile Met Leu Leu Asn Thr Trp Ile Ser Pro Ala Leu Leu Ser Phe
65                  70                  75                  80
Leu Pro Ile Phe Ile Gly Trp Tyr Thr Thr Pro Gln His Gln Gln Phe
                85                  90                  95
Val Ile Gln Asn Pro Thr Gln Cys Ser Phe Val Val Asn Lys Tyr Tyr
            100                 105                 110
Ala Val Ile Ser Ser Ser Ile Ser Phe Trp Ile Pro Cys Thr Ile Met
            115                 120                 125
Ile Phe Thr Tyr Leu Ala Ile Phe Arg Glu Ala Asn Arg Gln Glu Lys
    130                 135                 140
Gln Leu Met Met Arg His Gly Asn Ala Met Leu Met His Arg Pro Ser
145                 150                 155                 160
Met Gln Pro Ser Gly Glu Ala Leu Ser Gly Ser Gly Ser Ser Lys Thr
                165                 170                 175
Leu Thr Leu His Glu Val Glu Gln Glu His Thr Pro Thr Lys Asp Lys
            180                 185                 190
His Leu Ile Lys Met Lys Arg Glu His Lys Ala Ala Arg Thr Leu Gly
        195                 200                 205
Ile Ile Met Gly Thr Phe Ile Leu Cys Trp Leu Pro Phe Phe Leu Trp
    210                 215                 220
Tyr Thr Leu Ser Met Thr Cys Glu Glu Cys Gln Val Pro Asp Ile Val
225                 230                 235                 240
Val Ser Ile Leu Phe Trp Ile Gly Tyr Phe Asn Ser Thr Leu Asn Pro
                245                 250                 255
Leu Ile Tyr Ala Tyr Phe Asn Arg Asp Phe Arg Glu Ala Phe Arg Asn
            260                 265                 270
Thr Leu Leu Cys Leu Phe Cys Asn Trp Trp Lys Asp Arg His Leu Pro
        275                 280                 285
Leu Asp Ile Asp Ile Arg Arg Ser Ser Leu Arg Tyr Asp Gln Arg Ala
    290                 295                 300
Lys Ser Val Tyr Ser Glu Ser Tyr Leu Asn Ser Thr Thr Pro Ser His
305                 310                 315                 320
Arg Arg Gln Ser Gln Met Gln Gln Gln Arg Leu Ala Ala Gly Gly Ser
                325                 330                 335
Arg Leu Gly Gly Gln Leu Ala Ala Ala Ala Lys Asp Gly Arg Glu Ser
            340                 345                 350
Lys Asp Ala Lys Asp Thr Gly Lys Asp Ala Gly Lys Gly Lys Ser Asn
        355                 360                 365
Val Asp Cys Leu Ala Gly Asp Asp Val Gln Glu Ile Gln Ile Glu Ile
```

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242

SUBSTITUTE SHEET (RULE 26)

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<210> 189
<211> 603
<212> PRT
<213> Drosophila

<400> 189

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Ser Ala Thr Asn Ala Ser His Leu Gln Pro Ala Thr Leu Thr Gly His
            35                  40                  45
Ile Ser Thr Thr Ala Ala Ala Lys Thr Thr Thr Thr Pro Thr Ser Ser
    50                  55                  60
Leu Pro Ile Thr Ser Gln Phe Val Asp Ala Ser Leu Thr Ser Leu Ser
65                  70                  75                  80
Leu Thr Ala Thr Ser Ser Asp Ala Ser Tyr Ser Ser Pro Phe Ser Ser
                85                  90                  95
Tyr Leu Ser Ser Asp Ser Thr Phe Glu Leu Leu Ser Thr Val Gly Pro
            100                 105                 110
Asn Ile Thr Ala Asn Gly Ser Asp Ile Ala Val Asp Asn Gln Ala Glu
            115                 120                 125
Leu Glu Glu Ser Trp Leu Asp Leu Ser Leu Leu Leu Lys Gly Phe
    130                 135                 140
Ile Phe Ser Ser Ile Ile Leu Ala Ala Val Leu Gly Asn Ala Leu Val
145                 150                ·155                 160
Ile Ile Ser Val Gln Arg Asn Arg Lys Leu Arg Val Ile Thr Asn Tyr
                165                 170                 175
Phe Val Val Ser Leu Ala Met Ala Asp Met Leu Val Ala Leu Cys Ala
            180                 185                 190
Met Thr Phe Asn Ala Ser Val Glu Leu Ser Gly Gly Lys Trp Met Phe
            195                 200                 205
Gly Pro Phe Met Cys Asn Val Tyr Asn Ser Leu Asp Val Tyr Phe Ser
    210                 215                 220
Thr Ala Ser Ile Leu His Leu Cys Cys Ile Ser Val Asp Arg Tyr Tyr
225                 230                 235                 240
Ala Ile Val Arg Pro Leu Glu Tyr Pro Leu Asn Met Thr His Lys Thr
                245                 250                 255
Val Cys Phe Met Leu Ala Asn Val Trp Ile Leu Pro Ala Leu Ile Ser
            260                 265                 270
Phe Thr Pro Ile Phe Leu Gly Trp Tyr Thr Thr Glu Glu His Leu Arg
            275                 280                 285
Glu Ile Ser Leu His Pro Asp Gln Cys Ser Phe Val Val Asn Lys Ala
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SUBSTITUTE SHEET (RULE 26)

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Tyr Ala Leu Ile Ser Ser Ser Val Ser Phe Trp Ile Pro Gly Ile Val
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Met Leu Val Met Tyr Trp Arg Ile Phe Lys Glu Ala Ile Arg Gln Arg
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Lys Ala Leu Ser Arg Thr Ser Ser Asn Ile Leu Leu Asn Ser Val His
                340             345                 350
Met Gly His Thr Gln Gln Pro Thr Ser Leu Ser Tyr Leu His Pro Ser
            355             360             365
Asp Cys Asp Leu Asn Ala Thr Ser Ala Arg Glu Glu Thr His Ser Ala
    370             375             380
Leu Ser Asn Leu Glu Arg Pro Arg Gly Ile Thr Phe Ala Ala Val Pro
385             390             395                 400
Ser Pro Leu Pro Lys Cys Pro Leu Cys Gly Ala Asp Ile Ser Ser Thr
                405             410                 415
Thr Gly Thr Thr Ala Asn Ala Thr Ala Thr Ala Asn Ala Asp Ser Thr
            420             425             430
Ile Asp Thr Thr Val Thr Thr Ser Ser Lys Arg Ser Ile His Glu Gln
        435             440             445
Thr Pro Asp Leu Gly Gln Arg Pro Ala Ser Ser Ser Ser Ser Thr Arg
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Phe Trp His Lys Arg Thr Ala Ala Val Thr Ala Cys Trp Gln Gln Ser
465             470             475                 480
Lys Asn Arg Lys Arg Arg Phe Lys Thr Gly Cys Ser His Cys Gly Ala
                485             490                 495
Thr Gly Gly Ser Val Arg Pro Ala Lys Gly Trp Lys Ala Glu His Lys
            500             505             510
Ala Ala Arg Thr Leu Gly Ile Ile Met Gly Val Phe Leu Leu Cys Trp
            515             520             525
Leu Pro Phe Phe Leu Trp Tyr Val Ile Thr Ser Leu Cys Gly Pro Ala
    530             535             540
Cys Pro Cys Pro Asp Val Leu Val Val Val Leu Phe Trp Ile Gly Tyr
545             550             555                 560
Phe Asn Ser Thr Leu Asn Pro Leu Ile Tyr Ala Tyr Phe Asn Arg Asp
            565             570             575
Phe Arg Glu Ala Phe Arg Asn Thr Leu Glu Cys Val Leu Pro Cys Leu
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Glu Lys Arg Asn Pro Tyr Asn Ala Tyr Tyr Val
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<210> 190
<211> 6617
<212> DNA
<213> Drosophila

<400> 190
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ctagggtatt tgtgtgactt ttttctctct gcataagtga agatgtttac tattaataga 600
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agcctggctg gggattcaat ttaaattcat ccttgagtct aatgactttt aatgttgttt 780
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SUBSTITUTE SHEET (RULE 26)

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<211> 1983
<212> DNA
<213> Drosophila

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tga                                                                   1983
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<210> 192
<211> 660
<212> PRT
<213> Drosophila

<400> 192

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            20                  25                  30
Ser Pro Ser Ile Gly Val Gly Ile Gly Ile Ala Ser Ser Thr Met Ala
        35                  40                  45
Asn Pro Ser Glu Ser Pro Glu Met Leu Leu Leu Lys Asn Asp Lys Phe
    50                  55                  60
Leu Thr His Val Ala His Leu Leu Asn Ile Thr Thr Glu Asn Leu Ser
65                  70                  75                  80
Asn Leu Leu Gly Ser Thr Asn Gly Thr Asn Ala Ser Thr Met Ala Ala
                85                  90                  95
Asp Ser Pro Val Asp Glu Ser Leu Thr Leu Arg Thr Ala Leu Thr Val
            100                 105                 110
Cys Tyr Ala Leu Ile Phe Val Ala Gly Val Leu Gly Asn Leu Ile Thr
        115                 120                 125
Cys Ile Val Ile Ser Arg Asn Asn Phe Met His Thr Ala Thr Asn Phe
    130                 135                 140
Tyr Leu Phe Asn Leu Ala Val Ser Asp Leu Ile Leu Leu Val Ser Gly
145                 150                 155                 160
Ile Pro Gln Glu Leu Tyr Asn Leu Trp Tyr Pro Asp Met Tyr Pro Phe
                165                 170                 175
Thr Asp Ala Met Cys Ile Met Gly Ser Val Leu Ser Glu Met Ala Ala
            180                 185                 190
Asn Ala Thr Val Leu Thr Ile Thr Ala Phe Thr Val Glu Arg Tyr Ile
        195                 200                 205
Ala Ile Cys His Pro Phe Arg Gln His Thr Met Ser Lys Leu Ser Arg
    210                 215                 220
Ala Ile Lys Phe Ile Phe Ala Ile Trp Leu Ala Ala Phe Leu Leu Ala
225                 230                 235                 240
Leu Pro Gln Ala Met Gln Phe Ser Val Val Tyr Gln Asn Glu Gly Tyr
                245                 250                 255
Ser Cys Thr Met Glu Asn Asp Phe Tyr Ala His Val Phe Ala Val Ser
```

SUBSTITUTE SHEET (RULE 26)

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       290                    295                    300
Pro Arg Arg Thr Phe Asp Ala Asn Arg Gly Leu Asn Ala Gln Gly Arg
305                    310                    315                    320
Val Ile Arg Met Leu Val Ala Val Ala Val Ala Phe Phe Leu Cys Trp
               325                    330                    335
Ala Pro Phe His Ala Gln Arg Leu Met Ala Val Tyr Gly Leu Asn Leu
           340                    345                    350
Ile Asn Ile Gly Ile Ser Arg Asp Ala Phe Asn Asp Tyr Phe Arg Ile
           355                    360                    365
Leu Asp Tyr Thr Ser Gly Val Leu Tyr Phe Leu Ser Thr Cys Ile Asn
       370                    375                    380
Pro Leu Leu Tyr Asn Ile Met Ser His Lys Phe Arg Glu Ala Phe Lys
385                    390                    395                    400
Ile Thr Leu Thr Arg Gln Phe Gly Leu Ala Arg Asn His His His Gln
               405                    410                    415
Gln Ser Gln His His Gln His Asn Tyr Ser Ala Leu Leu Arg Gln Asn
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Gly Ser Met Arg Leu Gln Pro Ala Ser Cys Ser Val Asn Asn Asn Ala
           435                    440                    445
Leu Glu Pro Tyr Gly Ser Tyr Arg Val Val Gln Phe Arg Cys Arg Asp
       450                    455                    460
Ala Asn His Gln Leu Ser Leu Gln Asp Ser Ile Arg Thr Thr Thr Thr
465                    470                    475                    480
Thr Thr Thr Ile Asn Ser Asn Ser Met Ala Ala Gly Asn Gly Val Gly
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Gly Gly Ala Gly Gly Gly Gly Gly Gly Arg Arg Leu Arg Lys Gln Glu
           500                    505                    510
Leu Tyr Gly Pro Gly Pro Gly Thr Ala Val Pro His Arg Met Leu Gln
           515                    520                    525
Ala Gln Val Ser Gln Leu Ser Ser Leu Gly Asp Ala Asn Ser Leu Leu
       530                    535                    540
Glu Ala Glu Val Val Asp Arg His Tyr Ala Ser Gly Arg Ala Lys Arg
545                    550                    555                    560
Ala Leu Leu Ala Thr Lys Ser Gly Ala Leu Leu Val Thr Pro Pro Gln
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Ser Gly Asp Pro Ser Glu Val Ser Gln Pro Ala Thr Arg Leu Lys Leu
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Thr Arg Val Ile Ser Arg Arg Asp Glu Val Ala Asn Thr Ser Thr Pro
           595                    600                    605
Pro Phe Cys Gly Ser His Ser Leu Pro Asp Pro Glu Thr Cys Gln Ser
       610                    615                    620
Ala Ser Val Ala Gly Arg Ser Ser Arg Lys Phe Pro Trp Arg Lys Arg
625                    630                    635                    640
Arg Gln Lys Thr Glu Asp Pro Ser Ser Glu Gly Leu Thr Tyr Gly Ser
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Pro Lys Ser Gln
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<210> 193
<211> 4902
<212> DNA
<213> Drosophila

<400> 193
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SUBSTITUTE SHEET (RULE 26)

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<211> 1788
<212> DNA
<213> Drosophila
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<210> 195
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SUBSTITUTE SHEET (RULE 26)

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<212> PRT
<213> Drosophila

<400> 195
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Phe His Asn Glu Lys Phe Leu Leu Asn Leu Thr Gln Val Leu Asn Ile
            20                  25                  30
Ser Ala Asp Asn Leu Thr Ser Leu Leu Gln Gly Leu Glu Pro Glu Glu
        35                  40                  45
Leu Leu Pro Thr Val Thr Pro Met Thr Pro Leu Ser Leu Leu Ala Thr
    50                  55                  60
Leu Ser Val Gly Tyr Ala Leu Ile Phe Ile Ala Gly Val Leu Gly Asn
65                  70                  75                  80
Leu Ile Thr Cys Ile Val Ile Ser Arg Asn Asn Phe Met His Thr Ala
                85                  90                  95
Thr Asn Phe Tyr Leu Phe Asn Leu Ala Ile Ser Asp Met Ile Leu Leu
            100                 105                 110
Cys Ser Gly Met Pro Gln Asp Leu Tyr Asn Leu Trp His Pro Asp Asn
        115                 120                 125
Tyr Pro Phe Ser Asp Ser Ile Cys Ile Leu Glu Ser Val Leu Ser Glu
    130                 135                 140
Thr Ala Ala Asn Ala Thr Val Leu Thr Ile Thr Ala Phe Thr Val Glu
145                 150                 155                 160
Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Gln His Thr Met Ser Lys
                165                 170                 175
Leu Ser Arg Ala Val Lys Phe Ile Phe Ala Ile Trp Ile Ala Ala Leu
            180                 185                 190
Leu Leu Ala Leu Pro Gln Ala Ile Gln Phe Ser Val Val Met Gln Gly
        195                 200                 205
Met Gly Thr Ser Cys Thr Met Lys Asn Asp Phe Phe Ala His Val Phe
    210                 215                 220
Ala Val Ser Gly Phe Leu Phe Phe Gly Gly Pro Met Thr Ala Ile Cys
225                 230                 235                 240
Val Leu Tyr Val Leu Ile Gly Val Lys Leu Lys Arg Ser Arg Leu Leu
                245                 250                 255
Gln Ala Leu Pro Arg Arg Cys Tyr Asp Val Asn Arg Gly Ile Ser Ala
            260                 265                 270
Gln Thr Arg Val Ile Arg Met Leu Val Ala Val Ala Val Ala Phe Phe
        275                 280                 285
Ile Cys Trp Ala Pro Phe His Ala Gln Arg Leu Met Ala Val Tyr Gly
    290                 295                 300
Ser Thr Ser Gly Ile Glu Ser Gln Trp Phe Asn Asp Val Phe Ser Ile
305                 310                 315                 320
Leu Asp Tyr Thr Ser Gly Val Leu Tyr Phe Leu Ser Thr Cys Ile Asn
                325                 330                 335
Pro Leu Leu Tyr Asn Ile Met Ser His Lys Phe Arg Glu Ala Phe Lys
            340                 345                 350
Val Thr Leu Ala Arg His Phe Gly Leu Gly Gly Lys Asn Gln Gly Arg
        355                 360                 365
Gly Leu Pro His Thr Tyr Ser Ala Leu Arg Arg Asn Gln Thr Gly Ser
    370                 375                 380
Leu Arg Leu His Thr Thr Asp Ser Val Arg Thr Thr Met Thr Ser Met
385                 390                 395                 400
Ala Thr Thr Thr Thr Gly Leu Asn Gly Ser Ala Asn Gly Ser Gly Asn
                405                 410                 415
Gly Thr Thr Thr Gly Gln Ser Val Arg Leu Asn Arg Val Ser Leu Asp
            420                 425                 430
Ser Val Gln Met Gln Gly Gln Asn Arg Ser Arg Gln Asp Leu Phe Asp
```

254

SUBSTITUTE SHEET (RULE 26)

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          435                      440                      445
Asn Pro Arg Arg Met Leu Gln Thr Gln Ile Ser Gln Leu Ser Ser Val
        450                      455                      460
Gly Asp Ala His Ser Leu Leu Glu Glu Asp Leu Gln Phe Pro Gly Glu
465                      470                      475                      480
Pro Leu Gln Arg Gln Pro Thr Met Cys Ser Ile Asp Glu Leu Thr Asp
                485                      490                      495
Asp Leu Ala Ile Ser Arg Ser Arg Leu Lys Leu Thr Arg Ile Thr Arg
            500                      505                      510
Pro Pro Gly Gly Val Thr Gly Gly Val Ala Gly Gly Ser Thr Thr Gly
        515                      520                      525
Ala Ala Gly Ser Gly Gly Val Ser Gly Asp Glu Ser Ser Gly Lys Val
        530                      535                      540
Arg Lys Ala Lys Val Lys Val Leu Lys Ser Ser Ser Pro Phe Lys Gly
545                      550                      555                      560
Leu Arg Thr Lys Phe Asn Trp Arg Ala Arg Arg Lys Gly Ser His Lys
                565                      570                      575
Pro His Glu Lys Gly Ala Thr Val Asn Gly Gly Asp Thr Glu Glu Arg
            580                      585                      590
Ala Ala Phe
        595
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<210> 196
<211> 9889
<212> DNA
<213> Drosophila

<400> 196
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caagaactgg gagagcaaat aaatatgcga tttcctcgac ttatagttac ttgtgtgaaa  240
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caaaaggatt ttataacaat tccagtgtcc agcccatcgt actgatgtgg ctaattgttt  360
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aaggttgagt ttttgtttaa gatgattgca catggcacac aggttgattt taatctaaat  540
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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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     50                  55                  60
Asp Ile Ser Asn Leu Ser Val Pro Glu His Val Met Asp His Ala Pro
65                  70                  75                  80
Gln Leu Ser Arg Ser Gly Leu Leu Lys Val Tyr Val Leu Ala Val Met
             85                  90                  95
Ala Leu Phe Ser Leu Leu Gly Asn Leu Leu Thr Ile Trp Asn Ile Tyr
            100                 105                 110
Lys Thr Arg Ile Ser Arg Arg Asn Ser Arg His Thr Trp Ser Ala Ile
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Tyr Ser Leu Met Phe His Leu Ser Ile Ala Asp Val Leu Val Thr Trp
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SUBSTITUTE SHEET (RULE 26)

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SUBSTITUTE SHEET (RULE 26)

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TCAACAGAAAATTTCTGGCCCACAAGACCTGCCTGGAGAACGGCTCCTGGTACCGTCATCCGGTTAGCAATCAGACCTGGTCCAATTACACCAACTGCGTGGACTATGAGGA
CCTGGAGTTTCGCCAGTTCATCAACGAGCTGTACGTGAAGGGTTATGCCCTCTCCCTGCTGGCCCTGCTCATATCGATTATTATTTTCTTGGGCTTCAAATCCCTGCGCTGC
ACCCGCATCCGCATCCATGTACATCTGTTCGCCTCGCTGGCCTGCACCTGTGTGGCCTGGATATTATGGTATCGTCTGGTGGTGGAGCGTTCCGAAACCATAGCCGAAAATC
CGGTAAGATGCACTGAGAAAAGTAACTATGAAAATAACATAGCCCTACAAGTAGCTAGGCAATTATACAAAACCATAAACATAACTAACTTTCAGCTGTGGTGCATTGGGCT
CCATCTGCTGGTGCACTACTTTATGTTGGTCAACTATTTCTGGATGTTTTGCGAGGGCCTGCACCTGCACCTGGTGCTCGTTGTGGTGGAGTTATCCTTACTCGTCTGGCAAT
CTGGCAATTGCCTGCACAAGTCTGCATTCTTTATGGGCGACTTCTGTGCATGGCAGATGTGATTTCCTGCAGCCGCTGACATGGCAATGGTTCACCCCCAGCAATTTGTCTG
AGAGCAAATCGCAACGTTGGCCAACTGCTTTACGTCTGCGTCAAGTTGAGATGTCAGGAATGTCCGTTCAGATCCTGACGCCCCTTCTTCTTTCATTCGCCAGGTCTTTGT
CAAGGACACGATTGTGATGCGCTGGTTTATTGTCATCAGCTGGTTTTCACCCATACCCATAGCCATCGTCTACGTTTTTCTGATCAACGTACTGCGAGTGATCGTGCGAAAG
CGGATGCCGGCACCCAGCTGGACCACTTCTATCAGATGCTATCGGTGGTGTTGGTCAGCCTGCAGGGCTTTGTGGTCTCCTTCCTGTTCTGCTTCGCCAATCACGATGTCAC
CTTTGCCATTCGCACGCTGCTGAACAAGTTGCTGCCCAGTTTAGTGACCCCGCCGCCGGCCGGCGGGAGTAATACTGGACAGATGGCCACGACCACGCCCAGCCGAGAGTTGGGC
GTTTAA
(SEQ ID NO: 2)

FIGURE SHEET 1

Start ATG: 1 (Reverse strand: CAT)

MATTSSDSESQNVDVASQAQTQDNLRIFLKHLYAECVFRYQNVTYDTDDPSFSLGPATDYDSDLPENFSPVPRYLENAAMNEGVIDMRNVDEELAEKEELMATVVSATMATN
QKENRLFCPLNFDGYLCWPRTPAGTVLSQYCPDFVEGFNRKFLAHKTCLENGSWYRHPVSNQTWSNYTNCVDYEDLEFRQFINELYVKGYALSLLALLISIIIFLGFKSLRC
TRIRIHVHLFASLACTCVAWILWYRLVVERSETIAENPVRCTEKSNYENNIALQVARQLYKTINITNFQLWCIGLHLVVHYFMLVNYFWMFCEGLHLHLVLVVVSYPYSSGN
LAIACTSLHSLWATSVHGRCDFLQPLTWQWFTPSNLSESKSQRWPTALRLRQVEMSGMSVQILTPLLLSIRQVFVKDTIVMRWFIVISWFSPIPIAIVYVFLINVLRVIVRK
LHPQSAQPAPLAIRKAVRATIILVPLFGLQHFLLPYRPDAGTQLDHFYQMLSVVLVSLQGFVVSFLFCFANHDVTFAIRTLLNKLLPSLVTPPPAGSNTGQMATTTPSRELG
V*
(SEQ ID NO: 3)

Name: Calcitonin receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384694

GCCGTAAACTATGGCGATGCCCCACTGTGCCCGCACACAAATTCCGCCACCTCGCTCCGAAATCGTGTGTATTTGGTTAATAATAATCTAGTTGGGCATCGATTGTTCGG
CCAAAATGAAGCCACTATCCGTGGCGGAGTGTTAATTAATTTGCACTTAAGCGCAGCTGCTGGAAGCACTTGATAGAAGTGGGCATGCCGGTTCTCTTGGGAAGTTGGCT
TACTATAGTTTAGCGTTAAGGCGTTAACTTGTGGCCTTTAAAGTTCTTAGAGAAGACTTTCTGCAGCTGCTCAGGCTGTTCATTGCGGCATCTAGCATAAAATTTAGAGT
TTGAAAGTAAGTTTCTATGAAAAAAAAATACACGTATATATAAGTATAACAAGAAAAGGACCAAATCAAAGTTTATATACCATTGCTGTACTTATATATTTGAATATTAA
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CAACTAAGGTACATTTACTTCCATTTAATTTTCTATTGGCAGCTATATAATAAACAGTTCCGATCCAACGTGAACCGACCTATCACCATTTTTGATAAAGTTTTACGCAG
AAACGTAAAAATATCTAAAAGCATGCTATTTTGTATTTGTATTTTTGTATTTTGTAGAGAAAAGTTGTAGATCTATATTTAATTTTGCACACATGAGCATTTTAATCAGT
GTGGAAAAACCAGCTGCAATATAATTGCTTTTGAATAATGCGAATTTCGGGGGGAAGTTTCTTTTACCAGCACAATATAAACAAAACTGCTCAACTATTTCTCGATATTT
ACATTTTCAGGGTCCATCAGCAACATAGATGACGCGGAGTATCACTGCAATAAGACGCAGGTGCGCAAGGTCATCTCGGGGGTGGTGGGTGCCGCCTCCTCGGTCACATC
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TCCAGGAGCCACATGGTAACTGTTGCAATGGCTTGCAGGTCTTTCGGTTGGCTTTGCCGATTCCTAAGTGTCTGCACGTGCCACTAAATTAGTCGAGTCCCGCAGGCCAA
CTAGAGGAACATAGTGCTGCAGTTGCCCAAGAAGTGTACAGTAGGGACTCTCAGCAATCATAACAATTAATGTAATTATTTTACTATATGTTCAATTTATCTTTAATATAC
AATTCCAAAATGATGATTCTTAGCTGCTAAAGAACTGACTTACATATTAAATTTCCTACCAAAACCAATAACAAACTGGACAGATCGCTTCAGTTGAGTACTTCGACTATC
AGATACCCGTCACTTGCATTACCGCTTAAAAAGCTTGTATCTAGCATTGCTCGTATTTCAACTGCAAACGACATTGCAGTTTTTTGGGTGTTCCTCATGTAGTGACTAGA
GCGTGAAAAACGCCACAAACTAATATCCATTTCTGATTCAGGAAGGAATATAACATTTTCCGAGTGCCGGCATGAATCACGTGCAGGAAGTTGAAGGAGATTGAGTGCCC
GGTTCGGCTGCTCCAGCTACGTGAGCTGGAGCCAAAAGTCAACAACGCGACAATAACTAAGTAGCCAACTGCCAGATCCCTTCTCAGATATATATATAGTATGTACTCA
CTACTACTTGGATGCCATTAAACGCACACGAAGTGCCAGTCGAAGGAGCAGCAGCCGTTCCATGCAGGCCCAGCTATCGTCCCGAAAGGACCTCATAAATCAGCAATAAA
CATTTGATTGCATTTGGTTTGCACGCGTGGATTCTGCGCTGGCTTCGCATAAACAGCACTTTCGAGCAAATTTTGTGTGTTCTGCAATTCAAATTTCTGGTCGATAGCGA
CTTAGTGAGTTTCGTTTAGGCTTAGCGGAAATTGGCTGCAATGCAAAATGTTCGCAAGGACACAATTCAAATGACAATGCAGTTAAAAATTCCGTAAATGCAATATTTTA
TGGCTTATCGTATTTGGATAACAATGTTTTAAATGCTTGAACAAAGCATTGCTGTCTTTTGTTTTAAAGTAAAATTTTTGCCGTCAGAAGTTTGTGCATTGAATTAAAT
GGTTATTCAAACATTACATTTTATTTATCTTGAAAAAAGTACAAAAATATGTATTAAACTCGTAGTATTATATATAAATTAAATATATTTTATTATTTTTTGTTTTTATG
GACTGAGTAATAGCACTTGAATTTTCCAACTAGTTTTTCACAATTTTTCGTACTTTAATAAAAGTAAATATTTGCATCTCTAGTGTCAATTATCAAAAGTCAACAAAGCC
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TAACCAAACGGTTTATGTGTGCGTGAAATTGGTTTCCCGGCTTGGGCCAGGTCACCACAGTTGGCCTTTTGCTGCAGTTGCCACAGCTTTGGGTTTCGCAAGGTAATGCC
AGCTGATGTTTTCTTCGACAGCAGCATTGTTTGTGGTTTTTTGGAAAACAGCTTAAGCGAGAAAATATGAGCGAAAAACTGGGAAGGAGCTTACGAAAGGTTCTGCAGAAG
CGATAGCCCAGAACGAGTGCGAAAAAATATGAAAATTAAATGGCGACCTTAAAGTGAAAGGGGTTCTTACATAAAATATTGTAGCACATTGCCACTTTGTGCCACCCAA
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CAGCGATTCGAGTACTTCTCCCGCACTATTCCCTCGGATCACTACCAGGTGAAGGCCATGGTGGAGATAGTGAAGCGGATGGGATGGAGCTACGTGTCGATTATCTACGA
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CAATAATAAGTAAGTTCAATAAGTTTCAGCCACTTAAATTTCCTCTTTTTCAAAGGACTACATAAATTTCACCTAATAGGGCAAATCATTTAACTAGTAATCCTTAAACG
GTGGAACTTTAAAATAATGCCAAGTGCCGTTTAAAAGCGTTAGCAGCACTCCATTATCATATGTTTATATCCTTAGCCGCTTGCAGTGTAAACGATATACATTTTAAGTG
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CTGACGAAGCCGCGGGCTCGAGGTATGTAACTGGAGAGTGGGAAGTTGGGATTGCAGGAGGGGATCGGAGGCGATGTGGCGGAGGAAAAGTGCATTTCCAACCGGAACAG
CGACTGCAGTCTGCCAGTCAAAATGCAATTTAAAATGAAAATGTCAAAGCGAAGGCGCAGTGCAAATGCGAAAGGAAAGCCCTTCGCAACGCCCGCACAATGAATGCGAT
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AGCGGGAAATTAAAAAGTTCACGACAAAACAAACGGAAAAAGTTATTTGCAAATAAATTGAGAGATAGTCGCCCAGAAGTGGGCAAACTGATACGTCCAATACTGTAGTT
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GTTGTTTAATTTTGCATATCGAGGGTTCTTTCACTGCTCCTGGTCCTGGTCGTGGTTCTGGTGGGGGCTCCAGTTGGGTCCTGAAAAATGATGCCCTTCCGGATCCGTA
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GCATGTCTAAGGCAAAGTGAAATCCAAGGAAAATATCCTTAACTTCACAAAAGTATCGACAAGTTTCCCGTTGTCGCCGCCGCTTCCTTTGAATAAGATTCCCTCCTC
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AACTGCAGCTCACGTATCCCATACAAGTTTGTCCAGAGCGAAACAATAAGGGCTGAAAGCGTTGGAAAATTTGGTAAGCACCTAACCAAAGGATAGTTTTAGAAGCTTCCT
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TTCTGTTCGCTTCTTGGGACCAATTAAAATATTGTTTTCCTTGCAAATTGAAGACAACAATACCTTGGCAGAAAATCTAAATATAGTAAAGATACGTCGCCAAATGGCGAACT
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ATCCAACTTAATTTATATAGCATTTGCGTAATTAATATTCAAAGCGAAATAATGGGCTGTCATTTAATACTATAAAAACACTTTAATCCGCCCTCGGAAAGGAGAACACA
AGAGCAGTTGGCAGCTGCAGATTGTTTTCTTTTGCGCACAAAAGCCGCTCATTCACTATTGATTGCAATTAAAAATTAAATTCTTTCTTCCTCCTTTCGCATCCTTTTAAT

FIGURE SHEET 2

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ACGCCGCTGCCCAGGGGCCATTATCTTCGGTTCGGATCAAGAGGTGCGCCAAGTGATGCGGGCGGTGCGCCGGGCGAATGCAACTGGTTCCTTCTCCTGGATCGGATCCG
ATGGCTGGAGTGCCCGGAATTTGGTGTCCGACGACTACGAGCCGGAGGTAGGTGAACTATTCCGTCAGACCGGATGACGGGCCAGTTACCGTCAGCCGGAAATTATGAGC
CTAAATGGGCGGAACAACTCGGTTTGATTAATGACTCGGATTTCGGTCACATACTCACGCACGCACATACGAGGGCCCAACCCCATTACATGATAACCAAAAAATTATAA
ATGATGGCGGCCGAAAGAACACTTTCACACGCCCTTTCCCATGATGAATTATGGTTCAATTTGGATTAATCGTGCCTTTGTCTGTGCGTGGCTAATTAATTTGTCTAAGC
CCTTCAAGCCCAGAAATGGTCCTCCTCTCTGATCAAGCTCATTAAGTATACGCCCGCGTCGTGTCTTGGTGTCATCAACAGGTGGAAGGCACGCTGTCTGTGCAGCCGCAGG
CGAATCCGGTGCGCGGGTTCGAGGAGTACTTCCTCAGTCTGACGGTGGAGAACAATCAACGCAATCCCTGGTTTGTGGGTAAGTGAATTACCGATTAAAATTAAGCTGGT
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AGCCAACGAAGGGTGCAGACTTGCTGAAATATTTGCGAAAAGTGGAGTTTGAGGGTGAGTGAGTAATAGAAGCCGTGTATCCACTTTTGCCGGATAAAAGCAAGTTAAAT
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ATCCCTCCGCAGGCCTCAGCGGCGACGAGTTCCGCTTCGACGGGAACGGCGACGGTCCCGCCCGGTACAACATCATCCACTTCAAGCAGTCCCAGGCGGGACAGTACCAC
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ATTAAGTTTACCTGACTGAATTCGTGCATCCTTAGTCTCCTGTAACCTAATGTATTCGTGCTCACTGCTCCTCATCAATACTAATTTTGATCTCATTATCCCGCTAACCC
AGAGGTGAAGTTTAAGCGGCTGAGTCCCAAGCCGCCGGAGTCTGTCTGCAGCCTGCCATGCTCTTGTGGGTCAGGCCAAGAAGTACGTGGAAGGCGAGAGCTGCTGTTGGC
ACTGCTTCAATTGCACAACCTATCAAGTAAGTGAAGCCCATCTGAGGCCAGTAATTTATTTGTTGGCCCTTCGAATAGATTGAAATGTAGCGCCAAGTGAATTATTCCGG
TCCATTTATCAAGTGTTCCTTTGTGCGGTGCGTCCATTCTTTCCATTCACTCACCATTCGCAGATACTCATCAACGGCGTTTGTTGTGTGGTGCAAACATGCCGCCTTTGTGCTCGCCCCA
GCAGTACTGCCGCCCCATCCCGGAGATATATTTGCGTCCGGAGTCCGCTTGGGCCATCGGTGCTATGGCGTTCAGTGCGACCGGGATCTTAGTAACGCTCTTCGTAATGG
GCGTATTTGTCAGGTGAGCAGCGCATACACCGTGATAAAAACGGGTATAGGAAATTACTTTTAATAATATTTAATAGTTATTAATGGCTTTTATAAAACCATTTGAAACA
ATTCAGTCTTAAGATCGAACATTTAACAATGAAATTTGCTTTCTAAATCCAAAAACCCATCAGGATGTTATATTCCTTTTCTATTAAGACCATTTTTAATAATACATAGT
CCAATATTATCATAAAACCTTGTTAATGTATATATTTTCTCAACTTCAAATATTTAGACAATATATAATACTTTAACAATAATTAAATAATTTGAAGATAAGGTAACGG
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GAGGGCCTGTTTTCTAGCTATGTTTTTCTCTGACTGTATTTATTGGCACACAATTGTCCGCTTGCATGGATATGGAAAGCAATTAAAAAGTTTCACCCTTTCCGGGCAAA
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CACCCAACAGGCACAACGACACGCCCATAGTGCGTGCCTCTGGTCGGGAGCTGAGCTACATTCATGTGCTGGCGGGGATTTTCATGTGCTACGGTGTCACCTTTGCCTGGTC
CTGAAGCCGACCAACATAGTGTGTGCCATTCAGCGGTGAGTGTGCAAATTGCCGAGATGATGCGTGTGAATTTTCCTCCGAAACTCCCTCTTTTCCGCTTTTCCGCTTCC
ACACAGGTTTGGTGTCGGCTTCTGCTTCACGGTCGTTTATGCAGCACTGTTGACCAAAACGAATCGCATTGCACGGATCTTCAAAGCGGGCAAACAATCCGCCAAGAGGC
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CACAACATGTATGAATGAACTCCTTATAATTTAGTTATGTGTTTTGTATTTGGGTAATTTGGTTTATTTCGAAACAATACACGCATGAAATATTTATAAGTCTATATTTTA
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CAAATACAGTGTGCACAAGCACACGAACCGCACCGTACACCTTGAGCCATAAAAATGCAATTTACAACTGGTTGTGTCTGGCAAAAGGAAAACAATAAAAGGCTGCCATG
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GCCGCCTCGCTACGGCAACATGCACCGCACCGCTGGCACAGGACCCTCGTCCATGATGGCCGCCGCCGTGGTGACCGCCGCCACCTGTGCCCAGGAGGAGAAGATCCAGA
AGCATATCACTCCCACAAACACAGGTCAGTAATTAAGGGATATCGGTTAACGAGTCCCGGTCAGTAAGCGTAGCGCTCAAAATACACACACTTCGTGTCGGGCAAATGT
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CGGTGGATGGCAGCGAAACCATGTCCGTGGCTCCCAACAATGGGCATGGAAACAACGGGAGCCAACGTCCGCCGGTCCTGCAAACAAACTTATAGCTAAACGCGCAACAA
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FIGURE SHEET 3

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TTGCAGCAACAGCTGCTGAAGGAGCAGCAGCGACAACAAGCCGAGCTGCAAACGCAACATCCGCAGCAGCAACATGGAACACAAAGCTCTTCCAGCGACACCGCCAGCAC
GGGCAGCGGCAGTGCGGCGAAGAAGCGGGCCGCAATTCCCGTTTAGCTGCCCCCGGAGATTCGAGATTCTCGCAACCATACGTAAGTAGAGGAAAGTGTCTGTTGACCCA
AGCGATTCCCGGCATCAGTCTAGGGATGCGGAAAAGCAGACAAGAGGAGGGCAGGAGGTCGTGCTAGGACGGGACTAAATTGGGAGCAGCTGGGCCACAGAAATATCTTC
AGATCTTAGAAGGCGAAATAATTCATTTACCACTTTTGTTCGCTTATTAATTTGAGTGAATTCTGGTTATACCTTACCCCCATAGACACAAATTATCTTAACGTTCTTTT
ATATAAGTTTATCGATAGCTGTACAACAATGTATCTCAATAATGAAGATATTCCTGTGGCACTTAAGGCTTTCTTCAGATTTTAACATGCACGCAAGAGTCATAAGTAAG
TAAGACTCGGCTGATCAAAAACCTTCGCAACTCTTCCCAAAAACAAATGTGTTTCTCCATTT
(SEQ ID NO: 4)

Exon: 1001..1143
Exon: 3372..3542
Exon: 4058..4202
Exon: 6615..6757
Exon: 7120..7228
Exon: 7333..7504
Exon: 7648..7754
Exon: 8263..8412
Exon: 8583..8716
Exon: 8953..9143
Exon: 9801..9935
Exon: 10017..10179
Exon: 10294..10507
Exon: 10885..11036
Exon: 13701..13884
Exon: 14430..14572
Start ATG: 3468

Transcript No. : CT5032
GGTCCATCAGCAACATAGATGACGCGGAGTATCACTGCAATAAGACGCAGGTGCGCAAGGTCATCTCGGGGGTGGTGGGTGCCGCCTCCTCGGTCACATCCATACAAGTTGC
CAATTTATTGCGGTTATTCCGAATTCCCCAGGTGTCGTACTTCTCCACCAGCCCCGAGCTGAGCAACAAACAGCGATTCGAGTACTTCTCCCGCACTATTCCCTCGGATCAC
TACCAGGTGAAGGCCATGGTGGAGATAGTGAAGCGGATGGGATGGAGCTACGTGTCGATTATCTACGAGGAGAGCAATTACGGAATCAAGGCTTTCGAGGAACTGGAGGAGC
TCCTCGCACGCCATAACATTTGTATTGCCATCAAGGAGAAGCTGGTGAAGGATTCGGGAGTGGCCGAGGACATCGCCTACGACAATATAGTGCAGAAGCTGCTGACGGAAGCC
GCGGGCTCGAGGGGCCATTATCTTCGGTTCGGATCAAGAGGTGCGCCAAGTGATGCGGGCGGTGCGCCGGGCGAATGCAACTGGTTCCTTCTCCTGGATCGGATCCGATGGC
TGGAGTGCCCGGAATTTGGTGTCCGACGACTACGAGCCGGAGGTGGAAGGCACGCTGTCTGTGCAGCCGCAGGCGAATCCGGTGCGCGGGTTCGAGGAGTACTTCCTCAGTC
TGACGGTGGAGAACAATCAACGCAATCCCTGGTTTGTGGAATTCTGGGAGGATCACTTTCAGTGCCGATATCCCGGCAGTACGAGCACTCCGTACAATAACTACACCAAACA
GTGCACCACAAAGGAGCGACTTTCACGCCAGAACACTGACTTCGAGGACCAGTTGCAGTTTGTCAGCGATGCGGTGATGGCATTTGCATACGCCCTAAGGGATATGCACCGC
GACCTGTGCGGCGGAGGTCCTTCGCTCTGCGGAGGCCATGAAGCCAACGAAGGGTGCAGACTTGCTGAAATATTTGCGAAAAGTGGAGTTTGAGGGCCTCAGCGGCGACGAGT
TCCGCTTCGACGGGAACGGCGACGGTCCCGCCCGGTACAACATCATCCACTTCAAGCAGTCCCAGCGCGGGACAGTACCACTGGGTCAAGGTGGGCGAGTACACCGAGGGCGA
GCTGCGGCTTAATATGACGGAGGTGAAGTTTAAGCGGCTGAGTCCCAAGCCGCCGGAGTCTGTCTGCAGCCTGCTGTGGTGGGTCAGGCCAAGAAGTACGTGGAGGCAT
GAGAGCTGCTGTTGGCACTGCTTCAATTGCACAACCTATCAAATCCGCCACCCGGATGACGAGACCCATTGCAAGCTGTGCAAGCTGGGCACTCTTCCCGACGCCCACAAGC
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AAGCCGACCAACATAGTGTGTGCCATTCAGCGGTTTGGTGTCGGCTTCTGCTTCACGGTCGTTTATGCAGCACTGTTGACCAAAACGAATCGCATTGCACGGATCTTCAAAG
CGGGCAAACAATCCGCCAAGAGGCCCTCCTTCATTAGTCCCAAGTCCCAGCTGGTAATCTGTGCGTGCCTGGTTAGTGTGCAGATACTCATCAACGGCGTTTGGATGGTAAT
TGCGCCATCACTGCCATGCACCATTATCCCACACGCGAGGATAATCTGCTCGTCTGCGACTCGTACATCGACGCCTCCTACATGATTGCGTTCTCCTACCCAATCTTCCTG
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GCCGCCGTGGTGACCGCCGCCACCTGTGCCCAGGAGGAGAAGATCCAGAAGCATATCACTCCCACAAACACAGACGAAGAAATTGTGCGAAATGGCCACTCAGACAATTTCC
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(SEQ ID NO: 5)

Start ATG: 240

MVEIVKRMGWSYVSIIYEESNYGIKAFEELEELLARHNICIAIKEKLVKDSGVAEDIAYDNIVQKLLTKPRARGAIIFGSDQEVRQVMRAVRRANATGSFSWIGSDGWSARN
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GPSLCEAMKPTKGADLLKYLRKVEFEGLSGDEFRFDGNGDGPARYNIIHFKQSQAGQYHWVKVGEYTEGELRLNMTEVKFKRLSPKPPESVCSLPCLVGQAKKYVEGESCCW
HCFNCTTYQIRHPDDETHCKLCKLGTLPDAHKQYCRPIPEIYLRPESAWAIGAMAFSATGILVTLFVMGVFVRHNDTPIVRASGRELSYILLAGIFMCYGVTFALVLKPTNI
VCAIQRFGVGFCFTVVYAALLTKTNRIARIFKAGKQSAKRPSFISPKSQLVICACLVSVQILINGVWMVIAPSHAMHHYPTREDNLLVCDSYIDASYMIAFSYPIFLIVICT
VYAVLTRKIPEAFNESKHIGFTMYTTCVIWLAFVPLYFGTANHVPLRITSMSVTISLSASVTIACLFSPKLYIILIRPERNVRQSMMPPRYGNMHRTAGTGPSSMMAAAVVT
AATCAQEEKIQKHITPTNTDEEIVRNGHSDNFQYNHVAGHQCVQSNTICRSICAKQCHNGHDHAHR*
(SEQ ID NO: 6)

Name: metabotropic glutamate receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384693
CAGTTAGTTCCTAGTTAACAAGTGAGGTTTGGTTGAAATCTTTCTTTGCTATATAGGTATTTCATTTCCGTATGCTGTATCGGTTTTGTAAAATAATAAAGCATTTCGCGAG
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AATCAGCGTAAATCAAAAACAATTGATTTCTTACAAAATACATAAAACATAATTCGCCTGAATTCTATATATCATGTACATACAGTTCCTAGATCTTATACATATACCTACA
TCCATATATATATACTTGATTTTCTGGTTGTTTAAATTAGTTTTTAAGTATTTAAAAATGGCATGTGGTGACATGTATTACAATACATCATACATATATGGTACATACATTT
ATATTTAATATCGATTTCCAAGTTGGTATAAAATGCATGCAAGTCGAAGGGCCCGATTCCAATTCCAATTCCAACCCCCCATCGCTCGAGTTTTGGTTAAGCTTGCACGGCA
CCGCAGGGGTATGGATGTGCCCTATGGTCTAGGTTTTAGTTATTTCATATACATTTATAAAGTTTTGGGATTTTCGAATCACTGCACGTATAGCATGACAGCATGTTGTTTC
ACACAATGCTCCATATTTCGACTAACGACTAATACTAGGTATAGCTAGAGATCCTAAGCTACAATTTTTGCCTAAGACTGTTCCGGGGGAGTTGCGTTAACTGATCACTTAG

FIGURE SHEET 4

5/89

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CCAGTGGTTCCAGATAACATCGCACCGTGTTGTTCTCATCGAGCATGGCCGACAGGTGGCGCTGCTGATGGTGCGGAGGATGCTGATGGGGATGCGGATGGGTTAGCTGGTG
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GGGAGCCCTCACCAACGCCGCCGCTAACCCCAAAAACCGCACCGTTGTGCTCGGGTTGCGGTCCTGCTCCTGGTGGCAAAGCCCCGTAGTCAAGAGGCGCTCCATGTTTGCG
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CAGACGACGCATCCGCTCATCGCTCTGCGGTGGCAATCCATGAGCATCATCCTCCAAGTCGCTCTCGTCCTCCTCCTCATCCTCATCACAGACGCTGTCGTGCAATTGCTCC
GCGGCCGTTGCCTCCTCATCCTCCTCCTCGTCTTCGTCGTCATCGTCATCCGCCGTGCAGCGTCGAGCCGATCTTTGCTGAGCCAGCGACTGTTGTTGCTGCTGCTTCTTGA
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ACCACGCACTAAAACAAAAACATTAATTCGTATAAATTATTAGGCATATGAGCATGTGAGTCTTACTGGTCAATATAGTTCCAGAACACGCAGGTGGGATTCGTTACATTCT
CGGTCTTCAGATGTTTCAGTGTCAGGGTTATGGGCTGGGAGAGTTGTATGTGACGCCCCTTGCCCAAGCTGGCCGAGATCACCTTGCTGTTCAGGATGCGTAGGCGCTGTTG
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TAACTGCGGGAGCTCTTGAGATCGAAGTGATCATAGCTGGGCTTTAGAATGGATTCCAGGCGATCGAAGGCGGCGAATACAATTCGCACCAGACCGCCTTCACTATTATCTA
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CGGCGGCTCGCAGCTGCTGCTGTTGTGCAGACAGTCGCCACCGCTGGGTGCCGGAGTTGTCGAACTGATGTCATCATCGTACTCATCGTAGCCGGAGTCGGGTATCCTCTTC
CGCAAAACAACTTGGACTCATCATCGCCTCCGGACATCCCGGCTGCGGTTCAAATTAATATTGTTGATGGTGCGCACCACGCTGCCGTTCCCGGGGACAACGGATCCACTGGC
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GGACACTGAAAGGCGAAGGCTTCATAAGTCACAGGGTGCTGGGCAGGGTATGGGTTTATATGGACATGGTATATATATATGCGCATATAAAAAGAAATTTTTTGGTTAGCGGC
GATGATTGTTGTAGTTTGGTTTGGTTTGGATTGGATTGTTGGTGGGCCTGCAAAGACACTTACGATCTAACGATATATGCTCATAGGATATTGACAATATGGTTGGTAGCAT
GATACGCTTTTTACACTGCCTGGGATATACTTAGTAATGCTGAGGTTGATGGTGGAGTATGTGGGTCGTTAGCTTGGTAGCAAGTGCAATAGTAGTCATAAATACCAAATCCT
GCCGGCCCAGATCACGAATCATCGATCGTCCATCATTGGTTCTTATCGGCAATGCTCATTCGGCGACAGTGTTTCACTCGGTTTGAAGTATTCAAACTGAAAGGGAAGATAACAT
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AAGATAAGAAGATGGCCATGGGCAGGGGAGGGGGGTAGGGTAGGGGAGCTAAGAATACACACCCTTCTGTGTACACCCCACACTGTGGTTGTAGTTGTTGCATGGCCATCGATTC
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(SEQ ID NO: 7)

FIGURE SHEET 5

Exon: 8400..8352
Exon: 8181..7992
Exon: 7808..6337
Exon: 6274..6047
Exon: 5977..5779
Exon: 5720..4860
Exon: 3972..3833
Exon: 3777..3548
Exon: 3478..3381
Exon: 3315..1531
Exon: 1466..1001
Start ATG: 8400 (Reverse strand: CAT)

Transcript No. : CT8755
ATGCTACCAACCATATTGTCAATATCCTATGAGCATATATCGTTAGATCTGTCCAAGTACCAAACCGCCTACGCCTGCGAAGGTAAGAAACTGACCATCGAGTGCGATCCCG
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CCGGGGGTTGGAGCGGGTGCGCCGCCCCCGCCGAGACTTCCCACACTTCCCGGAGTGGTGGGAATCAGTGGGAATCCCGGCCTGTTCAACGTACCACCGCAACACACCGCCGT
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AATTTGTACTGGAACATGACTCGAGTGGGTGATGTGAATGTTCAGCCCTGTCCTGGCGGGACAGCCGGCATCGCCAAGTGGCGTTGCGTTCTAATGAAGAGGATACCCGACT
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GGTAAACCAGCGTCTGCGCAACTTTGAGCCCACCTGGCATCCCGCGACACCTGATCTGACGCAATGCCGCAGCCTTTGGCTCAACAATCTGGAAATGCGAGTAAACCAGCGG
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AGATGATGCACGACAAGGAGACCTTCCCGGATCAGCGACAGCGCCGAGGCTATGATCATGGAGTTGTTGCATTGTGTGGTCAAAACCGGCTCCAACCTGCTGGACGAATCGCA
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TGCCGTTAGGAGTGAGCGAAGAGGCGCATGACGATCCCCGAGCAGCAACAGCAGACCACCAGTGCCCATCACAGAGGATGCCATTATGGGAGCCACCTCTGATTGTGAACTGAA
CGAGGCCCAGCAAAGAAGAACCCTAAAAAGTGGCCTAATGACGGGCACACTACAGGCTCCACCGCAGACCCTTGGTGGCCATGTTGTGCTCGAAAGAGGTAGCACTCTCCGC
TCCACTGGTCATGCCTCACCCACCAGCTCTGCCGGGTCCACACACCTGATTTTTGCGCACAAGCAACAACAACAACAGCAGCAACAGGGACCTTTGGGCGAGTCTTACTACC
ATCAGCCGGACTACTACAGCTGGAAGCAACCATCAACTGGAACAGGAGGATTGAAAACACCGCGGGAGTACTACAATAATGCGGGTGCTGCTGCATCATCGCCGCAACAGGC
GCACGAGGTATTCTACTGGACTCAAAAGCCGAACAGCGACCCACATGGCAAAAAGAAGAGGGGCGCCGGAGGAGTTCCCGCCTCGCCTAGTGGATCTCTGCACAGTCGCACG
GCCGCCGCCTCCCAGGTGCTTTTCTATCCATCGTACAAGAAGACCAAGCCTGGCCAGCCAACAGGCTATCCGCAATACGCGGAGGCGTTGGACCCACCACTAGCCACTGGCA
ATGCGGCTGCCTACTACCAGCAGCAGCAACAGTTGCGTCGCCAGCAGCTACATCAGCAGCAGCAACAGCAGCAGCAGCAGCAACTCTCCTCGGACGAGGAGCAGGCCGAGCA
ACATGCTCACCTGTTGCACCTGCAACGACGAGCTGGTAGCCAGCAGCAGCTCCCTGCTCCACCGCCACACATGGCCGCAGTACCAGCAGGAGTTTATGCAGCGCCAGTATAGA
AATAAGCATTCCAACTGTGATCTGGGCATGGGCGATGCCTACTACAACCAAGGCAGCGTCGGCGGCGCGATGGTGGGCCGGTCTACGAGGAGATCCTCAGCAACCGCAACT
CGGATGTGCAGCATTACGAGGTGGGTGACTTCGATGTGGACGAGGTGTACAACAATAGCGTTGGCACTGGCGTCTTCAACAACATGGCAGGCGGCGGTGGCCGCCGGCGGTAG
TCGGTACGGCGGCGGAAGCCTGAGTGGCGGCAGTGTCTCGTCCAGGAGCCAACAGCAGCAGCTCAAGAAGCAGCAGCAACAACAGTCGCTGGCTCAGCAAAGATCGGCTCGA
CGCTGCACGGCGGATGACGATGACGACGAAGACGAGGAGGAGGATGAGGAGGCAACGGCCGCGGAGCAATTGCACGACAGCGTCTGTGATGAGGATGAGGAGGAGGACGAGA
GCGACTTGGAGGATGATGCTCATGGATTGCCACCGCACGGATGAGCGGATGCGTCGTCTGATGGCGATGCAGGACGAGGATTTTAAGCGGCCGGTTTCAACGTCAGCTGCCG
CAAACATGGAGCGCCTCTTGACTACGGGGCTTTGCCACCAGGAGCAGGACCGCAACCCGAGCACAACGGTGCGGTTTTTGGGGTTAGCGGCGGCGGCGGTTGGTGAGGGCTCCCTG
CGTGGCGCATTCCGGCAGCAGCAGCAGCAAGCACTGAATGCCAAGTCGCCAGGCGGCCGTTTGGCGGTAAATGAGCTATTCGGTCACGGCAACTCGGGACCACCGCTGCCGC
CGGCGAATCAGACGCCCGCGCAGAAGCGCCAGCAGCTACAGAAACTGTCACCACAGTCCACCACATCATCGTCGTCGCATACATCACACAGCAATCCCAATCCGCATCCCCA
CCAGCTAACCCATCCGCATCCCCATCAGCATCCTCCGCACCATCAGCAGCGCCACCTGTCGGCCATGCTCGATGAGAACAACACGGTGCGATGTTATCTGGAACCACTGGCT
AAGTGA
(SEQ ID NO: 8)

Start ATG: 1 (Reverse strand: CAT)

MLPTILSISYEHISLDLSKYQTAYACEGKKLTIECDPGDVINLIRANYGRFSITICNDHGNVEWSVNCMFPKSLSVLNSRCAHKQSCGVLAATSMFGDPCPGTHKYLEAHYQ
CISAAQTSTTTNRPSPPPWVLSNGPPIFGNGSGLIHPPGVGAGAPPPPRLPTLPGVVGISGNPGLFNVPPQHTAVTHSTPSSSTTAVGGGRLKGGATSTTTTKHPAGRHDGL
PPPPQLHHHNHHGEDTASPTKPSSKLPAGGNATSPSNTRILTGVGGSGTDDGTLLTTKSSPNRPPGTAASGSVVPGNGSVVRTINNINLNAAGMSGGDDESKLFCGPTHAR
NLYWNMTRVGDVNVQPCPGGAAGIAKWRCVLMKRIPDSGYDEYDDDISSTTPAPSGGDCLHNSSSCEPPVSMAHKVNQRLRNFEPTWHPATPDLTQCRSLWLNNLEMRVNQR
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RSVVQKVKNILLSVRVLETKTIQSSVVFPDSDQWPLSSDRIELPRAALIDNSEGGLVRIVFAAFDRLESILKPSYDHFDLKSSRSYAILSNDSDVNAGEIQQRLRILNSKVI
SASLGKGRHIQLSQPITLTLKHLKTENVTNPTCVFWNYIDHAWSANGCSLESTNRTHSVCSCNHLTNFAILMDVVDEHQHSLFTMFDGNMRIFIYISIGICVVFIVIALLTL
KLFNGVFVKVRNGSNPLPHQRSGSRRQQNNIRDQTHESLTLTTPTSQSNVPPPSHGNTNFIQHNSIRNSHRNNLNYNVQQQQQQQQQQVVAAAAAAVVLSNQPQRNMQHAMN
NLNLNLNHQHGQQTAAAAAAAASIAAALQQHAVQASNASNNLNISHNYLQQQHVQQQQQQQRGQQPQPHPHRNHHNLNVDGNGLDNTNNIIMQANMDDLQYKWWWCIYLCLLAI
ELLFLLGIEQTETSIFCGFITIFLHCAILSGTAWFCYEAFHSYSTLTSDELLLEVDQTPKVNCYYLLSYGLSLSVVAISLVIDPSTYTQNDYCVLMEANALFYATFVIPVLV
FFVAAIGYTFLSWIIMCRKSRTGLKTKEHTRLASVRFDIRCSFVFLLLLSAVWCSAYFYLRGAKMDDDTADVYGYCFICFNTLLGLYIFVFHCIQNEKIRREYRKYVRQHAW
LPKCLRCSKTSISSGIVTGNGPTAGTLCSVSTSKKPKLPLGVSEEAHDDPQQQQQTPVPITEDAIMGATSDCELNEAQQRRTLKSGLMTGTLQAPPQTLGGHVVLERGSTLR
STGHASPTSSAGSTHLIFAHKQQQQQQQQQGPLGESYYHQPDYYSWKQPSTGTGGLKTPREYYNNAGAAASSPQQAHEVFYWTQKPNSGHNGKKKRGAGGVPASPSGSLHSRT
AAASQVLFYPSYKKTKPGQPTGYPQYAEALDPPLATGNAAAYYQQQQQLRRQQLHQQQQQQQQQLSSDEEQAEQHAHLLHLQRRAGSQQQLPAPPPHMAQYQQEFMQRQYR
NKHSNCDLGMGDAYYNQGSVGGADGGPVYEEILSNRNSDVQHYEVGDFDVDEVYNNSVGTGVFNNMRAAVAAGGSRYGGGSLSGGSVSSRSQQQQLKKQQQQQSLAQQRSAR
RCTADDDDDEDEEEDEEATAAEQLHDSVCDEDEEEDESDLEDDAHGLPPQSDERMRRLMAMQDEDFKRRFQRQLRKHGAPLDYGALPPGAGPQPEHNGAVFGVSGGVGEGSL
RGAFRQQQQQALNAKSPGGRLAVNELFGHGNSGPPLPPANQTPAQKRQQLQKLSPQSTTSSSSHTSHSNPNPHPHQLTHPHPHQHPPHHQQRHLSAMLDENNTVRCYLEPLA
K*

(SEQ ID NO: 9)

Name: Latrophilin receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384743
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AAGTTGAAGGAAAACCCTCAGTAATTCCGCCAAAGTTCGTTGCTGGAAAAGGACTCTTTTAAGGTAATTTCATGATATTGACTCGTTTCAGTTAAGTCCCTAAAGCTAATGG
CACACTGAATACAATTAGGCATTACGGCTACGATTGCAATTGCGTTTTTTTTTTTCGATTGTTAAGTACACTTGTTCGGCATCGGGAGAAGACAGCAAAGTTGGAAACCTA
GTTTCTGGTTCCCATTTTTATTTTTTTGTTTTTGAAGACATGAACATGCGTATCACAGTATTTGGTTGCTGCGCGTTTCTCTCTCTCTAACTCAAAAAAAAAGAATTTAT
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GACATCTGATTCAGCGATATAGAGCCGGTACCAGGCGAAGTCTTCAGTTTGTACGGACTTGGCGGCAACGGAACACTGGCCATAGAAGTTCGCACCGAATGGTAGGAGACCA
CCGTGCTATTGCAAGCCGCATGCGATCCACGCGAGCTACTATGCCCGTCCAGGTGTCCAGTTGCTGCTCCGGCAGACGTATGCTTCACCATTTTGCCATTGCTGACTTGCCT
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GCGGCCATTCCAAAATAGTAGCGCATAAGGAAGACACTAGCGCAGGAGGCATTGGACAGTCCGTCCACGGTGAGTAGGGATTCATTGGGCGCCTGGGGATCCGTGCCGCACG
CAGTTCCCGTTCTTCCCACCATAAAGCGCACTGCCCAGCCCAAGGTGACCATGTTGTGGCACCAAATCAGCGGCGACAACAATCTGGACCACTTGGCGCTGGCCAAACGACT
GCCATCGCTGGCCAAAAGACACACGGTGGCTACCAGGGCCAAACCCAAAGCGGCATAGGCCCATGTGGAGACCCAGATCTCTGCCAGATGCTTCTCCGCCGGTGTGAACAGT
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GTATTCCTTGGCCCGGTAGCCCATACAAATCCTGCTCCTGCTGCGGCTGATGCAATTCACCGGGACCTTCCATACACATCGTCTCGTGGTTGTTCTCTCGCGGAAATTTATC
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GCATTTCGTTACCCACCAGATTTGGCATGGAGGTCTCATTGTAGCCGATCTTGCCGGCACATCTCAATGCGAATGGTTTCGCATTGCCGGAAGGCGGGGATTTCTGGCGGAGA
ACTGGAACTGGAACTGGCACTGGGGTTGCCGCTCGTTGAGGATTTTGAGATGCGCGGATGCAGGAGGATCACCACCAGGAGACACAATATGCAGGTTGGCTTCATTGCGGCT
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GTTTTCTTCGCGCTGGGTTCCCTCTTTTCTTTCCAAAGAATCCGAACTATATGCAGATTCTTCGTTCTTCGGTGGAACGAACGCTGGAAGGGGTAACCTGTTCCAGGTGCGT
TCGCCCTCTCTCGCTCGCACCCTCTCACTCGTTCCAACAACTTCCAGCTCTCCTTCTTTCCAGCTTGTTATTGTTGCTTTTGGCTTGTCAACTCGTTAACTACCTCTTTTT
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CGGGTTTTTCCTCAGGGATTAACCCGAAAACGATCTAGCAAACCATCGAATCTTTCACACATCTCAGTGAACGAATAGTGTATTTGTTTCGATGTGCTTAAACGAATGGCGC
AGTCAGTTTGTAGCCTTAGCGAATGTATTCTAATCTAATTGGTATTAACATCGAACGTTTATATATTTTATTTTGTTTTCGTGGTAAAATTCAACGCATACTGGTCACTCTG
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GCCCCTGGCGGAGTTATGCGTAATCAAAGAACATTGAGAAGGGCGCGCTTTTCAAAAACAAATTTGTCCAAATAATAAGAAACATTTAAGCATAATAAGAACATAAATGTT
CAATAAATTCTATAGGTGCAGTAAAATACGTGTTTTGCTAGCACAGCTATTTTAAGCTGAGAACTTACAATATTTTAGTACATTGTGCTTAAGGTTTAAAGATACATATATT
GAAAAAGTTCTGGAAATGCTTTTGAAGAACAAAGCTTTAAGAGGCGCGCTTTCCGAGTATGTGAGCTTTTTCAAATGGCACACTTTCTGCCGGAATATAAAATAAAAAAACC
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AATTCTGAGCCAAACCGCGATTGCCATTTCTGCATGTTGGTCCTCCGTCCGTTTCGCCATCTCCCTTTGGCCACCGCTTGGCCTCTCTTTCGCACACACATGGCAAACACAA
GCCACGCCCATGTATTTCAACCCCCCTTGACAAAAATACGTAACATGCCACTTTTTATGTATGAAACGTGACAAATACGCACATGTGTGAGAAAGAGATCCACCGAGCTGGCGA
GAAAGAGAGAGAGAGACGCTGGACGTTTATGTGTTTGGCAGGACTCGCGTATGCAGTGTGTGTGTGCGTGTGTGTGAGTGTGTGTGAGTGTTTGTTGTTGGTTAACGCAC
ACGCGCAGACGTAGCAACACATACACATATGTGGAAAGGATATGTACATACATACATACATACATACATATGCCCGCTGACTTTTTCGCCACTGCCAA

(SEQ ID NO: 10)

Exon: 3914..3576
Exon: 3322..2232
Exon: 2170..1932
Exon: 1854..1001
Start ATG: 3241 (Reverse strand: CAT)

Transcript No. : CT9057
GACCAGTATCCGTTGAATTTTACCACGAAAACAAAATAAAATATATAAACCTTCGATGTTAATACCAATTAGATTAGAATACATTCGCTAAGGCTACAAACTGACTGCGCCA
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GACGTCGATCAGCGGGGTTGGGCGGCCGTGCCGGTGGAGAAAGGGGAGTGGTTGGGGCTGAAGAACGAGTGGGGGAAGGAGGAGAAGCGATAACAAGAACGACGCCGAAAAAAAA

FIGURE SHEET 7

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GAGAGAAACGGAAATCGGAACACCAAGCGAAGAAACGTATCGAATTCGTATTCTTCGGAACGAAAGAACAACAAATCAGCCGCAATGAAGCCAACCTGCATATTGTGTCTCC
TGGTGGTGATCCTCCTGCATCCGCGCATCTCAAAATCCTCAACGAGCGGCAACCCCAGTGCCAGTTCCAGTTCCAGTTCTCCGCCAGAAATCCCCGCCTTCCGGCAATGCGA
AACCATTCGCATTGAGATGTGCCGCAAGATCGGCTACAATGAGACCTCCATGCCCAAATCTGGTGGGTAACGAAATGCAAACGGACGTGGAGTACACACTGCAAACCTTTGCA
CCACTGATCGAATACGACTGCAGTTCCCAGTTGAAGCTGTTCCTGTGCGCCGCCTACGTGCCCATGTGCACGCCCAAAGCTCCAGTCCATGCCATCGGTCCGTGCCGGAGTC
TCTGTGAGTCCGTGCGAATACGTTGTCATCCAGTTTTGCAGGGATTCGGATTTCCATGGCCACCGGCTCTCGACTGCGATAAATTTCCGCGAGAGAACAACCACGAGACGAT
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TCGGGACTGGCCAAATCGCATCTGTACGTAAGGCTACCCAGATCTGGACGCTGTGCACCACTCTGCGAGGCGGACATACTGTTCACCACCGGCGGAGAAGCATCTGGCAGAGA
TCTGGGTCTCCACATGGGCCTATGCCGCTTTGGGTTTGGCCCTGGTAGCCACCGTGTCTTTTGGCCAGCGATGGCAGTCGTTTGGCCAGCGCCAAGTGGTCCAGATTGTT
GTCGCCGCTGATTTGGTGCCACAACATGGTCACCTTGGGCTGGGCAGTGCGCTTTATGGTGGGAAGAACGGGAACTGCGTGCGGCACGGATCCCCAGGCGCCCAATGAATCC
CTACTCACCGTGGACGGACTGTCCAATGCCTCCTGCGCTAGTGTCTTCCTTATGCGCTACTATTTTGGAATGGCCGCCTGCGCTTGGTGGGCTGTGCTCTGTTTGGGCTGGC
ACCGGCGACATTCGTCGGCACAGTCCGGACTCCAAGGGCCATGTGGTCATTCCCTCGAACTTTGGAGGCAGTCCGGCGAAGAGGAACAGTGCCAAGACGGCTCAGCAGGATCT
AACGCAAAACAACTTTGTGTGCTTCGTGGCCTGGGGATTGCCGGCCTTTCAAACGTCAGCAGTGATCGTTGCCCGTTTCGTGGATGCTGACGAGTTGCTTGGCAATCAGTCG
GATAAGGCGCTACAGATATTGGTGGCTACGCCCGTTTTTTGCTACTGGATCTTTGGCTCGATGAATCTGATCTCCGGCTATTTGGTACACTGTCGCACCAAGGAGATCCTGA
GGAATAGCAATGCACTCAGCGTGCAACAGCAACTGCAACAGCTAAGCGCACACAGTAGTTCCGGCATTGGCATATTCCTTTTCATCTATGGACTTGCATGTGCCATGCTTCT
GTTGGCTGTCATTTACGAGTTTGCCAACATCGATGTCTGGCTGGGATCGGGTGATACCAATACGCCACTTTGGCCATTTTTGTTGCGCGCCTTCATGGAACTGATGCTGGGC
ATTTGCTGTTTTGCCTGGGTACTTGGACCAAGCATTTCCACTCTCTCTACAAGAGGCAAGTCAGCAATGGCAAAATGGTGAAGCATACGTCTGCGGAGCAGCAACTGGCACC
TGGACGGGCATAGTACCTCGCGTGGATCGCATGCGGCTTGCAATAGCACGGTGGTCTCCTACCATTCGGTGCGAACTTCTATGGCCAGTGTTCCGTTGCCGCCAAGTCCGTA
CAAACTGAAGACTTCGCCTGGTACCGGCTCTATATCGCTGAATCAGATGTCCAACTATTCGCTGGGCAGGAGCGTGCATCACCAGCAGCGCCATTCGCCGCATCATCATCAT
CACCAGCAGCAGCAGCATCATCAGTTCCATCCCCACCACAATCACCAGCATCACTCCACATCCTCGCATCGGCTGTATTATCCGCCAGGTAGCTATGCCTCGCAAAAGTACA
GCCAGCACGGCAGCTACTATCCCCACTTGCAGCAGTATGGCAATGAGACGCTACTCTAG
(SEQ ID NO: 11)
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Start ATG: 421 (Reverse strand: CAT)

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MKPTCILCLLVVILLHPRISKSSTSGNPSASSSSSSPPEIPAFRQCETIRIEMCRKIGYNETSMPNLVGNEMQTDVEYTLQTFAPLIEYDCSSQLKLFLCAAYVPMCTPKAP
VHAIGPCRSLCESVRICHPVLQGFGFPWPPALDCDKFPRENNHETMCMEGPGELHQPQQEQDLYGLPGQGIPGGLGGKLPMDCSGLAKSHLYVRLPRSGRCAPLCEADILF
TPAEKHLAEIWVSTWAYAALGLALVATVCLLASDGSRLASAKWSRLLSPLIWCHNMVTLGWAVRFMVGRTGTACGTDPQAPNESLLTVDGLSNASCASVFLMRYYFGMAACA
WWAVLCLGWHRDIRRHSPDSKGHVVIPSNFGGSPAKRNSAKTAQQDLTQNNFVCFVAWGLPAFQTSAVIVARFVDADELLGNQSDKALQILVATPVFCYWIFGSMNLISGYL
VHCRTKEILRNSNALSVQQQLQQLSAHSSSGIGIFLFIYGLACAMLLLAVIYEFANIDVWLGSGDTNTPLWPFLLRAFMELMLGICCFAWVLGPSISTLYKRQVSNGKMVKH
TSAGAATGHLDGHSSSRGSHAACNSTVVSYHSVRTSMASVPLPPSPYKLKTSPGTGSISLNQMSNYSLGRSVHHQQRHSPHHHHHQQQQHHQFHPHHNHQHHSTSSHRLYYP
PGSYASQKYSQHGSYYPHLQQYGNETLL*
(SEQ ID NO: 12)
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Name: Frizzled 4 -like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384825
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TAAGGAGCGGGTTAATCACAACTGGCTGGGAAACTGAAAGTGGCCGACAAGCGCATCTACTTAACCTAGATGATGGTCCTACGCGGCCCAGGGTCAATCACATTGCGGAGTA
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TCGTAAAATAATTGCTTGGTGTTTCGCTTCTAATTGACGAGGACTTGGACTTGGATTTGAAGTGTGGACCGTGTACAGAGTGGACAATGGACAGGGCATCTTATTTATTCGG
TGCCATTCGCAGGCGCCTGCTGCTCCTCTTCCTGGGAATCGCCGAGGGAAAGCCTCGACTTGCCCGCTGTTTCCATCGATTTCCAGGTGCCTCCACTGGTGGCCTGCTGCAG
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GGAAAGCGTGGCGAACCCCTTACCCTTTCCCTTAAACTGGGTGGCTGCTGCACCACCGAAGGTCTCCGGTTGCTGGGCAATTGGAAGTTCACCTTGGTCTCCAGCAGTTTCA
CATACTTTCCACCCAACGTTTGGTCCCCCTGTTCACCGCCAGAAATAGTGGGGATAGGCAGGAAATTCGGATCCTTGGTAAGGTGATCCAGGTGAGTACCGCTTTTGGTCAA
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AGTATTCCCGAGATACTTGGAGTTCTGTTTTTACTTGCAGCCGGAGTCTGCGAGATGCCACTGGTTACCGTCAGTTCTGGCTTTAGATGACCTCCCCCAGTTAAGAGTGATG
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GACTCGCTCCGAAATCAAGTTGGCCAGCACCACGACGATGGCGCTGGTGATGACCACACTGTATACAGACACTCCGATGTACTGCGAGTCATTGAGAGCAGGTATTTTTACG
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AATCCGCCGACGAGCAAGATCAGTTGAATGTCCTGCAGCATCTTGTCCTTGAAAACGCTGCCGGTACGAGTGAATATCCGATGCACTCTGTAGGTCTTGGCAAACATCGATC
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AAGTAACACACTAAGTGTCATGTCAGGCAGACCCAAAGAAAACAAGCCGGCGGCAACAATGGGGAAACAAGTCATCAATGGACCACAATTCTCAGAGTGCTTGAGACTTTG
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AACTGGAAAAGCGGAACGACAGTAGAAGTGGTTACAGAAACAGAAACAACAGCGACCAGCAAATTTCCCAGGAGTGGCGTTCGAGGCAGTTGTTAAGGGGGTCAAAGTGGAA
AGGCGCAGATCGGGATAGAAGAAAGCTCGTCAAACTTGACTTGACTTCGCAGTTGCAGCAGTTGCAGCGAAACCGAACGGCTATTTATAGCCACGACAGGGGCAGTC
GTGTATCTTGAAAAGACACGCGGAATAATCAATATTCAGTTTATATAATCCACTTTAAAATAATAGAAATTAACAAAAAATTGCCACAATTATCAGTAATTTTTATACTTCG
CAGGCTATTTTATCGCCATCTTCGTGTATACGAATACGACATTAGTTCAAGCAATATTCTTTCAGTGAATAAATAAAGCAAACACATGAGCGCGACTCGAAAGTTACCAG
CCTGAAACTGAAAGTCATATTTGATGAGGACCCCACATGCTTGCTTACACACAGAAGCCCGTCAAAGTCAAACAAAGACGGCTGAGAGGAAAGGCGGATGAGAATGCGGATT
CGGATAGGAATGGCGATAGGGATGGGGATGTCGGGAGCCGAAGGATAACAACTCACCGTGCAGACCGTTGCGAAAGAGTCCTCCGCCGAGGGCAGCGTCGAGTGGTCCAAGCC
CAAAAGGATGACGGTGGCGTACACCAAAGATGCAGCCCACTGCGGTGATGTTGCTCAGCTTCGGGCTGGAAAGTTTAATTGCCCTGTGGAGTGAGAAGGGGGGATGGTCATGGT
TATAAGCTGAGGCGCCGCAATCCTTTGCAGAGAAAGTGCAGAGTAACCGTAGAATGCGAAACATATATACGAACTCAACTAACGATGGGTCAGAAATACAGCTGGAAAGCCA
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<div align="center">

FIGURE SHEET 8

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AGCAATTACTTCACTTCAAAAACCGAAACAAGTCACATGTGTAATGGGTTCAATGGGTTGAGCACCGAAAGCAGTTAACTCATCATGGAATATAAAGAAACAGCCCGCACAA
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(SEQ ID NO: 13)

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Exon: 6893..6618
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Exon: 4786..4485
Exon: 4114..3976
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Exon: 2683..2365
Exon: 2235..1001
Start ATG: 8795 (Reverse strand: CAT)

Transcript No. : CT9836
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CTGCCGCCCACTTGCAGTCTCAGCGCCCTGGCCGAATCCGAGGACCGTCCCGGAGATAGCACCTCTATCTTGGGCAGCTGCAAGTCCATACCTCGCATTTCGCTGCAGCAGG
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(SEQ ID NO: 14)

Start ATG: 1 (Reverse strand: CAT)

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LPPTCSLSALAESEDRPGDSTSILGSCKSIPRISLQQATSGGTWKSMETAGKSRLSLGDSQEEEQQAPANGTE*
(SEQ ID NO: 15)

Name: GABA B-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000012808751
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11/89

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ATGAGACTCAAGGAATGTCACATTCACAAAAAATTTTCAATTTGAAATCTGAAAAGATTCAACAGCATAAGCAAATGAATTTAAGATTGCGATATTTGGGTATTATCCTTAAT
TGGCTGGCTGCCTAATGTAGATTTGTTTTTCTCGGTGTACCGATGCATCCTCTTTGCCCATCCACTTCTTTCTCCCCTCTTTGCTGATTTTTTTTTTTTTGTTTTGTGAGA
GGGTGGAATTCGGGATTTGGGATGTGAGCGAGAAGGATGGCCATATTTTGAATTGTGGAAACAGCCGTTCCATTATCGTTCCATTACAAATGCACACACACACACACACACA
CGCGCGCGTGCAGTTTGCGCTTCTCTGTGTGTGCGTTTGGACCAAATGCAATAACAATAAAAACGCGCAACTCAAATTGTTAACAAAGGTAAGGCCGTTTTTTGGCCGGAT
TTGGATTCTGGTCTTGAAAGAGAAACACACACACACACACGCACGCAAAAAACCAACGAAAATAATAACAAAACAACAACTCACCCGAACTCGAACCCGTTTCACTGTTT
TCCGCTTATTATAAATTTATACTTCGTTTGGCGTTTCTTAAATGCTTTCGAATTGCATTTTGGATTTGACATTAAATCGCTCCGCGCAGCACAGTAACAAAAATAAACGGAA
CAAAATAAATACAACCAGCCGATTCTGGCCTTCTCACAATTCCGACTTTTGAATTATCGAAACAGAAGCGCTGCTTGGGCCAACTAAGCCAACTTAACTAACCGATCGCAGA
GCGCAAAGTGTCGTATTTTCACTGTCGTCAATTAACAACAGCGGCAACAAGAACAACAAACGAAATGAGCGGCTGGGCTACAGTTTTTTAGTCCGAGCGCGATCGAACATGT
TGGCTGCCTGGCAACAAGTTCGATGCGAACTTTTCTATTGATCTAAGAAATCGGCGTTCTATCGATTGACGCGCTGCGCAGGCGCCTATCGATTTTTGAAATTCTAAGCCCG
CCTTAAAGGATATTTGTAGAAAAGTAGCTTGCAAAGAAATTAAATTCCTTGAAATAAAAAAGAAATTTAGTACTCTCGTTCTATACTCACTTCTATTCACTTGCGGTTAGTT
AGTTAGTTTTTAATGCCACATTTTTATGATGATGACTTTTTTTTCAGCTCATCTATGCGCAATCAATTTTGCGCCAAGCGACAGCTGCACATAGTTTCTTTTGACCAAGCAAT
CATTTATCATATAATTTTCCAAGTAGTAGTGCCAAGTTCATAACTGATGGAGTGTGCTGCCAATTTGCATGTTGTGGAGCCATTCAGTTTCAAGGTCGCGCTAATTAAATAC
TCGTTACAAGTGATGCCAAATGTATAAATATTTGAACAGAACGTATTAAATTAATATTATCCACTAAGAGCACTATTTTAAATTCTTAAAAACCAGATGCACGTCAAATAGA
TGTACATAAAAAGTATATTTACTTACAAATATCATACACGGACCTGTTTTATTCCTCATCACTGGCCATTAGTTGATAACATGTGGACTTCTATGATATCCTGCTGCATTTT
TGCCGTTTAGTCAGGATTTAGAGCTTGTACACAATGCGACAGCTGAAAGGGCGAAATCGGTGCAATCGTGCTGTTCGGCATCTGAAAGTTCAGGGCAAGATGTGGTTGAAAA
ATCTTAAAAGCGGTTTGGAACAAATTCGAGGTGAATCTATCCAAATCGTTAGAATCCCATGAGTACGTTCATC
(SEQ ID NO: 16)

Exon: 6913..6695
Exon: 2519..2365
Exon: 2292..2147
Exon: 2075..1975
Exon: 1908..1806
Exon: 1744..1257
Exon: 1187..1001
Start ATG: 2500 (Reverse strand: CAT)

Transcript No. : CT10621
GGCCCAAGCAGCGCTTCTGTTTCGATAATTCAAAAGTCGGAATTGTGAGAAGGCCAGAATCGGCTGGTTGTATTTATTTTGTTCCGTTTATTTTTGTTACTGTGCTGCGCGG
AGCGATTTAATGTCAAATCCAAAATGCAATTCGAAAGCATTTAAGAAACGCCAAACGAAGTATAAATTTATAATAAGCGGAAAACAGTGAAACGGGTTCGAGTTCGGAATGG
ATCAGGACATGGGCATGGCAACGGGCTACTTTCAGGACGCAGACATGCAGATGGATGAACCGGCGGCCGCCACGCAATCGATCTACCCGCATTCGGCGACATTATTCGCGGC
CATTAGTGCCTGTGTCTTTGTGACGATCGGCGTTCTTGGCAACCTGATTACCCTGCTGGCGCTGCTCAAGAGCCCCACGATACGGGAGCATGCCACAACCGCCTTCGTCATT
TCGCTAAGCATCTCCGACCTGCTTCTTCTGCTTCTTCAGCCTGCCACTGACCGCAGTGCAGTTTGGTACCACATTGTGCAAGATCTTTCCGG
TGATCTTCTATGGCAATGTGGCTGTTTCACTCCTCAGCATGGTGGGCATCACCCTGAACAGATATATACTCATCGCTTGCCACAGCCGCTACTCGCAGATATATAAGCCTAA
GTTCATAACCCTGCAGCTGTTGTTCGTTTGGGCCGTCTCCTTTCTGCTGTTGCTGCCGCCCATATTGGGCATCTGGGGCGAGATGGGCCTGGACGAGGCCACCTTCTCCTGC
ACAATACTCAAGAAGGAGGGGCGATCGATCAAGAAGACGCTGTTCGTGATCGGCTTCCTGCTGCCTTGCCTGGTGATCATCGTTTCGTACTCGTGCATCTACATTACGGTGC
GCGCGAAGACAATCGACTGACCGTCATGATGGTCACCATCTTTCTGTGCTTCCTCGTCTGCTTCCTGCCGCTAATGCTGGCCAATGTGGTGGACGACGAGCGCAATACCTCG
TACCCCTGGCTGCACATCATCGCCTCCGTGATGGCCTGGGCTTCCAGTGTCATTAACCCGATCATCTATGCGGCCAGCAATCGCAACTACAGAGTGGCCTACTACAAGATCT
TTGCGCTGCTCAAGTTCTGGGGCGAACCCGTTGTCGCCGATGCCGAGTAGAAACTATCACCAAAGCAAGAACTCCAAGGAGCTGTCGGGCGTCATCCGCAGCACGCCGCTGTT
TCACGCTGTGCAGAAGAATAGTATTAACCAAATGTGCCAAACATATTCAGTATGA
(SEQ ID NO: 17)

Start ATG: 239 (Reverse strand: CAT)

MATGYFQDADMQMDEPAAATQSIYPHSATLFAAISACVFVTIGVLGNLITLLALLKSPTIREHATTAFVISLSISDLLFCSFSLPLTAVRFFQESWTFGTTLCKIFPVIFYG
NVAVSLLSMVGITLNRYILIACHSRYSQIYKPKFITLQLLFVWAVSFLLLLPPILGIWGEMGLDEATFSCTILKKEGRSIKKTLFVIGFLLCLVIIVSYSCIYITVLHQKK
KIRNHDNFQIAAAKGSSSSGGGSYMTTTCTRKAREDNRLTVMMVTIFLCFLVCFLPLMLANVVDDERNTSYPWLHIIASVMAWASSVINPIIYAASNRNYRVAYYKIFALLK
FWGEPLSPMPSRNYHQSKNSKELSGVIRSTPLFHAVQKNSINQMCQTYSV*
(SEQ ID NO: 18)

FIGURE SHEET 11

Name: Melatonin receptor-like 2
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384305
GTTCGTTTGATCGGTTGACCTCGATTTATTTACTGCTATGCAAAGCTAAAATTCAAAAATCCCTACTCATAGATGAAGTTTTTTGCACACTTTAGGTGTAACTTGGTGCTTT
AACTTGGCGTTTCTAGTCTTAAATAATTGGCAAGATTATCTGCCTAACTTTTGGTGACCCCAACTTTTAATCACACACCAAGCGGAATTATACTAAGGTTTATTTCCCTTGG
CATCAGACTGTCTTCTTCTTCGCTCTTCCAGCTCTTGTCTTTATTAAACCTGGCCAAGGACCTGTAACTTCGTTTAATTAAGTAATTCAATGAAATTGACAGCTGTTTGCTT
GGGTCAAGCATAATTGATGACTACTCATAATCAAAACAGAAGTGCTGCCAATGAATGGGAAGCGGAAGTCTGGCATAAATTACAGGTCTGTCCATCCGAAGCGCAATCATCA
TATAATTGTCATGGAACCACACTTGGCACTCACTTTTGCCTGGCTTCTGCTCCTGCGAACGCTGATGTTGCTTTGTGCTTTGTGCTTTCTGCTTGATGCTTTTTGCTTTGTG
CCCAAGTCTCGTGACTCCACTCCACTCGGAGTGGCATCCATGGTTAGGAGAACAGCAATAATGAGGCACACCAACCGGCCAATTGGCAATTGTGCGAGGTCAAACACAACCG
GTGGAGGAAACTGGTGTCGGCCGCACAGGGAAGACTTAAATTTTCTTTAATTGCTCGAATTTATGGGTTGGTAGTGGCATAACGACAATTGTCCAAGTCAAGGTCACAAATG
ATGCTCCTGCCTTTTTAGTTCGATACACACAAAGAAAAGGGGACCATACATATACAAGCAACCAACTAGATGAAACCTATTTTAAGGACGGTTGAATTGTTGGCTTTTAACA
TAGTAGATTAACTTCAAAATTAGCAGTTACTACTACTAATAACGAGCTAAGCCACTCATTTGCGTAAACACTTTCTATCTGTGCACTTTTATCTGCTTGAATAGTGTCTGGG
TGATGGCCTCGATTGCCGTGGTTGGCAACCTATTGGTCCTGCTCGGTCGCTACTTCTACAAATCACGGAGCAACGTGGAGCACTCGCTCTACCTTCGCCATTTGGCCGCCAG
TGATTTCCTCATGGGCATTTACCTCACATTGATTGCCTGTGCGGATATCAGTTTTCGCGGCGAGTATATCAAATACGAGGAGACCTGGCGGCATAGCGGCGTTTGTGCCTTC
GCAGGTGCGTATCCTTCGACATCCTAGCCATTTCCATTTCGTAATGGAATGCTAATGTGTATTACGTATTCGCCGTGTAGGCTTCCTCAGCACCTTCAGCTGCCAGTCGTCG
ACGCTGCTGCTCACATTGGTCACCTGGGATCGTCTGATGTCGGTGACGAGGCCCCTCAAGCCACGGGATACGGAAAAAGTTCGGTAAGTGTGAACTACAATAGATATGTAAT
TTGAATTTTGTTCGTAAATGCAATTATGTTTGTTTTGACCGCCGCCTTACTATGTACAATATATATTTTCTGTTGCTTCATTTTAGTTTGCAAAAGCTATGGTTTTGTATGT
GTAAGCTATGATAAATTATTGAAATGACAACTTCCACAGCATTGTCCTACGCCTTCTGCTGTTGTGGGGCATAAGTTTCGGATTAGCTGCAGCTCCACTTCTTCCCAATCCG
TACTTTGGTAGCCATTTCTACGGCAACAATGGTGTCTGCTTATCGCTGCATATCCACGATCCCTATGCGAAGGTAATACACCATTTCCTTGGAAACGCCTGTTCTAATATTC
CAAAATGTATATTTTTAGGGTTGGGAGTACTCGGCGCTGCTGTTCATCCTGGTCAATACGTTGTCACTGATCTTCATCCTCTTTTCCTACATTCGAATGTTGCAAGCGATAA
GGGATTCGGGTGGCGGAATGCGAAGCACTCACAGCGGTCGCGAGAATGTGGTAGCAACTCGGTAAGTTTGGATAATTCAAGTAAAATGATTTAATTATTGAAATATCATGTT
TTTACAGCTTTGCCATCATTGTGACCACCGATTGCGCCTGCTGGCTGCCCATAATTGTGGTCAAATTGGCTGCTCTTTCAGGCAAGTTCATCGGCAACGCCTTTAAATGATT
TATTTTGATTATCAACTTATTCGTATATATATAACCCCTTTCAGGCTGCGAAATCTCGCCCGATCTTTACGCCTGGCTGGCGGTTCTTGTGCTGCCAGTGAACTCGGCCCTC
AATCCAGTGCTCTACACATTGACCACTGCGGCCCTTTAAGCAACAGCTGCGTCGCTACTGTCACACCCTGCCCAGCTGCTCGCTGGTGAACAACGAGACCCGATCCCAGACCC
AGACTGCCTACGAGTCCGGACTGAGTGTCAGTCTGGCGCACTTGGGCGGTGGTGTGGGCGGCGGGTCGGGGCGAAAGCGGATGTCACACCGGCAGATGAGCTATCTGTAGGC
GGGCGCAACTGGCTTAAAATGCAGCACGAGATCAACAGACTGGGGCTAGTGGGTGGGTGGCATTACAACAGGACACTTCCATGTAATTGGTCCCTTAGACTATTGGTATTAT
ACGTACTTATTGATACTTATTCTAATATCAATTTTAAATTACTTATAACATTTGAGGATATGATAACATAAACCTTAGACAAGAGATTCCAGCTATTTAAGTTTCTTTTTTG
TATATTATTTATTTTACCAATCGTTTTAAGGCAAACCTCTTACAACTGTCCAAAGAATATCCTAACTATTTGTTGCATCCCCATTTATTCGACCTGCCCAATGGGATATTGT
TACATGTGATCTAATAGTTAAATCAAATTTTAATTTTATAAATACATATTCAGATGTTAATTGAAGCTTTTGAACATAGGACTTGCAATCGAAGGCCGCAAATGCCTGCCAT
CCGGCTTTCTATGCGTTGCCCTGAGGTTCAGTGGCTACATCGAGATCCGCCTGGACGTGATAGGGTCCCTCGTTCACATAGGCCGTGAAACGGATGGTTTCGGTGGCGCGAAA
ACTCAGCGCTAGCGGACAGAATCTCCATAATTTGCCACTTCATATACTTAATGTCCCTGTGCAGATCCTTTTGACGCGAAAGAAGGAACTCCACAGCACCGCCGGTATTCTT
TAGAGCTACAATGCCCCAGTTGTACTTACAAATGGTTTTCAAGAACGACAAGGCGGCCATTTGAAGATCGGGGAACGGAGTGTTTATCAGGTCCATAATGATATTAGCATGC
GCTCCCCCAGCGAAGCACTCGTACCAGTTTTTACCAATGTTACTGAAAAAGAAGAGAATCATTAGAAGAAAAACTTCAATTATAGAGTTAAGCATTACATGATTTCTGTGGC
AGGCGGCGTCTTGAAGTCATAAATCACATCCAGGGAGTTGAGCAGCCTCTTCTTGATGTGCGCCGATAGCTTCTTAGTATGCGAGCCATACTTCTTAAAGGA
(SEQ ID NO: 19)

Exon: 1001..1236
Exon: 1313..1427
Exon: 1720..1864
Exon: 1923..2077
Exon: 2136..2209
Exon: 2285..2574
Start ATG: 1011

Transcript No. : CT13764
TGTCTGGGTGATGGCCTCGATTGCCGTGGTTGGCAACCTATTGGTCCTGCTCGGTCGCTACTTCTACAAATCACGGAGCAACGTGGAGCACTCGCTCTACCTTCGCCATTTG
GCCGCCAGTGATTTCCTCATGGGCATTTACCTCACATTGATTGCCTGTGCGGATATCAGTTTTCGCGGCGAGTATATCAAATACGAGGAGACCTGGCGGCATAGCGGCGTTT
GTGCCTTCGCAGGCCTTCCTCAGCACCTTCAGCTGCCAGTCGTCGACGCTGCTGCTCACATTGGTCACCTGGGATCGTCTGATGTCGGTGACGAGGCCCCTCAAGCCACGGGA
TACGGAAAAAGTTCGCATTGTCCTACGCCTTCTGCTGTTGTGGGGCATAAGTTTCGGATTAGCTGCAGCTCCACTTCTTCCCAATCCGTACTTTGGTAGCCATTTCTACGGC
AACAATGGTGTCTGCTTATCGCTGCATATCCACGATCCCTATGCGAAGGGTTGGGAGTACTCGGCGCTGCTGTTCATCCTGGTCAATACGTTGTCACTGATCTTCATCCTCT
TTTCCTACATTCGAATGTTGCAAGCGATAAGGGATTCGGGTGGCGGAATGCGAAGCACTCACAGCGGTCGCGAGAATGTGGTAGCAACTCGGTTGCCATCATTGTGACCAC
CGATTGCGCCTGCTGGCTGCCCATAATTGTGGTCAAATTGGCTGCTCTTTCAGGCTGCGAAATCTCGCCCGATCTTTACGCCTGGCTGGCGGTTCTTGTGCTGCCAGTGAAC
TCGGCCCTCAATCCAGTGCTCTACACATTGACCACTGCGGCCCTTTAAGCAACAGCTGCGTCGCTACTGTCACACCCTGCCCAGCTGCTCGCTGGTGAACAACGAGACCCGAT
CCCAGACCCAGACTGCCTACGAGTCCGGACTGAGTGTCAGTCTGGCGCACTTGGGCGGTGGTGTGGGCGGCGGGTCGGGGCGAAAGCGGATGTCACACCGGCAGATGAGCTA
TCTGTAG
(SEQ ID NO: 20)

Start ATG: 11

MASIAVVGNLLVLLGRYFYKSRSNVEHSLYLRHLAASDFLMGIYLTLIACADISFRGEYIKYEETWRHSGVCAFAGFLSTFSCQSSTLLLTLVTWDRLMSVTRPLKPRDTEK
VRIVLRLLLLWGISFGLAAAPLLPNPYFGSHFYGNNGVCLSLHIHDPYAKGWEYSALLFILVNTLSLIFILFSYIRMLQAIRDSGGGMRSTHSGRENVVATRFAIIVTTDCA
CWLPIIVVKLAALSGCEISPDLYAWLAVLVLPVNSALNPVLYTLTTAAFKQQLRRYCHTLPSCSLVNNETRSQTQTAYESGLSVSLAHLGGGVGGGSGRKRMSHRQMSYL*
(SEQ ID NO: 21)

Name: TSH/FSH receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013383844
TTTTCCGCCAAATTCGCTGGCTTTTAAGTGCTCACATAAATGAAATTTTCAAATAGCAAATAACATAGGAATAATCCTTCTAAATCGCAATATAAAAACATATATACAAGGA
GTGGTAAATGACAGTATTCTATTAATGGCAAAACGATTTATTTAAACAGACGTCGCATCCGCATAAACGATCTTTCACACTTTTTATTAACGGTTAGTATAAATAAAAAAAA
ACATTAATCCTTAGTTTATTTAACCAATTTTGTTTGCTGAAATCGATTCTTGAAAGAGAAGCTGACATTTTTTTTATATATGCCTCCCTACTTCAGGCAGTGCGAACATACC

13/89

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GCATCAACGCGACTTGTAGCGGCCGTGTGAAAAGGCTATTTTGTGGTTAGCGCAGATCTGCGCTGCAGTGTGACCCCGGCTACAGGTATTTCGGCATCGCACAGGGTCACAC
TCGCCCAGGCACCCGTATAAAATCCCCGCCCCCCTGATCGACGATAGTATTTCGAAAAAAACGCGAGGAAAAGTCTGATGCGCGTTAAAATCGGAGCGCAAATCGTGCATAT
ATTTTTTTTTACACACCGCGCGCCGTGTTTACGACTGAAAACGGAGACTGACTGAAAAGCCTTGGCGCACAAGCACGCAATGAAAACGCAACGATAAGAATGTGATATTGTG
ATAAATACATGATTCGCTGACAACTCTATTTTATATTGGAATGCATTCGAAATCGAACGCAGCGCAGCGTGTGTTGTTTACTTAACGATTTTCGGTGTTTGTTTGCCCAACT
TGCGGCGGTGAAATTCAGCATTTTCCATTTTGCCAACGAAAGAGAGGAAAAGTGAAAAGTGCTATTCGACGAAGCGAAACGCAAAATCAAAAGAAAAACA
GCATAGCTAAAGCTATGTGTAGTACATAGCCACATAAATTGCAAATTGAGGCCAAGAGACAAGAGAACCTGAAATCCACACAGATCTTGACGAGTGAGCTAACGATGGACAG
GAGTCGGAGTAGCAGAGCTGCCAGCAGCAACCAGTTCATCAGGCCATGTGGCCTACTGACGACCGTCATCCTGCTGCAGACGCTTGTGTCGATGAGTTTGGCCATCGAGGAG
ATGTCGCCACCACCGGCCGCCCCGCCACGTCCATCGCCGCCGCCCACCGTGAAGCTCAACAAGTGCTGCCATTCGGGCGAGTATCTGAACGATGGCACCTGCATCGCCGGCA
GCGAAGCCCTGTGGCTGCCCATGGTGACTTGGTGCAGCAGCAGCGCTTCTTCGAGCCCCATGGCGCCAGTTCTTGAAGTTCCTGCCCAATACGAGACCCACGTG
CCGAAAGGACCCAGACGACGGAGATCTTTCGCAGCCGCGGAGCCAATGTGATGCTCTTTCCCAATGGCACGCTCTATGTGCGGGAACGCGCTCTAATGGTCCAGCCGTCGGAT
TACTGTGTCGACTGGGAGGTGGCCGTCGTTTGCTTGAACGACAGTCAGCCGATCAATGCTCTGGAGGATCCCGATTATGCAGCCAATCCTCTCGTGCAGCAGGAGCCGCCCA
AGGCTAGCCTGCGACTGAGCAAGTGCTGCGGCAAGTGGGGCAGCTATAACACGCAGCTCCAGAACTGCGATCTGCAGCCCAACCATCAGGCAGCCGTCGATGGACTGCTGCG
ATTGTCGCCGCAGCTACCGGAGGGCAGCTATCAGACTAGCTACGGCCTGCCCCGACTGTGGCCAACCCGGTGGCTACTCCATTGCCGGTGATTGGCAGGATGCCAAGCTGGAT
CGGAACACGGCCATGCTCCAGTTGCCGCACAAGAACCTCAGCGCCCGGACAATACTGCCTGGAGCACACGCAGCGCGAGGGCGAGGTGAAGATCATAGCCTGCCAGCATTTGT
TTAGCTCCGCGGCAGGAGCCGGCATCCACGACGGCTCCATTGGAGGCACCATCGAGCAGGCCAATGGCCAGAATCTGCAGAAGGCCGTCCTGACTGGTGGCATACTTGTGTC
CATTGTCTTCCTGTCCGCCACTTTGGTGGCCGGCTTCCTGCTGCCCGCTGTGCATCATGCGCTTCATTGGCGCTGCCAAATCTGCTATGTCACCTGCTTGCTATTCGGCAAA
ATACTGCTGGCCATCGAGGAGCTGAGCTCCAGCCTGCAGCCGGGCAGTGCCGCCTGCCATACGCTTGCTATCACCATGCAGTTCTTCTTTCTGGCCGCCTTCTTTTGGCTGA
ACACCATGTGCTTCAACATCTGGTGACGTTCCGGGACTTTCGGCCCAGTTCGGTGGAACGCAATCAGGAGGCACTGCGTCGCTATCTGTACTCCCTGTACGCTTGGGGCGG
TCCTCTGCTTATCACCTTCGTGGCCGCCTGCGTGGACCAGCTGCCGGAGACGACGCTACTGCGTCCGGGATTCGGACAGCTCTACTGCTGGTTCGACAATCGCAATCTCTCG
ATCTTCGCCTACTTCTACGGACCCATTGGCCTGCTGCTGTGCGCCAATATAGCGCTCTTCGTGTCCACCACCCATCAGTTGACGTGCGGCCTGTGGAAACGGGACGATGTCA
AGTCCTCATCGGAGAAGTCCGCCCTGGGACGCGTCTGCCTGAAGCTAGTCGTCGTTATGGGTGTCACCTGGATAGCGGACATTCTGTCCTGGCTAGTGGGTGGACCGCATGG
CGTATGGTTCTTCACCGACCTGATCAACGCCCTGCAAGGCGTCTTCATCTTCATCGGTGGGCTGCCAGCCGCAGGTGTGGACCGCCTGCCGCAGGATCTTCTGTCCGCGA
TTGCGTCATGACATCACCAATACGACCAACGGTGTCCAGCATTCGAGCAGCTCGCAGGGTTTGCCCTCGATGGCCGGCGGCACGGAGATTACACAGAACACCACCACCACCA
CCACGACAACCAACACGACCGCCACTCACATGCCCAGCAATCCGGCGGAGGATGAGGTACCGGAGAAGGCTCCCATTGCCCCCGTCGCACCCATCGTCAAAATGGAGACCAT
TTGCTAAACGTAAGTTGAACACCCGATAGCCAATGAAGTGTGCTTGTAAAGAGATAGCTCTGTTTGCCAGCGCGCAAACAAAGCGCCTGCTGTTCCCACTCCCAGCGCAGTT
TGCCAAGTGGCTTACAAAACGCGGCTTTAAGCACACACACTCACACACACACACACTTGCTGATAGACTTATCGGCCTTAATGGGCTTTAGGGCCCAGCCGGGAATGCAAAGTA
TCTCAATGAGCTGGCTGGCTGGCTGGCTGGCTGTTTGCTCGCCGGTTACGCCATGCATCGCAGCAGTTTCGATCCTATAAAGCGCACGTATGTACAGGTGGGGCCACTTCAA
TATCACTAAGCAGCTTTAGCTTCAATAGACTTCAATCGGTGGAAGGTTTGGTATTTGGACCCAAGAACCTAAGTTTCTTATTAAGTTTTAGTCTTTCAAAAATAGCGTGCTA
CGTAGAAGATAGTGTGATAATTGCGTCTGTCTGTGGATTTAACCCAAATACCAATGAGGTATTCACAAAATGTGAAAACAAATAGGAAACCCCGAATTTGTCATGCGCCGACA
ACTTTCGAGAACCAACCACCACCATATGAAGATAAAAAACAAAAGAAACTAGTTTGGTTTTCTATGGGGGAAAACGATACGAACTTTTCAATTCAAAACCTTTGGAGTTTCA
ACGGTCAATGGCCATGTTGGAAAATACCCTTCTCTATAGGACACTATTCATCTCACACCCCCATGTGGACTATACGCTATCCAGATGAAATTTAAGGGTTCGAGATTTCCT
GACAACTTGCGGCTACCTGGAGCGTTTTTCCAACCAGGCGCCGGTTGAAAAAGTCTAGCACGTTTTCGTTTCGTTTTATGGTTTTATAGGGGGAAATTTACGTATTTACGTA
GGATAAGAAGATCGTCCTGCGATGGTCAAATAGTGACCATATTCTTCATTTGCATGACCGAAATTGTTTAACAACATGCGCCAAGTTTACGATTTCGGCTGCACCACTTGAG
TTCGAGTATGGTCATAAAGATGAAAATGTTGCCGCTGTGTGCCGTTATGTTTTTCATCGGAAAACTCTGACGCCGGGCCGGGCGAATTCGATTTTTGAATTTCCTGTCGATT
TCCACATTTCCACATGGCCATAAAGTAATCAGCGCAACCCTTGACACACACGCAAGCGAAGATAATGGAAATCGTTGCTGGCATCCGTATCGGTTGGATTCAAAAAATGTGT
GTTGCCGAATCCGTAAGGGAAAATCGAGTTTAAATTGGACTCACCGGCGACGATGGCGATGGTGATGGTGATAAGCACACAACACACCATCGTCTTGTTTGGATTTCGGCCC
CGAACTCGGCACAATCTACAATTATCTAAAAAGAAACCTCTGTGCGGCGATCATAAAGTTTTGAAAAACAATAATTCCATTTTCGGGCACTAAAAAAAAAAACAGGGCAACTT
GAAATCTAGCATTAAACTGGTGGCTTAATGTTCCAATGAAAAGATAAGGATTTAACAATAAAAAAAAAACTTTTTTTTTGTATGCACTGCATGTTGATAGCAACATTAATGAA
AGAAACTAATCAATGAAGTTTCTGTTTCTCTATATTAACAACAAATGCTGCTTTGTTTAGGCCATGTTTTTGTTATTAGAGCCCAAGAAACATTGGTTTGCATTGCACAAAG
GCGTATGGAAAATGTGTAATTACTTCAGTTTGTAACATTTTCGAATATGACAGCTGCTGGTGGCAGTTAATTCTTTGCCCTCGCGTTTTATTGTTTGTTACTTTTTACTTTT
ATTTTTTATTTTTTTTTTGGGCCCTGATCGCGTCATACTTTTTGGGATGCGTGTCTGTCCGGGTGAACAGATGTGCTGTCTGTCTGCCATTCGCTTGTGTGTAGGTCCGTG
TTGGAATCAGAGGTTTTGCCCAAACGAAAGAGAAAACAAAACAAACAGTGGGTTTTGGCCCATGGGCCCATTCGATGAGATTGCGCAACCGAGTTAAATGGCCTGGCCCCT
GAAAAGCTGAAAACCGAAACAGAAACATGAAATCTGAAATCTGAAATTGTGGAAATCTGAAATTGTGGCTGGCACACGCAACACTCGTAATCAGACTAAAAAAAAAAAGGGG
CAGTCAGTCGGCTTAAAACTGTGACCTGCATGCATTTGCCAACTGCAGACTGCAAACTGCAAACTGCAACTTCGAAGGCAACCCGAAATGCATCTGCAACTGCAACTGCAGC
TGCCGTGCCATTTGTGTTCATCTACATAATCCCAGAGCAGCGTGTCCACGTCACGCTCATCACAACGCGACGGTGCAAAAATGCAGCGAAATTGGATGCGTTGCGTTGTTTGT
CAACTGAAATGGTCCAGATGCACAATGCAAGGGAGGGAAGATGCGGCAGAAATGCGCCGGAATCGATGCAGTAATGCGTTTCAAGCTATCATTATGGGATCACATGGGGTCA
ACTATTTGACTTGAAAATATGACTAACAAATTGAGCAGGGAAAATGCTTTTCCTTCGGAAAAAATGATTGTGTGCCAAAAACTAAAAACGAAAGTTTCCCTACTATTACTTT
TGGCATCGCCCAAAAAAACACTTTCTTTCATTAGCCATTTCACTGATTATCTTTTTTGGTAACCAAGCGGAGTAATCATCATAAGCACACAGCGTTAAACTATTCAGCTATTT
CCAGCTTGTTGAGATAACTAAAAGCTCGGACACGCTTGAGTTCCACTTTTTTTTTTTTTTTTTTTATCTCCATCAACATTTAATAATTAAGTGATTTCGCTTATTGTTCTAGT
ATTTATTAGCGCATTACCTAATTGTTTGACACGACGAAACATGAAATGATTACTAATTTCATCATAGAATGCCAGTGACCCATGCTCGTTGGCATTTCGATTATAATAATAT
TCGCAGTTGCATAAATATAGATTGTTTCCGAACGTGACCTGTACTTCCTAGTGCAACTGAATCTTTTGCGTTTCTGGGTCAGCTTTTATCTGCCTAGTTCGCTGACATTTCA
AAAGTTTGCAACACTTGGCAGCTTGGCAGCGTAATGAATTCCTTCCTGTTGACTCCGCCCGAAATTGGCACAAATTTGCCAATAAGAATACTTAATGTCCAACTCCAGAC
GCAATCGCAGCGGCACACGCACACATGCTCTGCCGTTAATTTGAGTTTAGCGGCAATTTTTAATTTGAACGTTCTGCAGTTTTTCAACTTATAATTGCACTCTGGCCCATTTA
CATTTTACGCAGGGCATTATTATTATTTCTTTTTTTTTTTTTAATTTTTGCCTGCTGAGTCGGTCGACATCGGATTCCTCGTTGGAGGCCGAAGGAAGCGAAGTAGGGGGCA
CATTGCGTTTGGTACATGAATTTCATTGGCAAATAATAAGTATTTCATCTGGCAGCGATTCTACACCTCAAATCATATCGCGCAAGATTCGCACCTTTTCGCAAGAATTTGAAAT
CAAAATAAATCTCAGAATTCCTGATTACGCGATGCCTGGAAATCTAAACAGATCATGAGTAAGCCGCAAATGTTTCAGCTAAGAAAAATGAAAAGAACAAAGTTTCCGCTAA
GCCATTTTCAACACTGCTTCTAAGTACTAATGTCTTGAGTGCACTGTACCCACATGCGCACGCATATCATATGAAAATTTGTACTTATTTGTGCCCCTTTTCTTTCTTATTT
AAAGAAAGAATGGAAAAAACACGAAAAAAAAACGCTGCCAAAGCTGGAGTTTCGAGACGAGCCGCGGCACACACTTGCGCAATCGCAGCAACAAAACCAAGCTGACCAGCTAA
TTGTGCGAGTGTACGAGCGAATGAGTGTGTGTGTGGTTGTGTGTGTGCAAGCGACTTGCGCGTGATTTTGAAATCGGCCAACAACCGCTGGGGAACAAAACGTACTCAGT
ATGCCAGTATTCAACTTCAATTTAAGCCAGCGCACAAAAGAAACGTATTATTTTATTCATCATCATCATCATAATCGCATAGCATCGCATCGCATCGCATCGTATCG
CAGAATAACGGTAAAGCAGTTCGGGTCACATTAACACGTTCTAATTGGCACTCCGGTCAGTGTTGCGAAATGGAATGTGCAGCATAACGAAACAGGAATTCAGCCTAGACA
AAACAAAGCAGCGCTATTGTGGCTCTTTCTTTCTTTTTAAGCACTTTTAGCCAACAGAAATAAAAAACACGAGGGCTTTATGTGTGTGCATCTGGCTGTATGTATGTGTGGC
AACCACAAGGAATTTTCTGTTGAGGCACTTTTGTTGTTTAGTTTAGATCGCGTTGCTCTGGTTTTTTTTTTTTTTACTCAAATCTCAAGTGTGAGAAAAACAGCAGGCGCACC
ACACACACAAACACACACACATGCATGCACATATCGGATGTTTAACATTTAAATTAGCTGCTTCTGATTGGCATTTTCGGTATGACACTGCTTGCATTCAGTTCTTTATGTG
GTTTGCCCCATAATGTTTTTCAACCGAAAAATTGTATATTTTTTTTTTTTACGTCTAGTGTAAACAATTGAAATTTATTTACTTCAGGGCATAAACAAAATCGTTATACACACA
CATTGATAGGCG
(SEQ ID NO: 22)
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Exon: 1001..3033

FIGURE SHEET 13

Exon: 7293..7412
Start ATG: 1001

Transcript No. : CT14539
ATGGACAGGAGTCGGAGTAGCAGAGCTGCCAGCAGCAACCAGTTCATCAGGCCATGTGGCCTACTGACGACCGTCATCCTGCTGCAGACGCTTGTGTCGATGAGTTTGGCCA
TCGAGGAGATGTCGCCACCACCGGCCGCCCCGCCACGTCCATCGCCGCCGCCCACCGTGAAGCTCAACAAGTGCTGCCATTCGGGCGAGTATCTGAACGATGGCACCTGCAT
CGCCGGCAGCGAAGCCCTGTGGCTGCCCATGGTGTACTTGGTGCAGCAGCAGCGCTTCTTCGAGCCCCATGGCGCCAGTCCGCGATTCTTGAAGTTCCTGCCCAATACGAGA
CCCACGTGCCGAAAGGACCAGACGACGGAGATCTTTCGCAGCCGCGGAGCCAATGTGATGCTCTTTCCCAATGGCACGCTCTATGTGCGGGAACGCGCTCTAATGGTCCAGC
CGTCGGATTACTGTGTCGACTGGGAGGTGGCCGTCGTTTGCTTGAACGACAGTCAGCCGATCAATGCTCTGGAGGATCCCGATTATGCAGCCAATCCTCTCGTCGCAGCAGGA
GCCGCCCAAGGCTAGCCTGCGACTGAGCAAGTGCTGCGGCAAGTGGGGCAGCTATAACACGCAGCTCCAGAACTGCGATCTGCAGCCCAACCATCAGGCAGCCGTCGATGGA
CTGCTGCGATTGTCGCCGCAGCTACCGGAGGGCAGCTATCAGACTAGCTACGGCCTGCCCGACTGTGGCCAACCCGGTGGCTACTCCATTGCCGGTGATTGGCAGGATGCCA
AGCTGGATCGGAACACGGCCATGCTCCAGTTGCCGCACAAGAACCTCAGCGCCGGACAATACTGCCTGGAGCACACGCAGCGCGAGGGCGAGGTGAAGATCATAGCCTGCCA
GCATTTGTTTAGCTCCGCGGCAGGAGCCGGCATCCACGACGGCTCCATTGGAGGCACCATCGAGCAGGCCAATGGCCAGAATCTGCAGAAGGCCGTCCTGACTGGTGGCATA
CTTGTGTCCATTGTCTTCCTGTCCGCCACTTTGGTGGCCGGCTTCCTGCTGCCCGCTGTGCATCATGCGCTTCATTGGCGCTGCCAAATCTGCTATGTCACCTGCTTGCTAT
TCGGCAAAATACTGCTGGCCATCGAGGAGCTGAGCTCCAGCCTGCAGCCGGGCAGTGCCGCCTGCCATACGCTTGCTATCACCATGCAGTTCTTCTTTCTGGCCGCCTTCTT
TTGGCTGAACACCATGTGCTTCAACATCTGGTGGACGTTCCGGGACTTTCGGCCCAGTTCGTTGGAACGCAATCAGGAGGCACTGCGTCGCTATCTGTACTCCCTGTACGCT
TGGGGCGGTCCTCTGCTTATCACCTTCGTGGCCGTGTGCGTGGACCAGCTGCCGGAGACGACGCTACTGCGTCCGGATTCGGACAGCTCTACTGCTGGTTCGACAATCGCA
ATCTCTCGATCTTCGCCTACTTCTACGGACCCATTGGCCTGCTGCTGTGCGCCAATATAGCGCTCTTCGTGTCCACCACCCATCAGTTGACGTGCGGCCTGTGGAAACGGGA
CGATGTCAAGTCCTCATCGGAGAAGTCCGCCCTGGGACGCGTCTGCCTGAAGCTAGTCGTCGTTATGGGTGTCACCTGGATAGCGGACATTCTGTCCTGGCTAGTGGGTGGA
CCGCATGGCGTATGGTTCTTCACCGACCTGATCAACGCCCTGCAAGGCGTCTTCATCTTCATCGTGGTGGGCTGCCAGCCGCAGGTGTGGACCGCCTGCCGCAGGATCTTCT
GTCCGCGATTGCGTCATGACATCACCAATACGACCAACGGTGTCCAGCATTCGAGCAGCTCGCAGGGTTTGCCCTCGATGGCCCGGCGGCACGGAGATTACACAGAACACCAC
CACCACCACCACGACAACCAACACGACCGCCCACTCACATGCCCAGCAATCCGGCGGAGGATGAGGTACCGGAGAAGGCTCCCATTGCCCCCGTCGCACCCATCGTCAAAATG
GAGACCATTTGCTAAACACAACTGAGACGACGAGCGACAATGCGAAAGTCAGGCCCGGATACAAAAGTCCAGACCTCGAGCGAGCGAAATAATGGCAATGGGCAGCTCAGAA
ATAAGAAAGAAAGAATGGAAAAAAAC
(SEQ ID NO: 23)

Start ATG: 1

MDRSRSSRAASSNQFIRPCGLLTTVILLQTLVSMSLAIEEMSPPPAAPPRPSPPPTVKLNKCCHSGEYLNDGTCIAGSEALWLPMVYLVQQQRFFEPHGASPRFLKFLPNTR
PTCRKDQTTEIFRSRGANVMLFPNGTLYVRERALMVQPSDYCVDWEVAVVCLNDSQPINALEDPDYAANPLVQQEPPKASLRLSKCCGKWGSYNTQLQNCDLQPNHQAAVDG
LLRLSPQLPEGSYQTSYGLPDCGQPGGYSIAGDWQDAKLDRNTAMLQLPHKNLSAGQYCLEHTQREGEVKIIACQHLFSSAAGAGIHDGSIGGTIEQANGQNLQKAVLTGGI
LVSIVFLSATLVAGFLLPAVHHALHWRCQICYVTCLLFGKILLAIEELSSSLQPGSAACHTLAITMQFFFLAAFFWLNTMCFNIWWTFRDFRPSSLERNQEALRRYLYSLYA
WGGPLLITFVAACVDQLPETTLLRPGFGQLYCWFDNRNLSIFAYFYGPIGLLLCANIALFVSTTHQLTCGLWKRDDVKSSSEKSALGRVCLKLVVVMGVTWIADILSWLVGG
PHGVWFFTDLINALQGVFIFIVVGCQPQVWTACRRIFCPRLRHDITNTTNGVQHSSSSQGLPSMAGGTEITQNTTTTTTTTNTTATHMPSNPAEDEVPEKAPIAPVAPIVKM
ETIC*
(SEQ ID NO: 24)

Name: mth-like 1
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384553
GACCAGACAAGTGCAAGCAATGGAGCTCAGCGTCAGTATCCACTGTCTCACACACATCCACAAAAGCATCTTCATCAGATTCAGTTCCTCAGATCTCGCATCAGCTGCTGCG
ATTCCCATGGACGTGACACGGTGGAGCGGTGGAGAAAACATCATCATAATAATAATAAAGCCGAATAACTTTCTCCACACGTAGTGTGTGTCAATAAATCGGTTGTTTCTCG
CAGAGTTTGAAAGGAAACTTTTAGAGTTCTTAAACAAAGAATGTGGTTTTGGAACCACTGTGCCGCATCCTGTCTGCCATGAATGATGCGTCCTTTCCTGCCAGCACATAAA
GCCCCGGCCAGTTGCATCTATTCCACACACTGATAGACAATGTTTGTGCACTGATTTATACTCAGCCAGCTATTAAATAAGAATTTTCGTTATTACGCTGCCCGGGATTTTA
TTATGTGACTTTCAAAAGCCCCCGCCAACTTGTTGTGGCTTTGGCTTAAAGCCGCGCCAAGCTGAAAATTGTTATTTTAACCTTTTAAAGTCAGCTTTATCAGCACCAAATG
CAGGGCCATTATGCGTGGCCCACGCGGCGTATGAGCAACGTTAAATCTGCGAATAATTCAAAGACGTGCGTTTCTTTTTACAGCCGCCTTGTCGGTAATCCCATTAAGGAGT
TATCTGGCGAAACATTTTTGCACAACACTCGACTGGAGGCACTGTGAGTATACTTTGTTTGTTTTAATTTAAAAAAATCACAAAATATATCATGAAGTTGTTAAAACGGGATT
GAATTGATTTGAATATATGATTTCATTTAATTTCTCACCAATATTTAAGTTCGTTGGCCCTAATGCCAGTTAATTGGAGCCACTGAATATTCGAT
TTTTGAATCTCACGGGAATTCGGTATGATCACATCGACTTCGAGGCCATCAATTCAATGCGCAACCTGACGTACATCATCTACGATCGATTCTTCTACTGCTCAATGACGCC
GCGGGTGAGAATGTGCAAGCCGTCCACCGATGGAGTCAGCTCCTTTCAAGATCTTCTGAGCAAACCAGTGTTACGTTACTCCGCCTGGGTGATGGCCACGTTGACAATAGCT
GGAAATGTGCTAGTCCTATGGGGACGCTTTATCTACCGCGATGAGAATGTGGCTGTGACAATGGTGATTCGGAATCTGGCTCTGGCTGATATGCTGATGGGCTTCTATTTGG
TCACCATTGCAGGACTATCGCTACCGCAACGAGTATTACAAGTAAGTCAAATGTGATGGATTGGCATTTGTTACGCCCCAATCTTTTAGGGTTGTGCTGACTGGAT
AACCTCGTGGCAGTGCACACTGATTGGAACGCTGGCCGTGAGCTCCTCGGAGGTTTCGATGCTTATCCTGGCTTTTATGTCGCTGGAGCGGTTTCTCTTGATCGCCGATCCC
CCCTACCCTACTACGGATCCTATTCCGGAACCTGTGAGCACAATGTTTATGATAAAAATGTAGTTTACCAAGTGACGAAATTAAACTTAACAGGCTTTCCATTGCACATCCAC
GAGGCCTTCCCGATGGGCTGGCTTTACTCGGCTTTCGTGTTCCTGGGCGTCAATCTGCTGCTGCTGGTGATGATTGCGATGCTCTACACGGCACTCCTTATTTCGATATGGC
GAACGAGGACGCGCCACTCCGCTCACTCGTTGGATTGCGAATTCGCTGTGCGATTCTTTTTCATCGTGCTGACCGACTTCCTGTGCTGGGTGCCCATCATCGTTATGAAGAT
CTGGGTTTTTTTTCAACTACAATATCTCCGATGACATCTACGCCTGGTTGGTGGTCTTTGTGCTGCCACTTAACTCGGCGGTTAATCCTCTCTTGTACACCTTCACCACGCCC
AAGTACCGAAATCAAATCTTCCTTCGCGGCTGGAAGAAGATAACTTCTAGAAAGCGAGCGGAGGCTGGCAATGGAAATGTGGCCACCACAACGACGGGCACGGCAACTGGAT
CCTCTCAGCATCCGGATGACTTCACGATCTTTGCCAAAGCCGCGATGAGATGCCATTAGGTCCTAACGCTGTCGAACTGAAGGATTCTTGTGGCGCAGATCGAACTGTGTATA
CCACCAGATTTAGCAGCATTTATTTTGTCTATGATATCGAAAATCTATATATGTATGTGAATATCTATCCCTGTCCGTGTAAGATAACCAAATGAAAGTGTGAAATAAATTG
AATGTGATATTTGTAAGGCAATTTTACGGAATTTAAAATGGGATGCGAGTTAGTGTAAGATTAAGCTATTATCTAAGTTTTGGTAATAGTTTTAAATACTTTTTATTTAGAA
ATAGCAGCGCTATCATTTTTGGCATGGTGTGATTCTTTCTGGTCCGAGTAAATCTTTGCCATTACCAACTTGGAGCGCACGATGTGAAACTTTCGCATTTCCTCCAGGTCCT
CCATCTGCACCACCATGTTATGCTTACGCTCCAGGTGCATGCGTAGTCTAAAAAAATTATTAAGGAGTGTTACTTTCAAATAATGTACACTTTAAACAAAATAACTAACTTGT
TACGAGCTGGATAGCTCTGATGGCAGTGGGCGCACTCAAATGGCATGGCGTATGCGTGCACTCGTGATTCCTGAGAGATGAAGATGAGGTAAAGGACTTCTGGCAGCCGGG
AAACTCGCAAATGAAGCGAGATCCAGAGTGCTTAACCTGCTGGTGGACAGTCAAATGGGATCGCTGTGCGAAACGACGATCACAGGAGATCACAGGAATAGGGAAAGTCTCTG
TTATGATAGCGTTTATGAATCTCCAGGGCTTTGGCAATGGCAAAAACCTTGCCGCATGTGTCGCAGTGGACTCCAGACTGCCTGTGCTTCGAATCGACGTGAACTTTCAGCG
CCTGCTTTGTGAGGTAAACCCGGTCGCACTGGCTGCAACGAAAGTTGGGACGATTGGCCAAATGAATCATCTGGTGCTTGGCCATGCGGGAATGGTTCCTGAACTCCTTGTG
GCAGAACTTGCAGTTGGATTTTCCCGTATGCCGATTGCGTGGCACAATGTC
(SEQ ID NO: 25)

Exon: 1001..1278
Exon: 1327..1601
Exon: 1661..2187

FIGURE SHEET 14

Start ATG: 1001

Transcript No. : CT16185
ATGACGCCGCGGGTGAGAATGTGCAAGCCGTCCACCGATGGAGTCAGCTCCTTTCAAGATCTTCTGAGCAAACCAGTGTTACGTTACTCCGCCTGGGTGATGGCCACGTTGA
CAATAGCTGGAAATGTGCTAGTCCTATGGGGACGCTTTATCTACCGCGATGAGAATGTGGCTGTGACAATGGTGATTCGGAATCTGGCTCTGGCTGATATGCTGATGGGCTT
CTATTTGGTCACCATTGGAGTGCAGGACTATCGCTACCGCAACGAGTATTACAAGGTTGTGTCGGACTGGATAACCTCGTGGCAGTGCACACTGATTGGAACGCTGGCCGTG
AGCTCCTCGGAGGTTTCGATGCTTATCCTGGCTTTTATGTCGCTGGAGCCGGTTTCTCTTGATCGCCGATCCCTTTCGCGGCCATCGCAGCATTGGAAATCGGGTGATGTGGC
TGGCTTTGATTTGCATTTGGATTACGGGCGTGGGCTTGGCTGTGGCACCGGTGCTCCTGTGGCGGACCAGTACCCTACCCTACTACGGATCCTATTCCGGAACCTGCTTTCC
ATTGCACATCCCACGAGGCCTTCCCGATGGGCTGGCTTTACTCGGCTTCGTGTTCCTGGGCGTCAATCTGCTGCTGCTGGTGATGATTGCGATGCTCTACACGGCACTCCTT
ATTTCGATATGGCGAACGAGGAGCGCCACTCCGCTCACTCTGTTGGATTGCGAATTCGCTGTGCGATTCTTTTTCATCGTGCTGACCGACTTCCTGTGCTGGGTGCCCATCA
TCGTTATGAAGATCTGGGTTTTTTTCAACTACAATATCTCCGATGACATCTACGCCTGGTTGGTGGTCTTTGTGCTGCCACTTAACTCGGCCGGTTAATCCTCTCTTGTACAC
CTTCACCACGCCCAAGTACCGAAATCAAATCTTCCTTCGCGGCTGGAAGAAGATAACTTCTAGAAAGCGAGCGGAGGCTGGCAATGGAAATGTGGCCACCACAACGACGGGC
ACGGCAACTGGATCCTCTCAGCATCCGGATGACTTCACGATCTTTGCCAAAGCCGCGATGAGATGCCATTAG
(SEQ ID NO: 26)

Start ATG: 1

MTPRVRMCKPSTDGVSSFQDLLSKPVLRYSAWVMATLTIAGNVLVLWGRFIYRDENVAVTMVIRNLALADMLMGFYLVTIGVQDYRYRNEYYKVVLDWITSWQCTLIGTLAV
SSSEVSMLILAFMSLERFLLIADPFRGHRSIGNRVMWLALICIWITGVGLAVAPVLLWRTSTLPYYGSYSGTCFPLHIHEAFPMGWLYSAFVFLGVNLLLLVMIAMLYTALL
ISIWRTRSATPLTLLDCEFAVRFFFIVLTDFLCWVPIIVMKIWVFFNYNISDDIYAWLVVFVLPLNSAVNPLLYTFTTPKYRNQIFLRGWKKITSRKRAEAGNGNVATTTTG
TATGSSQHPDDFTIFAKAAMRCH*
(SEQ ID NO: 27)

Name: TSH, FH, LH receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013383791
CACTCACATTTGCCGACAGCAGAAATATTTTAGGGTTGTATCTTAGAGGTGGAGAAACATCGATGCCAACATCGATGTCATCGATGTTTTCGAAAAATCAAAAACGTCGATG
TTTTTCGAGGAATCGTCGATGTTTTCAGCGCATAGAAACAGCAAAGTGTGTAAATTGTAAGTCTAAATTAATTTCCATATTTTCTAATACAATTATTAATAGCATATTGCAT
ATTTATTGTGACTCGCCGGTGGTGTAGGCTGGTGTCTTGGAAGACATGGATAAATATCTGAAATGTAAGTTTTTTTTTTAAAGATCAATTTATTTGTTTTTTGCCAAAGACA
TCGAAAACATGGATGTTCGCCAACATCGATGTTTCTCCACTTCTAATGCCAACGAAACGTGACTGGGAACGTATCGATGGGAAAAACGTTACAAAAATACCAACTATCGCA
TAGCGGAATCACCTTGGCGGGCTATTCGAATGTATCTCACAAATAGTTTTTAAGGAACCTACAGTCAGTACCAAATACTTAAAATTCCATTTATATTTTATTTTATGCTACA
GAAAACTGATAAGCTGCATTACTTTTGAAAAGTTAAAAATTGTGTTTTTTAAATGATTTATTTATATAAATAAGCTTATGTAATACTATTGTTAATATGTAAAAAAAAAAGA
ATAAAAGAAAAAGAATAGTTTACCTAAGCAGTTGCTTGAATAATACATACATAATTTAAGTTTTATACATAATTTATCAACCCTCGCTCAGTAGGAAAAAAAGATGGCTCAG
AAATGAGCAACGAATTGGAATGTCCGATAAGCCTTTTTTATCAAAATAATAATTTTTACATTCCCTTTTCATAACGCTTTCCCAGTTAGTTTGTGCCAATCGTAAAACAGCA
TTCTGCATCGATCCTAATATATTTCTTGCTGAATCTGCAATCTTCGAGTGCTGAGAATTCGCGACTGCAGTTTCTTATGATACCGTTGATATCTCGGAAGGAGGGTCTCG
AATGGATCATACCTCTACGAGGGATTACTTATTCCCGCCCATTTGACGGCCAAGTATGAATTCAAGCTTCTGGCGAATGGAGATAAGGAGCAGGTGCCAAGTCACGTGAGAG
GATGTGTGTGCAAGCTAAGGACTTGCGTCAGGTTTTGCTGCCCACATGACCACATAATGGATATGGGCGAATGCTACGCCAACATGACGACGGAGGAGAACGAATTACTGGA
CCCCATGCTAAATGTGACCCTGGACGACGGATCAGTGGTGCAAAGGCACTATAAGAAGGAGCTCATGGTGCAGTGGGATCTGCCAAAGCCCTGCGATGATATGTTTTACCTA
GACAACCGGGATATAATGGATGAGTACACCTTGTTCGAGGTATGGCTGCTCGAAAAATAAGCATTTTTGGGCAGGATTTATTTATGCTTTGGCTCTCTGCAGAATGGAAGAT
TGCTGCGCCACTACGATCAAGTGTATTTGGACAAGTCGGAGTACTGTCTGCAGCACCGAACATTCGGCGAAGGTAACAACAACTCCATTCGCATTATACCCCACAACTGCTT
GATACTGCCATCCAGAACGGGACAGACCGTTGGTAAGATGATGCCCATTGCTTGCATGGTAGCTCCCAGTTCTATATCTTTCCTATTTCATAGTGATGATCACATCGTTGA
TATGCTTGGTTCTTACCATCGCCGTGTACCTGTGCGTTAAGAAGCTAATGAATTTGGAGGGCAAGTGTTTCATCTGTTACATGATGTGCCTATTTTTCGGATACCTGTTCCT
ACTCCTTGATCTGTGGGAGTTATCGCTCGATTTCTGTAAAGCAGCAGGTTAGCTTAGAGGGGATGCATTTCAACACAACTTGACAAACCATTGACCATTTACGACAGGTTTC
TTGGGATACTTTTTCGTCATGGCTGCGTTCTTTTGGCTATCTATCATCAGTCGGCACTATTGGAAATGTCTTACCAATCCCTGTGCCTCGATGAACATTCGGTCAGAACGTG
CGTTTCTGCTATACAGCTGCTTCGCCTGGGCAATGCCTTTGGCCTTGACCGGAGTCACCTATCTGGCTGATAACGTTGTGAACAACGAGGAGTGGCAGCCTCGCGTGGGCGA
CGAAGGGCATTGCTGGATCTATAGTGGGTTCTGTTTTGTATCCGGCTTGTGGTACCAGCTCACCAATGTTTTTCTTTCCACCCTCAGCTAAAAGCTGGTCTGCAATGGTGTA
GGTAGAATACAGAAGCTGAATTCGGACAAACAGAAGTATATCAATTATAATAGTTGAAAATGTCAGTTTAAGATAAATATTATCAATTCGTTACAGTTACACACAATTTCTG
CTGCTCTTCACTGTGATGGGGATGTCGTGGAGCTTTGAGATATTCTCCTACTTGGTGCAACGCGAGAAACTGTGGGTCAATATCTTTCTGGTAGCTGACTACTTCAACTGGT
CCCAAGGCGTCATTATATTTGTGCTATTCATTCTGCGGCGCAAAACTCTTGTACTATTCAAGAAACAGTAAGTCTTATAGTTCATAGTTCGGGTAACCAGTTCCCTAAAATG
TTCTCTTTTCAGAATATTTCCCAAACAGAGAGCCTTTAGTAGATCTGCAACTCAAAGTACGATTGAATCCATTTCTCAAACAAAAAGGCATTTTAACATGACATAGTATTTTC
TTCTCTTCGAATTAATCAATTTAATAGTAAAGTATAACTTTTTTTTTCTCACAAAATGTATGAATATATTTCACTTCATTCTACATTCTATATAGAATTCATTTAATCACAAAA
TGTATGAATATTTTTCTTTATATGACGTGCATCGACTATAGAAAATCGACTATAGTGTGCCACAATATATTTTACTCATCATTTCCTAATCAAACTATTGCAAACTTAACTT
TGAGCCGAGGAAAAACCCTGTATGTCTATCAAAACTATGAGTCAAAAGTATGACGCGATGCTGAAAGTAGTTGCCTTTAAATATTGAAGTGATAAATGTAGAAAGAAGACAT
TTGTATGGAAATAAACTAAGTTTGTAAATCTACATTCGCTTTATTTCATGTACAAATTTTAATTTAAAAAACTTTGAAGGTAAATAGTGCTTTATCAGATGCGGATTACACGG
TAGCAGTTATCATCGATGTCGAATCTTCTTGTTTATGTGACCGCTTTTCTTCGCTGTCGCACTGGAGTTCGTGGATAGTTTGCTCTTTGTATTCGAAGTGGGTGTGCCGAGG
AGATCCTTGTTCCCTCCACTGTTCGTAGATCCAGACACCATTCCGCTCACTACGCTGCCCTCATTGCGATGCGAGGGTGAATCTGTAAATAAAAAGGTGTAATTAAACATAT
ATACTTTTCTGGAGAAAAGCGCTAAAGTTGAATCTCAATGTGCTGTGCTGCCTTACCCTTTTCGTCTTTCGGTGTGCTCTTGATTGTCGTGGTTCCGTCGTGGGCCGTTGTG
GTGTTCTGATTGATTGAGATCTGATTGTCGCTGGAGTCTTCATTTGTGATGGAATCCGATTCG
(SEQ ID NO: 28)

Exon: 1001..1495
Exon: 1559..1712
Exon: 1775..1951
Exon: 2012..2263
Exon: 2328..2499
Exon: 2561..2759
Start ATG: 1001

Transcript No. : CT16507
ATGTTACTTTCTGCATCGATCCTAATATATTTCTTGCTGAATCTGCAATCTTCGAGTGCTGAGATTGCCGACTGCAGTTTCTATGATACCGTTGATATCTCGGAAGGCCAGA
GGCTCTCGAATGGATCATACCTCTACGAGGGATTACTTATTCCCGCCCATTTGACGGCCAAGTATGAATTCAAGCTTCTGGCGAATGGAGATAAGGAGCAGGTGCCAAGTCA
CGTGAGAGGATGTGTGTGCAAGCTAAGGACTTGCGTCAGGTTTTGCTGCCCACATGACCACATAATGGATATGGGCGAATGCTACGCCAACATGACGACGGAGGAGAACGAA

FIGURE SHEET 15

16/89

TTACTGGACCCCATGCTAAATGTGACCCTGGACGACGGATCAGTGGTGCAAAGGCACTATAAGAAGGAGCTCATGGTGCAGTGGGATCTGCCAAAGCCCTGCGATGATATGT
TTTACCTAGACAACCGGGATATAATGGATGAGTACACCTTGTTCGAGAATGGAAGATTGCTGCGCCACTACGATCAAGTGTATTGGACAAGTCGGAGTACTGTCTGCAGCA
CCGAACATTCGGCGAAGGTAACAACAACTCCATTCGCATTATACCCCACAACTGCTTGATACTGCCATCCAGAACGGGACAGACCGTTGTGATGATCACATCGTTGATATGC
TTGGTTCTTACCATCGCCGTGTACCTGTGCGTTAAGAAGCTAATGAATTTGGAGGGCAAGTGTTTCATCTGTTACATGATGTGCCTATTTTTCGGATACCTGTTCCTACTCC
TTGATCTGTGTGGGAGTTATCGCTCGATTTCTGTAAAGCAGCAGGTTTCTTGGGATACTTTTTCGTCATGGCTGCGTTCTTTTGGCTATCTATCATCAGTCGGCACTATTGGAA
ATGTCTTACCAATCCCTGTGCCTCGATGAACATTCGGTCAGAACGTGCGTTTCTGCTATACAGCTGCTTCGCCTGGGCAATGCCTTGGCCTTGACCGGAGTCACCTATCTG
GCTGATAACGTTGTGAACAACGAGGAGTGGCAGCCTCGCGTGGGCGACGAAGGGCATTGCTGGATCTATACTAAAAGCTGGTCTGCAATGGTGTACTTCTATGGACCGATGG
TGCTCCTGATTCTCTTCAACATAACTATGTTTGTTCTGACGGCTAAACACATAATAGATTCCAAGAGGACTCTTCGAAAGATTGCTCGCAATGAAGGTAGAATACAGAAGCT
GAATTCGGACAAACAGAATTACACACAATTTCTGCTGCTCTTCACTGTGATGGGGATGTCGTGGAGCTTTGAGATATTCTCCTACTTGGTGCAACGCGAGAAACTGTGGGTC
AATATCTTTCTGGTAGCTGACTACTTCAACTGGTCCCAAGGCGTCATTATATTTGTGTATTCATTCTGCGGCGCAAAACTCTTGTACTATTCAAGAAACAGTAA
(SEQ ID NO: 29)

Start ATG: 1

MLLSASILIYFLLNLQSSSAEIADCSFYDTVDISEGQRLSNGSYLYEGLLIPAHLTAKYEFKLLANGDKEQVPSHVRGCVCKLRTCVRFCCPHDHIMDMGECYANMTTEENE
LLDPMLNVTLDDGSVVQRHYKKELMVQWDLPKPCDDMFYLDNRDIMDEYTLFENGRLLRHYDQVYLDKSEYCLQHRTFGEGNNNSIRIIPHNCLILPSRTGQTVVMITSLIC
LVLTIAVYLCVKKLMNLEGKCFICYMMCLFFGYLFLLLDLWELSLDFCKAAGFLGYFFVMAAFFWLSIISRHYWKCLTNPCASMNIRSERAFLLYSCFAWAMPLALTGVTYL
ADNVVNNEEWQPRVGDEGHCWIYTKSWSAMVYFYGPMVLLILFNITMFVLTAKHIIDSKRTLRKIARNEGRIQKLNSDKQNYTQFLLLFTVMGMSWSFEIFSYLVQREKLWV
NIFLVADYFNWSQGVIIFVLFILRRKTLVLFKKQ*
(SEQ ID NO: 30)

Name: mth-like 2
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384913
ACGTTGTCAGTGTGTGTGACGGTTGTTAATTTCATTTGACTTGCGAGGGTTTTAATATTGCAATGGAAATTCGGTACAATTTGCCGTCCATTAAATAAGCACGCAATTAATT
GTGGCAGCCATGACAGGCGTGGCTTGCCACCAATTAAGTGGAATACTATATGGCTATATCGCTATATCGCTATATGTCTATATGGCATATAGATGCCCACAGCCCCTTGGGG
TCGATCGCCTACGCCGTCTATAATCCCCAGCTAAACTTCGAGACATCGCATCCGGCACCGCAATCCGAAATCGCAAATGCTGATGAGGCAACAGAGTGGACGCGGCCGGAAAC
AAGGCACTCCTCCCATCAATCTGTCAGACGGGCCAGTGAGTCCTGGATGTCCTGGTGAACGCAGCTCAGCTCCCAGCGGGTGAGGCCAGTTGCCCAGACAGTTAGTCCGCCA
GGCAGTCAGTCGGTCTGTCAGTGAGTCAGTTAGTCAGTGAGCGAGTGAGTCAGTCAGTCAATCGAACAATCAATCATACGGAATGACAGCTACGTCGGCTTAAGTCAAAGGC
AGTCGGCCAAGAAGGGGATCTTGTCTAACTTACAGTCGCAAAATTCAATAGCCTGTGGCAATCGCACTTGCAACTTTAATAATTCCAAGAACGAAGCAGTCATAATGTTTACT
GAAATAATGTTATGCCACAATTGGCACATACAAGCTCATAATAGTGTTTTATTCTGTTTTTAATTGCACTTTAAAATTGATGATTGTATTAGCCATCATAGGCATGGCTTGA
GCTGTTCATTTAGCCATTTGATTTTGTCTACGTTGGTTTTTTATCAAGTTTCTTGCCGTGTAACCTTTTTTTTTTTTTTGGGCTCTCCCAACAATTTGAGCTCCTTTTTCGT
TTTCGCATTCCCTTAAACATTTGCTGGGGAAACACATTGATTTATATGCCGGCATCGCCAAAAATTGAATGTTATTGCTTGAATGGCCCCAATTTACTTAAAAGCTACGCTC
CTCCGCCCCACTGCCCCTCTGCCGCTCCACTGACCCCTGACCCCCATTATACATGTTGTGGGCTCCACTGGCTCCTGATTGGTATTTATGAGCGTGTTTATTTATTATATGAC
CCAACACTTGATAAAATTAAACGGAAATGGTTGGCAATTTTGCATTTGATTTGATTCTGACACCCAAACACACAGGCAGGCAAATTCGCAAATGAACTCATCTGCCCAATATTCCGA
CCATAAAGCATCCCGACCAACGGCACTCACATATAAGTTAGTTAAGTATGTATATTAGTGGCTTGGCAACTTACCAGAAAGTAGACAGCAAATGGCATCACGACCACGGCGA
CCAGGAGATCGGCGATGGCCAACGAGACTATAAAATAATTCGTGACCGTCTGCAGGGAGCGCTCGCGGCACACGGACAGGATGACCAGGATGTTGCCGAAGAGGGTCAGGAT
GGGGAACAGAATCAGGATGAGCGCCCAGTAGTTGTGGTCCACTGAAACGAAGCGAGTTGTAGTTACATTATATCCGGGATGCATCCATCCGCAGGCTCTCCTGCTGCTGCCA
CCCAAATTCCCTGGCCAAAGTTCACCTTGCAGGAAGATTTCAGGGAAAGCTCAACGGGCACGTAAGTCAATTACACAGGCAGTCCGTTTAATCAAGGACTCTGGCTGACAAC
TAATTTTAATGGCAACACAAGTAAGGACTAGCACACAAAGACGTGAATCTTAAAGGCTGTTTTAATATAATCTATCTAATATAGAGTGATGCATGTTACCAACAGCTGCGTT
GTTAAAAATTAAAGTTATTTCACATATTAAAAATGGCAAAATATGGCTATGTAATATGAAAGTTATTAAACTTGAAATACCTTTATCTTCATTATGAAACAAATTAAACAAA
CAAATATGTAGGAACTTTTCTTGAGATTGCACGAATAAATGAGTTATGTAACGCGTTTAAATTAAATTCTTGCTATCAAAACTGATTTCTAAATGAACATCTTTATAAATAA
ATTAATTATCGGCGGTTTCATTCAAATACTCCCATCTTAGAAATCTAAGGAATTCTGTTCTCAAAACCTAGTCACCTCACTATCCGATGAAAATATATTATACTAAAGAAGT
TGCTGTTGCAAGGTTTAAATGATGCTCCAACTTGATGATAATGTTTAAAGGTATTTAATGAGATTCAAGGCTATCTAATCTAATTTAATTTAATTTTAAAGCCTTTGAATGATA
TTCAATAATATCTAATGAGCTTTAATGATTTTTAAAGATTTATAATGCGGTTTTAAGATGTTAAGTTGTAGTAGTTTGATGATTTCGAATGGTAATCCTGCCTCGTACTCAC
CCACTCTCAGCTCGCCGCAGGAGTCGGTTAGGTTGAGCGTCTCGTTGGTGCAGTTCAGCCGGTAGCCGTCGAGGTACAGTCCCGTCAGGTTCTGCTCGAGGAGCAGTCCGCT
GCCCCTGCTCCCCGTGATGGCCACTCCCGGCGCAATGGTGCTTGTTCCCGAAACCGTGCTCCCATTGTAGTTGGGAAAATAATCGTTAAAGTTTTCGAGCAGCAGCATGAAG
GTGCTGCCCCTGATCCTCCAGCGCGCCGCCTACACCTCCGCCCGCCGTACCGGCCAGTCCGCTGCAACCCACGCCCACATCCCCAGAGCCGCCTCCATCGTAACTGGTCGGCAGG
GCGCCGTTCGATTGCCCAGCGTCTCGCGCGCCACCGTTGCTGTCCGCTGGAGCAGTTCCGCATCACCGAAGCCGCCCAGCATGCCATAGTCCGTTTCCGCATCAGCCACATT
GTCCAGGGCTGCCTCCTCCCCGCTGTCGATCAGCGCGATGCCAGCATCGCCGCCGTCGCCCGCTCCTGCTGCCCCTCCGCCCGCCAGCTGTTGTTCCACAAAGCTGCGCAGC
GAGTAACGCCCCCGCTCACCATCCTCCGCACTGGAGTTGCTCTGGGCTGGCTGCGTGCTGTTCAGTGCCTCCAGCCAGGCCAGGGTTCCGTTGGCGCCCGTCACCGCCAAGT
TTGTGCTGTTCTCGGGCCCGCCCACTGCCGCCTCACTGCCCACCGAACCCAAGAGCCATTCGCTGATGTCGTCGATCAGCGCGTAGCCGGCGTCCTCCGCCGCCGTTTCCAC
ATCCTCGTAGAGCGGCAAGTAGCCGGCTGGCATTGTGGGGCCCTCAACGCCCGCCTGCGCATCGCTGCCGTTCGCCGGTTGAGAGCTGTCCGCTTCCACCGCCAGGTGGTGA
TTTATCCACGTGGCTCCCGCGGATGGGGCTGCCGTGGTCGAGGTGGAAGCAGCGGCTGTGCTCAAGGTCGCCGATGTGGTTGCTGCCGTTGCTGCAGTTGCCGCAGTTGCTC
CCGTTGCCGCCGCAGTTGTTGCCGCCGTGCTGCTCAGTGGCTGGGCTGCCATGGTGCCGCCGGTTCCGCTGCTGCTGATGCCCGCCGCCAATCGAATGGGCTCAACATCTA
GTGGGGCGGGGGCGTGGCAGCGGAGGCGAGCTGCAACTCCTGCAACGCCAGCGGCATGTTTCCGTTTCCTGCAGCGAAAGAGACGAAGTTCGGAGGTGAGAAAACATAAATC
ACAAAAATTTCCATTATAATCAAAGTTCTTGAAGATAGTTCTTAACGATACGCACAACTAAGATTACAATTTTAAGCCTAATTGGTCGCGTTAATGTTGCTTAATTTGATAA
ATTCTTGTAATCCGCAAATGAGAGTCATGGTTCTTTTCGACTTAATATTTTTAGGATATCTAAAAAACAAAGTCGTTCTCAATTTTTCCTACTTACACATTACACATTGCAT
GCCCCTTCGTTTGCATTTTCAACACAAGGCGTACTTCATGCTTGACCACGCCCCCCCAACCAACACAACAACATACCATCCAGCACCACGCCCCCATGCCATTTTGGACGTA
CGGACCCTTTGCCCAACTGCCATGGCCGCATGTTTAATTAACTCTTTAATCAATTTATTGTCAATTATTCTACAAAAAGCGACAGCGAAATTGTGTAATTTAATTAAATTA
GCAAAAGGTTTTTGTGTCTCTCTCGCCCCCACCAACCATTCCGCCCACTCCCACTTCCATTCTCGCAACCAAAATGCCACGCCCCCATGCTCGACGCTGTCTTGCTTTTACAC
ATTTTGCAATTTTCGCTTTTGTATTTGCCAATTGGCGCTGATTAAAGCCGCCGAGTCGATGGGCCATAATTAAAAGATGGCCTAATGAGAGGCGAGGCGAGTACGTCTCGA
GTTGGCTGGGGGTCAAAGGTAATCGGATCGGAGTGGTCTTAAGTCCCCTGCCTTCTGCCTCTGTCTTCCGGAGATCGGGTTATTCGAACTCTGAGCTTGTCGGATTCTGGACT
CTGAATTCTGGATTCCGGATCGGAGGCAGAGATCCGAGAGCTGCACACCCAGACGGCTGGCACTAATCCAATTTGGGCACACTTCCAGGCGACGAGAGGCA
(SEQ ID NO: 31)

Exon: 3469..2353
Exon: 1497..1307
Exon: 1081..1001
Start ATG: 3469 (Reverse strand: CAT)

Transcript No. : CT17758
ATGTTGAGCCCATTCGATTGGCGGCGGGGCATCAGCAGCAGCGGAACCGGCGGCACCATGGCAGCCCAGCCACTGAGCAGCACGGCGGCAACAACTGCGGCGGCAACGGGAG
CAACTGCGGCAACTGCAGCAACGGCAGCAACCACATCGGCGACCTTGAGCACAGCCGCTGCTTCCACCTCGACCACGGCAGCCCCATCCGCGGGAGCCACGTGGATAAATCA

FIGURE SHEET 16

CCACCTGGCGGTGGAAGCGGACAGCTCTCAACCGGCGAACGGCAGCGATGCGCAGGCGGGCGTTGAGGGCCCCACAATGCCAGCCGGCTACTTGCCGCTCTACGAGGATGTG
GAAACGGCGGCGGAGGACGCCGGCTACGCGCTGATCGACGACATCAGCGAATGGCTCTTGGGTTCGGTGGGCAGTGAGGCGGCAGTGGGCGGGCCCGAGAACAGCACAAACT
TGGCGGTGACGGGCGCCAACGGAACCCTGGCCTGGCTGGAGGCACTGAACAGCACGCAGCCAGCCCAGAGCAACTCCAGTGCGGAGGATGGTGAGCGGGGGCGTTACTCGCT
GCGCAGCTTTGTGGAACAACAGCTGGCGGGCGGAGGGGCAGCAGGAGCGGGCGACGGCCGCGGCGATGCTGGCATCGCGCTGATCGACAGCGGGGAGGAGGCAGCCCTGGACAAT
GTGGCTGATGCGGAAACGGACTATGGCATGCTGGGCGGCTTCGGTGGCTCGGGGGAACTGCTCCAGCGGACAGCAACGGTGGCGCGCGAGACGCTGGGCAATCGAACGGCGCCCT
CGACGACCAGTTACGATGGAGGCGGCTCTGGGGATGTGGGCGTGGCTGGCGGACTGGCCGGTACGGCGGGCGGAGGTGTAGGCGGCGCTGGAGGATCAGGGGGCAGCACCTT
CATGCTGCTGCTCGAAAACTTTAACGATTATTTTCCCAACTACAATGGGAGCACGGTTTCGGGAACAAGCACCATTGCGCCGGGAGTGGCCATCACGGGGAGCAGGGGCAGC
GGACTGCTCCTCGAGCAGAACCTGACGGGACTGTACCTCGACGGCTACCGGCTGAACTGCACCAACGAGACGCTCAACCTAACCGACTCCTGCGGCGAGCTGAGAGTGGTGG
ACCACAACTACTGGGCGCTCATCCTGATTCTGTTCCCCATCCTGACCCTCTTCGGCAACATCCTGGTCATCCTGTCCGTGTGCCGCGAGCGCTCCCTGCAGACGGTCACGAA
TTATTTTATAGTCTCGTTGGCCATCGCCGATCTCCTGGTCGCCGTGGTCGTGATGCCATTTGCTGTCTACTTTCTGGAGCCAGTGGAGCCCACAACATGTATAATGGGGTCA
GGGGTCAGTGGAGCGGCAGAGGGGCAGTGGGGCGGAGGAGCGTAG
(SEQ ID NO: 32)

Start ATG: 1 (Reverse strand: CAT)

MLSPFDWRRGISSSGTGGTMAAQPLSSTAATTAAATGATAATAATAATTSATLSTAAASTSTTAAPSAGATWINHHLAVEADSSQPANGSDAQAGVEGPTMPAGYLPLYEDV
ETAAEDAGYALIDDISEWLLGSVGSEAAVGGPENSTNLAVTGANGTLAWLEALNSTQPAQSNSSAEDGERGRYSLRSFVEQQLAGGGAAGAGDGGDAGIALIDSGEEAALDN
VADAETDYGMLGGFGDAELLQRTATVARETLGNRTAPSTTSYDGGGSGDVGVAGGLAGTAGGGVGGAGGSGGSTFMLLLENFNDYFPNYNGSTVSGTSTIAPGVAITGSRGS
GLLLEQNLTGLYLDGYRLNCTNETLNLTDSCGELRVVDHNYWALILILFPILTLFGNILVILSVCRERSLQTVTNYFIVSLAIADLLVAVVVMPFAVYFLEPVEPTTCIMGS
GVSGAAEGQWGGGA*
(SEQ ID NO: 33)

Name: G-protein coupled receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384638
TTTGTACCGCAGTCAAGCGCAAAAATTCCTCGAAAAACCATAGACCAAGGTGTTTATGAGTTTATTAATACTGTGTAATTATTATTTGTGATATATGTGTGGGAAATTGGTA
ATAGATCAAACATGAAAGTAATGGTATCTGTTTTTCTGTATTAAAATAACATATCTGATAATTTCCTAAAGGATGTTAATGTTAATTTAATAGGTATTCCAAAACTAAGAGT
GAACTGGCAAAATGTAAAATTAGTTGGTATTTCCTTTTGAATAAGCTTGACCTTTAACTTACTTCATAGCCTATGACAACTCATATATTATTAAATATAAAATAATAAATAAATG
AGTGCTAATAATAATTTTTAATCAAAAATTCTCACAAGCTAACCTTGTAATGATGGTACGCCTAACTGATACCCATTATGTTACCATGGCCAGGCATAAATTCCTGTTACTG
GCACCGCATCATCATCATACTGGCATTCGGTCATATTAAAATAATATCACCTATCTATAGGGCTGCGGCTCTTTTGACACGCACACGTGCTGCTCAGCAGACCAAGTGAACT
TATCAATGAACACCCGCCACACCCACACGGTGGCCCAAGCACCTGACCCACCCATGCCCAGTGGCCAGCACCACCCGAACTCGCAGAAGCCAATGAATGGCCGGCAGACCAA
GAAACACCCACTAACATCTCGGGAGATTCTTCGTCTGCCGAGTTCAAGAACAACACACAAGTGGCCGTAATGAAATGTGAATAGCCTTGGCAAACATGAGTCCGGAAAGCCA
ACTTATGATGGCTTCTGAATAGCCAACCGCATAGTACACGGCTAAGAGCGGGGACCAAAAAAGGACCTGCTCTTTGCTCGCTCGTTGGCTTTCTCTTTCGCAGCCTCGGCTC
GGAAAAAGGATGCCGACAAGCAACAATTTTCATTGATAAAAACACCAGCTGCTGGGTCCTGAAACTCAGTCGTACGCGAGTCCTCAGTCAGTCAGTTTCGAGCTCTGGGATG
CAACGGATGCGGATGCCTTAAATCCCCGAGCCGTTTGGCGGTGTTATTGAAAATTGCGTATTCGCCGCGTATTACCAAGTAATAGCTTGTCCAAAGCCACTACGCTGTCAAA
TTGGTGCTGGCCAACTTTCGGACCCGAACGATGACAAACTGAAAAGTAAACTTTGTAAAGACTCAGCACCTTACAAACAAATTCAAGTGTTTCGCGAAAAAAAATAAAAAAT
TTTGAATTGAAGAGGACACAGTTCGGTGAAAAAAAAAATATTTGCAATGCACAATGGAAAATCAGCAAAGTGACCTCCAAGTTTACGAAAACAGAAACTAACTCAATAACCAT
CCCTGCAGGTGAGCAGAGGCAACATTTTTTCTTTAAAACATTTTTTACCATATTTCCGTAAACGGTTTGCGTCCTTTGGCAAATTTATGGTTGTCTTGGAATAAAATGAACT
TTATTTACTTGGCAACAAAACGAGTGTTTATTCGTGTCGCATAGGGAATCAAGCAGCCAACATAAGGACTATATTTTGTTTAATTCGATTTAATGTGAGTTGCAGAATTAAA
TTTCTTTTTAATTCAACACGCATCTGTACACCATTTGTAAAATTACAAGCTAAAGCTCAGCAAACACTAAATTTTAATCAGTGAAACGAACTGTATTCTGTCAATTTTAATA
TCAAAAGCATATACATTGCTCTTAAAAAATATTAAACTGCGTTAGTAACGTAAACAGAAAATGCTATGAAATTTGTTATAATCAAAATTCACTTGAAAGAGATTTCAACAAAA
TTACCAATCTCGTGTTCTAAGGAATTAATATAATAATTATAATAATATCATAGCTTGTTCCCTGTCACCTAATATATACCATTTAAATAAAAGTAATGCCTAGGTAATTGTT
GAGGGCGGCCTTAGCTGGCAATAAGCGGCTTTTGCCTAATGGAAAATAAGTGGAATGCCTAGGAATTATTGGCCAAGTGGACGGGCTGCTCTCTTTCTGGCAATCCTGAGTC
CTTTCGACTGATTCGTTTTTGGCTCCTTTGGCCCCATCTCCGCACGCTTTGTTCGGCTTGACACACCTGAGTGGCGATGTTCCACACAGGCACTTTCCCAAACAAATGGAAC
CCGGCATCTCGCATTTGGTTGCCCGAACGTAAGTCCCATGAAGTGGTCTTCTCCAGTGGACAGCCAGTCAGCCGCATTTCTTGGGGGCGCTCTTCTCGAGCGCTTGGCCTCT
GAGATGGCCTCTTTGGATGTCTTGGAGATATGCAGCTCATCCTGGCCACCCACTTCGCCGAGCCATTCCATTTCATTTCCCTGGCCAACATACCCGTATGAAACGATGAGTG
CTCTTCACAGTTTTTGCCTACATTCCGGCCACTGCACCGACTGATGGTTGATGGAGACCCATTCTCCGGTTAGTGTTCGTCTTGGTCGTCTTGGGTCTCGGTCCTGG
TCACAATGGGAATTCGCAGCTTAAAGCGCCGTGGCTTTATTCAGGCCAGATTGGATACTTGACATGTTCTAATGCGGCCAGATCTCAGTTTCTGCAACGTGCTCTCCCTA
TCTCAGTTACATGAATTAGCATTCATCGCCACTGCACTGAGCAAAAAATAGGACCACAAATCGCTCTAACTGCTGTAAATTGATATCCATTCAATTATTTTATTTAAGTATT
ATAACACATTGATAGAACATTAACATGTCATATATTTTTGAACACAATTCAGCATTACACTTTAATAAAGTCGAATTTGAATTTATCCAACTGACGCGTTGGGTGATATCAT
AAATTCAATTTCGAGAATGACAGGTCATTAAAATGTTGTCACCTACACTGTCAAATATTTAAGTCAAAATATTAAGTTATAAAATATCAAAAAGCTTTGATAGCTTTAGAGT
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TTAAAATGTCCTTTGGGATTTTTCTGAAATTTTTTTCAAACGCTTCCCCCTTTTTGTTTCCTGCATGTTTAGGCCGTTAAGAGCCTGTTGATGATGGCGGCATGGTAGAACT
GCAGGACGAAAGCGCTGAGTGCAGATGAGGACTGCAATAAACTGCCATACATAAGTGAAAATTGTGAAATGAAAACTTGCGCGAGCATAAATCAATACACCCAAGGGGGGTC
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GTTATCCTTTGATTGCCGGGCACACGACAAAAGTGGTGGACCAGGACACATGTGATGATTGCTTGCGTGGGTCGCAGGAATGAGCCAACTCAGATTGGTAATATTGTGTATG
AACGTGATTTCGTGACTTTGCAATGTTTCTATTTAACAAAAACTCTTGTTAAAGAAATACACACAAAACATCACTTATAACCCTTTTTGGATATCTATGAGGATTTAAGGTT
TGTAAACTAAGGCAATGGTATACCTTAAAAAGTCTATAGTAAATCGCATATATTACATCAATTTTAACGTTCATGCTGATCTTCCAGTTCCAAAATATATATTTTGAAATAG
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GCGCATATCCGCTTTGTAAAAATACGAGTCTAAGTGATGGGTTCCGTTTTTGTTTAGTAGTGCTCACTAGTGAACGGCCTTGTCGCATTTGGGGCTGATAGTGGATGTAGTG
TGGGGTGTATTGTGGTGTGCATGGGGGTGTTTGAATCGCAGAAGTCGGCCCAGCCCGTTGGCCGTCAAGAGGACCTGGCCTAATCGAATGAATGTAGAATGGGCACAAACAA
GTCACGCCTGCCTGCGCATTTCATCAAAGAACGGCGAACAAGAGGCTAACAGCTCTTCGTTTCTCTCTCTCTTTCTCTGCTCAGCTGGGTCCTTTGAAGATCCTGAATGACA
CTCAATTGGCCTAATCGGTTTCTGAAAACCATAGTATGAATTTCATACGGTACGCTAATTTCGAATATAACAAAAAAGCAAAAACGCTTTTGTGATATCTAAATTGTATTTGCCA
TTGAAAAGTTTATACCTATATGTATAATATGGAACCTTTCTAAATATAGTAATTGATACGAAATTGCAAAAATGATGGATGAACATCTCAACATTCAACAGGTTGCCCAGTT
ACTTAATCAATCCATCGGTGTTGAAAGTGAGCACTTTATACAAAAATACTCATGAGTGGTTCTAAAGCGGATAAGAGGATTTATCTTGAGCTCAAAAACTGATGCAGTGATG
CAATATTCAAGATGTGTGCCTTAGTATTCAACATTTTTGCCAGATTTATCGAAACGTAAATAAATAAAAATATACATGAAATTTAATAACATTGCGCAGCTTTTTGGTGAAA
GCAGTTTTAATTTAATAAAGCAATCGTTGCGTTGAAACTAATATTATTTTAAATTATACAGGATACAAAAAATAATATACATATACATTTAAATTTTGAATTTAAAAAGGGG

FIGURE SHEET 17

18/89

TGTGACAGATTTACTGAATAATAATAACTTTAAACATGCCACCTAACAAAAGCGAAAACAATTGTTTAATTACATTTGTGCAACTTGTGGCATTTAGTAAAAGCGAATATCT
AAGCAAATAAGTCGTGTAATTTGATATGCAATATAGCAACCAAACAAAAATGCGTGTTATTAAAATCATGATTACTGCCATACGTATAGATGTTTCATGTCCTGTCCCTTGT
TGATTTCATGCTGATAAAGGACATACACTTTTAAATCTTGCTAACTTGGTACTTTTAACGAGCATTCGAAGGTATCCTGTGCCCATTTCAAAAAAGCTGTAAGCTCTTTGGC
AGCCAAAAAAGCTGACAAATTTGTGCCGGAAAGGAAACAACTTCCTATTTGCATGATTTATTGCCAATGGAATAACAGGTTGGCTTCAGTTGCGTATGTCCCTGCTATTCGA
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ACCTTTACACTGAGTTCCTTTCCAGTTGCTCAAGTTTTGCTCCTTGGCAGCTGCACTTGTTGTTCCTGTTTGCCAGAAAGTTAGTTTCTGGCCAAGAATTTGTCTTTGGCCA
AGTACTGCTCACGCTCGGTTTCTTTGGGCAAAAGTTGGTATTTGAGTTTCGCAGTGGAAAAGCACTTGCGGCAGATCTTCAAATTCTGCCAAACCCGGCGGGCTCACGTGGC
CGCCTTCTAGTTATTTAATAAGTAATTAAGTTCCCTAATTAAATACATTCTCGCAGAGATTTACATAATAAGTAATCTACGCCGAACGTCTTCCTCCATTGCGGCGTTAATT
AAATTTGCAGACCGATTGCATTCGGAAACTTGATTTGGTTTGCGTCTGGCTGCCAGTCGTTAACAAATCATGATTGCTGAAATGGTCAACTTTGGGCATCGCACTTCGTAT
ACACTTGAGATTAAAAATTCTTTAATAAGGGGAAATAAACACTTATTTATAGAAGTATTTTTAAAATATATACAATTAATCTAGTCAGCGCTTTTGACGTAATTTATATTGAG
TTCGAACAACTCATTTGACAACATCAAAGAATCCAATATTCAGCAATTTTAAACATACTCACATGCGAAGGGGGAATCGAATTTCCAATAATTTAAAAAGGAATCGGAATTT
TACATTTTCTCGCGCTTTTGCGGAGAAGCCGTGATATGGTGACTGTATTTATGAAATTTGCTTTTACGCCACTTCCATGAACTGAAAATTGGTTTTCACTGCCTGTTTTTGG
TCGATATAATAATGCTGAGATATATATATGATATGTAATGTCTTTCTATATATTGTAGCATTTACGAAGGGTTATAGCTTGATATAAAAAAAGAAAGAAACTTTGAACAAAC
TCAAGTATATAAAAAGGTTTCAATAAAATATATAAAGTCCATTAGCTGTAGCTTACAGGAGCATAAGTTTTCTTGTTTAAGACGAAGCTTTATCGAACTTTATCTTATAGAT
ACATATATCTATTACTAGGATAAGTAAGTAATTACAATTATTTATGCACGCTGCATTGACATATGCCAAACACTTAAAGTATTCCCACCCAGCCGCACTTGCTACATTTATC
AGCAATTGAATTAATTTCAGGTTGCGGTTCAGCTGAGTTTGGTTTGTAAAATACATTATAATGTTTAATAATCAGCAGAGAGCAGGAAAAATATGTATTAAGTTCGGCATTG
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AAATGAAGAAAAAAAGTTTGGCTCAAGTTTATTGGTTTCGCGCTGCTTTCATCAATTGCTGCACGCAAATGCTTCTCAAAAAAAAAAAAAAAAAAAACTAACTCTTCATTTA
TGGCATTTCTTAGTTGCGAATAAATTCCGATTTAAGCTGGTTGAAAAAAACCCATCCTTTCAACGGTGACTAAACATATTTTAAGCAGACCGCTCAAACTCAAACCGTGGGT
GGTTAATTAAATAAGAGCATCGATTAAGTCAACTGTCTTTTTATCTGTCCCACTTTTAGGGTCACCCGGTGGACAGCTAATTGCAGCTAACCCCATTGGCATTTAGCAAACG
GAAAATGCATCGTGACCGCTGCAACCACATTGCACCACTACCACCAGCAGCATCAGCGCCACCACTTCCACCTCCAGCAGCAGCAAGGGAATCCGCACCGCTGAAACTGAAT
CTGAAGGCATCCCAGTGGCGGCGACACACGGAATCCTTGCCAAATGCGGCCAAATGCGAGGCGCTGGCAAGTAAATAAGCGTAATCCTTTGCGGGCACGTACCACCACTACT
AACCGGTGCCCTCTCGCTCTCCGAGATGTTGGCCAACTCGAGCCACAGCCATTCCACTGGGAGCACAACCTCGACGGCTGGGAGTTCGGCCACCGAATCATCCGCTGTGAAT
GTAGGCAAGGACCACGACAAGCACGTGAATGACAGCGTTTCCACGGGTCTGAGGTAAGTGCATGTGCCTAGGCTTTTCCATTTCCATGGCAACACACACACAGATTCCATTA
AGCTCATGACTGCGGGCTCAACAAGTCATCGCGATAAGCTCAGCTTCATTTTCCAGGAGATGCATTCAACTAATGTGCTTAGAATTCTACTATTGTACATAACTAACATATA
GGGAATATAATCAGATTACTTAGAACCTCAGAACAGTCAATACAATCCACTTAATATAAATGAATTAAAAGTATCTATCGAAACTGAAAAGAAGAGGATCATTAGCTTGGGT
ACAACATTTATAAGAATTTTGGCTTATGAAGTTGCAAAAAGAATTCTTAAAAAATTCAATACAATGTCAAATAGTTCTGAAAACCATAAATTATTAACAATTAAATATTAAAT
TATTTATATTGATTTAATTCATACATTTAAACATAAGTTACACTACTGCAAGGAGGAAAGTATCAGATGACTTGAGCTATACTTTCATAAACTTAGCTTAGAGCAATCTAAA
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AGTACGACCTGAGCTACATTGCCAAGGTGAATCCCTTTTGGCTACAGTTCGAGCCACCTAAGTCGAGCACCTTCCTGATTATGGCCGCCCTGTATTGCCTGATTTCGGTGGT
GGGATGTGTGGGCAATGCGTTCGTCATCTTTATGTTTGCCAACCGCAAATCTCTGCGGACTCCTGCCAATATCCTGGTGATGAATCTGGCCATCTGCGACTTTCTGATCGTC
ATCAAATGCCCGATTGCCATTTACAATAACATCAAAGAGGGTCCAGCTTTAGGAGCATTGGTAAGCTTAAAACTTGGGGAAATAACTTACTAAATATCTATATAAATGAAA
TTCATTCGGCTTGCATTTATGTCAAAAATCGATCAACAAAAGCAATCTACATAATAAATAAAATTAAATTGGCCCAAAATGCTTGGACTGATTTCAGCTGTTTCTTGCAGAA
ATTCATTTGTGGGATTCTCTTTTCCCGAAAGCAATTAATAGAATTTAAATGAAACAATAAAAGTTCAATTTGTAGCCTACACATCTTGGTTCATGAAAAACATATTCCAAAA
TGTAATGGCTATTAAAATTTCACCGAGCCTTTTGTTTGCCTTGAAACGGGTGGTTCATTAAAAATCCTACTGACTTTCCGTCCCACAGCCTGTCGCCTCTATGGATTTGTGG
GTGGCCTAAGTGGCACCTGTGCCATCGGTACCCTCACCGCCATCGCTTTGGATCGGTACAATGTGGTGGTGCATCCACTGCAACCGCTGAGACGCTGCTCCCGCCTGCGATC
CTACCTGATCATCCTGCTGATCTGGTGCTACAGCTTCCTGTTCGCTGTGATGCCGGCCCTGGATATCGGACTATCTGTCTATGTGCCAGAGGGCTTCCTCACCACCTGCAGC
TTCGATTATCTGAACAAGGAGATGCCAGCTCGCATTTTCATGGCACTGTTCTTTGTGGCTGCCTACTGCATTCCACTGACCTCCATTGTGTACTCCTACTTCTATATACTGA
AGGTGCTCTTCACAGCGAGTCGAATACAATCGAACAAGGATAAGGCCAAGACGGAGCAGAAGTTGGCCTTCATTGTGGCGGCTATCATTGGTTTGTGGTTCCTGGCCTGGTC
ACCGTACGCCATCGTTGCCATGATGGGTGCTTCGGCCTGGAGAGGCACATAACGCCACTGGGATCGATGATACCCGCGCTCTTCTGCAAGACAGCTGCCTGCGTGGATCCC
TACTTGTATGCGGCCACCCATCCGCGGTTTCGTGTCGAGGTGCGAATGCTCTTCTACGGACGCGGAGTGCTGCGAAGGGTCTCCACGACCAGATCATCGTACGATGACCCGAT
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GGAGACGGAGGAGAACGAGGAGATCGTTGTGGTGGCCGAGATCAACCAATTCGATTAGCAGCGTCATGGAACAGAGTAAGTTCTGAAGGCTGACGATTATGCCAGTTAAGAGA
ACGGAAATTCTGTCAATCTGTTTCGGAACCAACTAACATAAACATTTTTAATCAGTTTTAAGTTTTACAGACGTGTTTTATATAATTTGAAAATTAGTCAAACCTATGATCAC
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TTCCTATCTCGAAAAGTAAACTGTTCGCTGTTAATTGAAAATGTTTGTGCACTGCACTGCAAGGCATATCAAAATGGAAGCTATCAATAATCGTAAATTGAATGGATCGGAC
TCAAGTTTCATTGTTGAACTAATCTAATCTAATTTGTATGTAGAAATAATAGACCGAACTGAAATCAGCAATGGCAGCAAAGTAATTTCGCTCGGCAATGATATATGCCAAT
GGCATTGTTCATCTGAGTGAATGCGTTGTCATTGATGGACCTACAATTGAAATGAAAATAATAATAATAAATAGAAATGAAGCAGGGAAATCCGCCGAGCAGTGGGAAA
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TAGGGGCCGAAGTGGAAATTCAATAGTCAGATTATACATCATTTCAGGGAAAGTCACTCGGACCCAAGGTCAAGCCGTGGTATTGGATGTTAACAAGCGGATGTGCAGATTG
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(SEQ ID NO: 34)

Exon: 1001..1464
Exon: 7788..8022
Exon: 8083..8341
Exon: 8920..9245
Exon: 9609..10501
Start ATG: 7845

Transcript No. : CT17820
CTGGGATGCAACGGATGCGGATGCCTTAAATCCCCGAGCCGTTTGGCGGTGTTATTGAAAATTGCGTATTCGCCGCGTATTACCAAGTAATAGCTTGTCCAAAGCCACTACG
CTGTCAAAGGACGGGCTTAAAACGCTACTTGCATTTTTACGTACTATACATAGATAAATTTTCCGGGTAATCGGCGGAAATTGAGTTAAAGTTTTGTGTCCGGTTGGCGCCA
GTTGGCAATTGGTGCTGGCCAACTTTCGGCACCCGAACGATGACAAACTGAAAAGTAAACTCAGCACCTTACAAACAAATTCAAGTGTTTCGCGAAAAAAAA
TAAAAAAATTTTGAATTGAAGAGGACACAGTTCGGTGAAAAAAAAAATATTTGCAATGCACAATGGAAAATCAGCAAAGTGACCTCCAAGTTTACGAAAACAGAAACTAACTCA
ATAACCATCCCTGCAGGGTCACCCGGTGGACAGCTAATTGCAGCTAACCCCATTGGCATTTAGCAAACGGAAAATGCATCGTGACCGCTGCAACCACATTGCACCACTACCA
CCAGCAGCATCAGCGCCACCACTTCCACCTCCAGCAGCAGCAAGGGAATCCGCACCGCTGAAACTGAATCTGAAGGCATCCCAGTGGCGGCGACACACGGAATCCTTGCCAA
ATGCGGCCAAATGCGAGGCGCTGGCAACTCGTAAATATTTGGCCAAGTCAGTCATGGAGGCCATCATCATGACGACCCTGCCCAACCTGACAACGGATGCAGGTGACAGCAGCAG
CTTCTGGCTAACCGGTGCCCTCTCGCTCTCCGAGATGTTGGCCAACTCGAGCCACAGCCATTCCACTGGGAGCACAACCTCGACGGCTGGGAGTTCGGCCACCGAATCATCC
GCTGTGAATGTAGGCAAGGACCACGACAAGCACGTGAATGACAGCGTTTCCACGGGTCTGAGCAATTACAGTAATTACCCAGCTACATTCACTACAGGGACAAGTACGACC
TGAGCTACATTGCCAAGGTGAATCCCTTTTGGCTACAGTTCGAGCCACCTAAGTCGAGCACCTTCCTGATTATGGCCGCCCTGTATTGCCTGATTTCGGTGGTGGGATGTGT
GGGCAATGCGTTCGTCATCTTTATGTTTGCCAACCGCAAATCTCTGCGGACTCCTGCCAATATCCTGGTGATGAATCTGGCCATCTGCGACTTTCTGATCGTCATCAAATGC
CCGATTGCCATTTACAATAACATCAAAGAGGGTCCAGCTTTAGGAGACATTGCCTGTCGCCTCTATGGATTTGTGGGTGGCCTAAGTGGCACCTGTGCCATCGGTACCCTCA

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AGGATAAGGCCAAGACGGAGCAGAAGTTGGCCTTCATTGTGGCGGCTATCATTGGTTTGTGGTTCCTGGCCTGGTCACCGTACGCCATCGTTGCCATGATGGGTGTCTTCGG
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GAGGTGCGAATGCTCTTCTACGGACGCGGAGTGCTGCGAAGGGTCTCCACGACCAGATCATCGTACATGACCCGATCACGATCGTCGTTCACCCACCGATTGAGGACGAGCA
CCACCGGTGAGGGCGGAATGGGTGATCACCGCATGGAAAACTATCTGATGAACAACAATCTGATGATGGTGCCCGAGGAGACGGAGGAGAACGAGGAGATCGTTGTGGTGGC
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(SEQ ID NO: 35)

Start ATG: 522

MHRDRCNHIAPLPPAASAPPLPPPAAARESAPLKLNLKASQWRRHTESLPNAAKCEALATRKYLAKSVMEAIIMTTLPNLTTDAGDSSFWLTGALSLSEMLANSSHSHSTGS
TTSTAGSSATESSAVNVGKDHDKHVNDSVSTGLSNYSNYPSYIHYRDKYDLSYIAKVNPFWLQFEPPKSSTFLIMAALYCLISVVGCVGNAFVIFMFANRKSLRTPANILVM
NLAICDFLMLIKCPIAIYNNIKEGPALGDIACRLYGFVGGLSGTCAIGTLTAIALDRYNVVVHPLQPLRRCSRLRSYLIILLIWCYSFLFAVMPALDIGLSVYVPEGFLTTC
SFDYLNKEMPARIFMALFFVAAYCIPLTSIVYSYFYILKVVFTASRIQSNKDKAKTEQKLAFIVAAIIGLWFLAWSPYAIVAMMGVFGLERHITPLGSMIPALFCKTAACVD
PYLYAATHPRFRVEVRMLFYGRGVLRRVSTTRSSYMTRSRSSFTHRLRTSTTGEGGMGDHRMENYLMNNNLMMVPEETEENEEIVVVAEINNSISSVMEQSKF*
(SEQ ID NO: 36)

Name: Rhodopsin 3 and 4-like (Rhodopsin 7)
Classification: G_protein_linked_receptor


Celera Sequence No. : 142000013384543
TATGCGCAACTCGACAAACATCTTCCTAACCAACCTGAGCATTGCGGACCTGCTGGTGCTGCTCGTCTGCACGCCCACCGTCCTCGTGGAGGTCAACACTCGCCCGGAGACC
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GGGCCATCCTCATCTGCGTCCTGGCCTGGGGCATTGCTGCGCTCTTTACGAGGTAAGCGATTAGGCTCGTACTTGATTTTCTTAAATTTATTTGTAAACTAGCATTATACTT
TAAATATCTTAATTAGTTTGGTCGCTTTTCATCGCATGCTTTTTGGTGTTTGTAGTCCTACATTTCGTATGTACATATGGTATTATCCTGTTTAGATCTACTTCGTTTGTGG
CATTTTTCCCCGTTTTGTTTATTTTCCATTATGACGTGGAATTTCTGGTCTTGGTGTTTGGCCTTTTGTGCGCCATCTACGCTGGCGGCGTGTCCATTTGTCCATTTACATG
CTAAACTGCGACTGTCGCCTATCTATTCCATTTCCACTCCTGTCCTACCACTTCTCCTGCTTCACTCGCTTCATCGTTGCCATTGCCATTTCCATTCCCAATCCCATTCCCA
TTGACATCCGTCGCCTCAAGTTGCGGACGGCTTTTGTCCAAGTTCCGGAAGCTTGCCGTTATCAGCGCCCTGTCATCTTTAATAAGCACCGATGTCCGCTATCATGGATTTC
ATTTCATTGACACTTTATTATTGTGCGCTCCGTCCAAGGACGAGCGGCGGCGACCCTTTTTAATTTTGCAAATCTTGCCGCGTCCATAACAATGAAATAAACAGCACATTGTCGA
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TACACTAAAGATACACGGTATACATTTTTTTTCTAGACAGAAATATACTTTAATTCAACTAAATTAATATATATATGTACCTCTCCCATCTTTTAGCTATTAAATAGTCGAG
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GTGGTCCTAATGCTCGGCGCCGTTGTGCTGCTGTCCTTCTTCGTCTGCCTGCCTGCCCTTCCGCGTCCTCACCCGTGGATCATCCTCAGCACGGACCAAACACTGCACGATCTGG
GATTGGTGCGCTACTACAGCTTGCTGTACTTCGTAGGATCATGTTGTACCTCAACTCGGCCATGAATCCGATTCTTTACAACCTGATGTCGACCAAGTTTCGAAGGGGTTT
CAAGCGGCTTTGTCAGGACGCAGGGCGATTACTGCTGGAATTGGTGACATTGGGAAGAAGGAAGGAAGACTCTTCTCGCGGGCGCAGAGGTACCTTGTCACTGGGCATGGGC
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TTAAGATCGAGATGCAGATGCCATGTGGCAGCGACCTGGAGGCCATGGCCATGCTGCAGCATTCCACCTTGGGCAAGGGAATTGCCAGGCGAGTGAGTGATAGCCGTCTCAT
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AAGCTTCCTGGAATAGCAAGAGAAATAGTAAATCTGACCGAAAATACCCTCTAAGCGAGATGGGCGTGAAAAATCGCCTTTAACCCGTTTACACACTCGCTTCACTTGGCTG
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CAGCTGCCGAGAATCCCGAATCGTAGTTGGGCTGCCGCCTTGGACATTTCCGTACCAAAAACAATCAATTTTTCGGGCTATTAAACTCGAATGAATGTGCCAAAGATAAATA
ACAGCAACGACAGCCGAACAGCACTAAAACTACCACTACTGGTCAGGGTTAGGAGTCCAGATATCGACTGGCAGTAAGGGGTAAGCCATTAGGTGGCCTTCGAGGAGCGGAG
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TAGACTCCCACTTTTGTAGAGTAAAAAGTAATAAGTAGCTTGAACCCACACCATCCTGCGAGTATGATGAGTATGAGCAGACGCTGCCGTTTCCGTTTCCGTTCCGGTCTGTGATTA
AGTTGAGTGCTTCGCCCCCGAAACTTTTCCAGTAGTTAGCCGTTGAGTAGCTTTTAAATATTTGTTTGTTTCCTGCCCGCAGCGCGATAAAACTTTGCAGACAGCGCTAGTC
ACTCTAGTCCCCGCTAAAACTGATAATATGATTCTTGCAGTCCCATCATCGCCATATCCACCTACAGCGTGGAACCCTACGGGGACGGAACCGATGCTCCCGTTTGCACCAC
CGCCGCCGATGGTTTCTGGTCGATCTTCTACTTCGTGGGCTGCATCACGGTGTTTTTCTTCCTGCCCTTCGGCATCCTGGTTCTTCTATACGCGGCCATCGCTTACAAGCTG
CTCCGTCCCAACAACGCCTTCCACCGACCAACCTCCCCGCAGCCACAGCAGCCGTCCGGCGGAGCCACCAGTGGCTCCTCACAGGTGCCCAGCACCAAGGGTAACAGCCATC
AACAAAGCAACGGGATGAGGAAGCATCGCAAGCAGGTAATCTTCATGCTGGTGGCCGTGGTGTCTAGCTTTTTTGTTTGCCTTCTACCCTTCCGGGCCTTCACCCTCTGGGT
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CAACGGCAGGCGGAAGTGGGCGCAATGCGTCCACGCGACAGGAACAGGATGCCGAGGAAGGAGCTGCGCTGGCGGGAACGACCAGCGCCCGACATCCACGTCGCACACTCCG
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CGGGAGCGCGGCCATACTGGGAGCCGCTATCATCGGCCAACGGCTGCCACCGTTACAACCGCCTGTCTGCAGGAGCGGACGCGCCCAGCAAGATCTGAATCCCATCTCTAAATAT
GCATCCTTCGAGTCCCTGTCCACTGCCAGCAACCGTTAAAGTATTTAGTTGAATTCCAACAGCAAATAGTCATAGTTTTAGAAAAATTTTGTTGTAAAGACTGAAGTACCTC
AGAAGAAGTCAATAAACGCAAGAGAAGATGTTTTTGAAAATCGAAACTAATTTTCTTCGGGCTTCGAAAAATTGAAGTTTGCAAGATTCGAAATAGCTTTAACTTGATTTTT
AGAACAGAAACGAGTATGAACTTTTCATACGATCATTTTTATCGCACCTATTGTGATTTAATGGGAGATAGGAGGAGACCAATTGGGATATGCAAAAATAACGCAACTATTA
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20/89

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TTATCTTTGTATGTACGATTAATTTTAATCTCTAAAGAGTCAAAGTACTTCAATAATTTTACAAATCTGTCGGAGGGAATGTAAGCTTGCCCAAATCAAATGGAAGCTACAA
TCGTTGTCAGATGGAGATATTTTATGTTAGAAGGAATATCTCGGATACGAAATATTTAATTTAAAATTCCTTTTCATATTATTCTTTTTAAAAAATAATAAGTCCTGTATGT
ATACAATGCAATACATAAAGGTAGAGTATGTCCTAAAAAGAAAAATATCTTTCCGAATATATGTATATAATTTATAAAATAAGTGGATACATACATTTTTCGTAAGTATCCT
AGAAGATTTGCCAACGTATCAGGTTTACAAAAATTGATTACCTATGTGCAGTTAACTTAACGGCAGTGCACTAACTAATCTGATTTGTGAAATAATGCAGATATAAAACATT
TTTAAATAGAAATATATTTATACATCTGATTCTTCAACATCTAAGCACTCGTATAGAGTGCTTTGAATATATTCTAAATACATTGGCATGATCCAAGTTTTAAATCAGCCAA
AAACTTGCTCCAAAAACAGGAAGATTCTACACAAATCGCCTCGCCCTTAAAGTTTCTGCCAAGTATTTGGGTGCGTGCGGATCAGTTC
(SEQ ID NO: 37)


Exon: 2..134
Exon: 208..388
Exon: 2321..3216
Exon: 3631..3664
Exon: 4521..5472
Start ATG: 2


Transcript No. : CT18539
ATGCGCAACTCGACAAACATCTTCCTAACCAACCTGAGCATTGCGGACCTGCTGGTGCTGCTCGTCTGCACGCCCACCGTCCTCGTGGAGGTCAACACTCGCCCGGAGACCT
GGGTACTTGGCCACGAGATGTGCAAGGCTGTGCCGTTCGTGGAGCTCACGGTGGCCCACGCCAGTGTGCTGACCATCTTGGCCATCTCGTTCGAGCGCTATTACGCAATCTG
CGAGCCATTAAAGGCCGGCTACGTCTGCACCAAGGGGCGGGCCATCCTCATCTGCGTCCTGGCCTGGGGCATTGCTGCGCTCTTTACGAGCCCCATTCTGTGGGTGGCCGAG
TACAAGCTGGCCGAGTACATTGATGGATCGTCGGTGGCCGTGTGCCTGACCCAGGCCATCAGCGACTGGACGCTGGCCTTCTTCCTGATGACCATCTCGGTGTTCTTCGTGG
TGCCGTTCGTGACCCTGGTGGTGCTGTACGGCATCATCGCCCGGAATCTGGTCTCCAACAGGGCGGCCATGCTGCGCGCCCGTCCCACGAAGCCGGAGCTTAGTCTGAAGGC
CCGCAAGCAGGTGGTCCTAATGCTCGGCGCCGTTGTGCTGTCCTTCTTCGTCTGCCTGCTGCCCTTCCGCGTCCTCACCCTGTGGATCATCCTCAGCACGGACCAAACACTG
CACGATCTGGGATTGGTGCGCTACTACAGCTTGCTGTACTTCTGTAGGATCATGTTGTACCTCAACTCGGCCATGAATCCGATTCTTTACAACCTGATGTCGACCAAGTTTC
GAAGGGGTTTCAAGCGGCTTTGTCAGGACGCAGGGCGATTACTGCTGGAATTGGTGACATTGGGAAGAAGGAAGGAAGACTCTTCTCGCGGGCGCAGAGGTACCTTGTCACT
CGCACCCGCCTTAAGATCGAGATGCAGATGCCATGTGGCAGCGACCTGGAGGCCATGGCCATGCTGCAGCATTCCACCTTGGGCAAGGGAATTGCCAGGCGAGTGAGTGATA
GCCGTCTCATGCCTCTGAGAAATCATCAACCACGACGCCACAAGCCGCAAATAAGTTTCGACGAGGAGTCACTGGAGGAGAATAAGCGTAGGTTAGGAGTCCAGATATCGAC
TGGCAGTAAGGGTCCCATCATCGCCATATCCACCTACAGCGTGGAACCCTACGGGGACGGAACCGATGCTCCCGTTTGCACCACCGCCGCCGATGGTTTCTGGTCGATCTTC
TACTTCGTGGGCTGCATCACGGTGTTTTTCTTCCTGCCCCTTCGGCATCCTGGTTCTTCTATACGCGGCCATCGCTTACAAGCTGCTCCGTCCCAACAACGCCTTCCACCGAC
CAACCTCCCCGCAGCCACAGCAGCCGTCCGGCGGAGCCACCAGTGGCTCCTCACAGGTGCCCAGCACCAAGGGTAACAGCCATCAACAAAGCAACGGGATGAGGAAGCATCG
CAAGCAGGTAATCTTCATGCTGGTGGCCGTGGTGTCTAGCTTTTTTGTTTGCCTTCTACCCTTCCGGGCCTTCACCCTCTGGGTGATCCTGGCCAGCGCCGAGGATGTCGAG
GGTCTGGGCATTGCCGGCTACTACAACCTGCTGTACTTCTCGCGCTTCATGCTCTACCTAAACTCAGCCATGAACCCGATCCTCTACAACCTGATGTCCTCCAAATTTCGCA
GCGGCTTCTGGCGGCTGCTGCTCACTTGTCTGGGCCAACGGCCACATCACCACCATCGCCACCACTACCATCAGAGGCAGCATCAACGGCAGGCGGAAGTGGGCGCAATGC
GTCCACGCGACAGGAACAGGATGCCGAGGAAGGAGCTGCGCTGGCGGGAACGAGCCAGCGCCCGACATCCACGTCGCACACTCCGCCGCGAGGCCACCTTCTTGATCAACTCC
ATATCCACCTCCTCGGGTACGGATCGCACCACATCATCATCGGCGTGGCGCAACAGTCTGTCCATTTCCGGTCTGAGCGAACGGGAGCGCGGCATACTGGGAGCCGCTA
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(SEQ ID NO: 38)


Start ATG: 1


MRNSTNIFLTNLSIADLLVLLVCTPTVLVEVNTRPETWVLGHEMCKAVPFVELTVAHASVLTILAISFERYYAICEPLKAGYVCTKGRAILICVLAWGIAALFTSPILWVAE
YKLAEYIDGSSVAVCLTQAISDWTLAFFLMTISVFFVVPFVTLVVLYGIIARNLVSNRAAMLRARPTKPELSLKARKQVVLMLGAVVLSFFVCLLPFRVLTLWIILSTDQTL
HDLGLVRYYSLLYFCRIMLYLNSAMNPILYNLMSTKFRRGFKRLCQDAGRLLLELVTLGRRKEDSSRGRRGTLSLGMGTNTNTNTNSSNATGATSSSILSRSSNRRCSEDIS
RTRLKIEMQMPCGSDLEAMAMLQHSTLGKGIARRVSDSRLMPLRNHQPRRHKPQISFDEESLEENKRRLGVQISTGSKGPIIAISTYSVEPYGDGTDAPVCTTAADGFWSIF
YFVGCITVFFFLPFGILVLLYAAIAYKLLRPNNAFHRPTSPQPQQPSGGATSGSSQVPSTKGNSHQQSNGMRKHRKQVIFMLVAVVSSFFVCLLPFRAFTLWVILASAEDVE
GLGIAGYYNLLYFSRFMLYLNSAMNPILYNLMSSKFRSGFWRLLLTCLGQRPHHHRHHYHQRQHPTAGGSGRNASTRQEQDAEEGAALAGTTSARHPRRTLRREATFLINS
ISTSSGTDRTTSSSAWRSNSLSISGLSERERGILGAAIIGTTAATVTTACLQERRASKI*
(SEQ ID NO: 39)

Name: Thyrotropin-releasing hormone receptor-like
Classification: G_protein_linked_receptor


Celera Sequence No. : 142000012807287
CAGAAAGTGTAGGGAATGTAGGGAAATGCAAAGCGAGACCCTTTGGCTGCTCACTGACTGAAATATCACCAGACTCGGCTCGGTTCTGCCGCTCAAGTGGCAGTAAATAAAA
GTTGTGAGGAGCCTTGGCGGCATGAGTAATAATGACCGAAATCAGAGCACCATCACCATCACCAACCATCGCTACCACCGCCCAACGCGTTGCTCATTTTATTAAAATAACA
AAAATATTTTGCCGCTCGCAGCCTTTTTACGATGCCGAACCGACTGGCGGCCCATTTGTTATTTGGCGGTCATTGCCACCAAATGGTGTCCTGTCGCTCTTTCTCGTCCTCG
TCCTCGTCCTTGTCCGTTCCACTGGGCCAACTCGTGTGTCGTGTGTGTTTTGACCAGAGTTATGCAGCTGCGGATGGGCAAAAATGTTTTATTGCCAGCTGGGGAATGCCAA
AGTGGCAAGAGGCAGATTGCCCGATCTTAGCTGTTTAAATAAATTTAAGAGAGAGAGAGAGAGATCTGGCACGAAGCACTCCATCACTGGTCCAGCGATCCGTTAA
GCCATCGAGGGTCCTTCGAATGAAATGCCAGCGCTGACAAGGCAAACACTGGAGATTTGTATAATAAGGGTGGGTGGTTGTGCCGAAATTTGGCACTGATAGGCAGGACAC
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CAGAGCAGAGGAAGTGAAGAAAAGGGAACCGGAAAGGAAAGCCATTCATTTGGCCCCGCGACTCAAGTGCCGTTGTCTACGTTTGCGAATGTGTGTGGTTGTGTGCGTGGCA
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CTACCGCACCCATCTCTCATGTCCTTTTTATCCGCACATCCTTTCAGCTTACTCCACCGCCGCCCTGCTGGCCATCGTGTTCGCCATTCCCTTCGGTATCCGCATGCTGGTC
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AGGAGGAGCTTTCAAGGGTCGAAGCTCTTCTAAAAGGTTCAAAAGTTGGACTCAGCTTTAAGTTCACTCGGATATACTAAAAATATATAAAAACAACACGTTATGAAACTG
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GCCATCCAGGATTTGCTCGACCAGTGATGGGACCACCTGGGTAAGTCGCATTGAAAGTCTGTAGATGGTCTATTTAATTGATCCAACCTAGCGTTGTGGTATTCCTCACCTT
CTTGGCCACGGTAATCGTCTATCTACCGAGCATCTTTCGTGGCGAACTGATCAAATGCATCCTTGGATCGAGTGGAGTGACGTATATGTATATTTGCGACGCGACAACACTATCTAC
CAGCAGACCATCTTCTATCGCGTCTACAAGATCATGTGGAGGTGATCTTTAAACTGGTGCCCACTTTGGTGATCGGTGGCCTCAACATGCGCATCATGATGGTCTACAGGC
GGACCTGCGAGCGCCGCCGCAAGATGGTGCTCAGTCGTCCGCATGCCCAGGGACATGGTCACGGACATGGGCACGGACATGGTCATGGACATGGACATGCACATGGACACGG
CTATTTGAAGGACGACGATCCGCGCAAAGTTCGCCGAGGAGCGGCGCCTTGTTCCTGCTGCTCGGCAGCACATCGATTTGTTCCTGGTCTGCGTCTCGCCGATGGCCATTCTC
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FIGURE SHEET 20

21/89

CACATGACGATCGCCTCGGAGGTCTATCCGAGCTTCCCCTTCCAGGTGTTCCGTGCCAGCGCCAATCTGCTGGAGTTGATTAACTACTCGCTGACCTTCTACATCTACTGCC
TGTTCAGCGAGGATTTCCGCAACACCCTGGTGAGGACGATCAAGTGGCCCTGGTTGAAGGGCAAGTTCTGCCACCAGGCCGAGCACGAGGTGAGTGCCAGTCCACCGGCCAC
AGCCGGAACCGTAGCGGTAGCCGGAACCGGAAATGGCCACGTTTCTATTTTTCATCCGGCAATACCGGCGCTGACTCTCACACCCGCAGAACCCGACGAACGGCCCCGGTGT
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CTTCCACTTACCCCCCAGGTCGTCGAGGTTAAAGGGTGCCCTTTCTCTCGCTTGAGATCCTGCGACATTTGAACGTGTTCAAGTATCCGATGAACGAAAAATGATATACGATA
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CCGGATTCCAACC
(SEQ ID NO: 40)

Exon: 1001..1088
Exon: 1280..1429
Exon: 1851..1944
Exon: 1996..2821
Start ATG: 1001

Transcript No. : CT18637
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CAACGGCTGTTTGGGCGTTGGCGTAATGATGTTACTAGTGCTGACCATTGAACGTTACGTGTCCGTTTGCCATCCAGGATTTGCTCGACCAGTGATGGGACCACCTGGCGTT
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GCGACAACACTATCTACCAGCAGACCATCTTCTATCGCGTCTACAAGATCATGCTGGAGGTGATCTTTAAACTGGTGCCCACTTTGGTGATCGGTGGCCTCAACATGCGCAT
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CGGCGATGGCCATTCTCCACATGACGATCGCCTCGGAGGTCTATCCGAGCTCCCTTCCAGGTGTTCCGTGCCAGCGCCAATCTGCTGGAGTTGATTAACTACTCGCTGAC
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GCCAGTCCACCGGCCACAGCCGGAACCGTAGCGGTAGCCGGAACCGGAAATGGCCACGTTTCTATTTTTCATCCGGCAATACCGGCGCTGACTCTCACACCCGCAGAACCCG
ACGAACGGCCCCGGTGTGCCAATGGCGTGCTTCACTAA
(SEQ ID NO: 41)

Start ATG: 1

MGGRAEEVKKREPERKAIHLAPRLKCRCLPYSTAALLAIVFAIPFGIRMLVHKDRGQWEEFGPAFYTAHLELYLGNGCLGVGVMMLLVLTIERYVSVCHPGFARPVMGPPGV
VVFLTCLATVIVYLPSIFRGELIKCILGSSDVYVYLRRDNTIYQQTIFYRVYKIMLEVIFKLVPTLVIGGLNMRIMMVYRRTCERRRKMVLSRPHAQGHGHGHGHGHGHGHG
HAHGHGYLKDDDPRKFAEERRLFLLLGSTSILFLVCVSPMAILHMTIASEVYPSFPFQVFRASANLLELINYSLTFYIYCLFSEDFRNTLVRTIKWPWLKGKFCHQAEHEVS
ASPPATAGTVAVAGTGNGHVSIFHPAIPALTLTPAEPDERPRCANGVLH*
(SEQ ID NO: 42)

Name: G-protein coupled receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384543
AATAATCCACCTTCGAAGGTAAACCATCTTAATTATGCTTTAAAATTGCTGGATTATATAAACCCCTAAGGTAGTTCATCCCACTTGTTCAACTGAAATCGACCCACACAAA
TGGTGGTTGGTATCTATCTACCAGAGTTAGGAGCTCGTTTAACCCAATATTGCCTATTCGTAGAGATCCGCATTCCTGCGAGGAGAAGTCGAACTGCCGTAGCTGAGCTGCG
AGTCGGTCTTCTTCAGAATGGAAACGTGGTGGGTGGGTGCATCACCCGTCCGGTTGGCCATCAGCGAGTCCTGTTTGTGGAGCAGGCCGCGTCGCTGGTCGGCGAAGGAGAT
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AAGGTGGAAAAAGGGTTTTTATCGAAGGGAACACGATTTCTTACAAATCTTCATATCAATTTTGAAGGCCTTCACATATTTTATCAATATATTTGAGGTTAGAAATTAACTA
ACCTGAGGCGTCCGCAGCAGCTGCGCGACTTGATGATGGCCGCGAATCCGCGTCGGTACTTCTTGTTCACTGAGTAGAGTATGGGGTTGATGCAGCTGTTCGAGGAGCCCAG
CCACTGGGCCACCGGCATCACCTTCTTGAGGATCTCGAACTCCTCCTGCGAGATGTCCGCAAAGATGACATAGAGCGGCAGCCAGGACAAAACA
AACAGGATGACCACGGCCACCAACATCTTGATGACCTTCACCTTGCTCTTCTGCTGCATGCGGTCCATTTGCGCGTCCTTGGACTCGCCGGGGATGGACCTCGTGGAGACCT
TGATCCAGATGAGCACGTAGCAGAGCGTGATCAGGGACATGGGCAGCAGGTAGCAGGCCACCAGGTTGGCTAGCAGGAAGTAGAGGTTCCCATCCGTGCCCGGGGGCCACAC
CTCCTGGCAGAGGAACTGCGGCTGCGAGTAGGCCGAGACCAGGGCGTCGGAGAAGACCTCCTCGGCGGGCACCAGGTCGAAGAAGAGCAGCCAAGGAATGGTGGTCACCAGC
TTTACCAAGTAGTCAAAGAAGGAGTCTTCGTAGGAGCAGCAGCAGCAGCAGGAGCTCCGGCTTCAGATGCCACTGACGGCTTTGAGCCGTCAAGGATAATGCGCAATCATCAA
GCTGTCGAGTCGAGTCGAGGCGACGATGACGATGACGACACCGTTTCAACTAGGAGGAGCAGCTCGGCATGCAAATATCTCCGCTGATTAATTCGCACACGCAGGATGCCGA
TGCCAGCAGCCATCCTTAAGCCTTTTTCTGCTGAGTGTTCGCTTTCCAATCTCGACTATTGAACCCGCCTGCTACTCCTGCTCCTGCTCCTCCGCCCCAAAAAAGCGGCGCT
ATTTAGCTTAGTGCAGCCGGCTCATTGTGGCGCCCGCTCAGTGGTCATAGACAAGACTTGTCCCGGACGAACGAAACTGGTTGTCTGCTCCTGGCCCGAAACCATGTAATTA
CGTGCATTGTGTTCGTATTTTCGACTTGGACCTTGGGTTGTCGCCTGCGTCTGTCCGCCAAAACATTTGGCAGATAACACAGCGGTAATTCCATTAGAGGGCGGCCATGCCA
GGCCACTACCCCAGAATCCTATTCCTCACCGACTAAAAATAGCCAGCTTAACAATGTGGCCGAGACCCTCATCTCTGCGAAAAAAAAAGGTGGGCCGCCTGGGCGACCAAA
CAAAGCTGTCCGCAAAGCCAATAATCAAATTGTCATAACGTTTATTTATAGGAGCAAACCAATTGCATTTGCATAATTTGCCCATGCGACTTCTATGGTCATAAATCAGGCG
AGAGCTTAATTGAGTTCTTTTTGGGTAAAAACAGCGGAGTCGGAAAAAGTAATCAGCAGTTTTCGCTGGTGCAGACTAATTCAAACTAAACCTCTAATTTGATGTTGAAATT
TTGTTAAATCGTATTAACTACACTTTTGATGATGTAAACCATTTTATGAGCTTTAAAAACTAAAAATTTCTCTTATGAGTTCTCTTATACGATTTATGTATGATTTGTTTCAC
AAATAAACTCTCCTTATAGATTCAATTGCTGTCGGAAAATTAAATTATTAATATTATTTTGGTAATCACGGGTAATTGTTGCCCATCAATTCCGTTGAGTACCATATGCGTA
AATCTCTAAGGACGTCAGTTCAGTATTGTTAGCATATTTATTTAAGAAAAATCTTGCCACAATCAACTTAAACAAAGTAGTTAATACTCGCGCTTTTAAAGCATTTAATAAGC
CGCAAGTGTATTAATTTAAATATTTGCCACACAATCCTGTGTTTCTGTCTAGATCCACGTGGTTTTTATGGCTCCTATTTCGCTTCCTACTGCGGTTACCCATACGCACTGTTG

```
ACATTTGCGACGCAAAGAAGACACAAAAGCCGCAATGCCAGCACCGTAAAGACACAACTATGTCTATAAGCGAGTGTGCTTTCTTATAGACTTTATGATTATAAGCAATCTA
GTTATATACATATACGTATTCAGACAAGAAAAGACCCTAATTAAATGACAGTGGCATAAGTATAAATATAAGTAGAAGTAGAAGTATAAGCAAGTGATAAGCTAAGTCGAAG
GGGCATTACGGGCTCTAAGACCGTGGAGAGATTTAAGTTTCATGTTACAGATAATAAATCTTAAATTTCGATTCAGTTTACGATGGCTCGTAAAAGGAGAGAATAACAGCAA
AACAACTGGATAAACGGACATCAATGACGCTGGACTCGGACTTCGACTGGGACTTGGAAGTGGAAGTGGAATTGGAAGTGGATGAGGATGTGGATGTGGATTTGGACTCGGT
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TGGCGGCCAATCATCAATGGTATCAATATTCGCGGTATCGCGGCCAACAACATTCTAAGGCAATTGAAATGCACATAAAATGAGAAACATGAAATTGATTGTAAGCAGCGCC
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CACCCGGCGGTGGTCCACACGCCCATCATCCATCATGGAGCCCACTCGGTGCACTCGTAAGGCCATTCATGTCCAATCTGCTTATCACCACCGAACAACTCACCCCTTTCAT
TTTCAGCCATGTTGTTCATCATCCGGCAGCCGTCAAGGTCATCACACCCGTCGTCCACAAGCCCGTGGTGGCGGTGCATGCTGTCAGGCCGGTGGTTCCATTGGTTCCAGTG
CATCATGCCGCCCCCGCCGTCGTCGTGCATCATTAAGTGCAGCGAATACGGTTCACTTTCAATACCTTTCCCGCTCCCGATCCCGTTCCCGATCCCCACCAGACCCAGACCA
ATCCCTTCCTGAGCACCATAACCACGATCCCACAATAAAAGTTCATAGCCACGTAATTGGAGCGAGTGTTTTCAACTTACCTGTCCAGGGAAACGGCAATCAGGCTGTAGAC
CGAGGCTGCCACGGGAGCACACCTTGTATGTAGGGCACAAACTTGCACATCAGCCATCCGAGCATCCAGGCTGCGAGTTCCAGCAGTTCGCGAAACATGAAAGGGGGAAAGTG
TATGGCAACAAAAAAAGAAGAAGATGCAGATTTTTCTAAAATACCCCAAGGACACTTTGCCGAAGGAGTTTACCGAGTTCAATGCTCGACCAGGAGCACC
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CCAGCCATCGTAGTGGGTGGGGCAGAATGTGGAGTCCTGGGGGGGCAGAGCATTGTTGCCCAGACCCAGACTCAAAGCCGCGGTGGACCGCAGGACTGCCTAACTTAATTTG
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GCTAACTTTAATATGATTTGGCACATAAAAATATAAATATTATTGGCGCTGTGGCGCTTCGTCAAGTGAACTCTGTGGCTGTGGACAGGTTTTGGTTCTGGACAGGATCAT
GTGTGTCTGCTGGGAGGACATACACATCCTCCCGCCTGGCAAACAATCAACAGTGTGTACACAGGACAGCAGACCGAATTGGTTTTTCGGTTTTATTCCTCCGATTTGAAAT
GGCTTTCGGGCAGACCTGCAAGTGCAACAGACTGGATCCGAGGCTATTAATGCGAGTGTATTTGGCCACTCACTTGATATTATGCTGATAAGGGTGAACTTTGATATATAGC
TGTCTGCGGGAGCTCTTGACTCGGCAAACTTTATGCTTTCAAGTTGTTTGAAAACAATTTAAATTCAAATTCGGTTCCGAAATGCTTCATCACTTGCGGGACACCGGATTAG
CAGTGCCACTGGGTGAACTTTTTTTTTTTTTTAAATACATGTTCTTCCAACTTCCCTTCGGCAAATAAACTATCTAATTGTGTATGCAATTCTATTAGGACAGGCAAACGTG
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CAAAAACCGCATTATATATAAAAAAAAATCAAATAGGTCAAGGGTTATGCCAGTAGTTATTTATAGATACCACAAGCTTAGGTAAGACATGATTATTTCAAGGAACACCGAGT
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CGAACCTCCTTGTGGCATTACCCATTTGAGGACTCAAGTGAAACCAAACACTCCACAGTTTGCTCGGCCAACATCCAGCCTCCCCGTCAAGGTGAGAATGGGATGGGTGTTT
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AACAAACTGGCAACGTGACTGAAAGATTTAGCCAACGGGAGATGCTGATCTAAAAAGGGCCGTAATGATAACGATTCCCATTGATAAAATAGCACAACAATGGCCATAAAG
CGCCATCTGAGACAATTGCCGTTGCTGTTGCAAGGATATCCTTCGTCTCAAGGCGGCATCGTTGCTGGGAAATCAATTCATTTCGCATTTTATTGGATTTCAAAGCACACAC
ATAAATAAAGGGCCAGCGCCACATTCCGACCAACAACCACCCACCCACCCCCCAGGCCCACCAGCCAGGAACCACCCACAAAGAGTACACGGCCCAATACCAATACA
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TATTTAGGTCAATTCATCCAGCCGCAAAGAGCCTTGAATGCAAACAACCTTCCATTGCAATTCTGAGGCTTGAAGGTGTGCTTAGATAATGGCGCTGCCAGCGGCGATGGCC
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CATGTTTTTTCCCCTGCATTAGTGCTATTTCACCGTTGCCGCTGTGAAACCGTTGCCTTCGTTTTAACTTCAGCAGGTTGTCGAAAGTGAATAGGAATGTAAGTGGGGTTGA
GAGTTGTGGGGATGAAGAGGTGAAGCTGAAATGAGCCACCCCAAAAGCCCCAATGCCAGCGGGAGGGCTGCAATTTGTTGTGACTGGCGTTTTTGCTAGGCATCGGCGGCTC
AGCTGAAGCTAAGACATGCCAAGCGAAAATTGCGGAGTGGGCGGCCAAAAGGGTGCCCCATCCAAACAACCATACAACCATCTAGCCCACCCAATCTACCATCCACCGCCAG
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TCCCCCACAGTGGGCTTCTCTGGGGAGTGTATTGGTATGGGGTGGGTCGAGTGCAGTGCCGAGTCTAAGAGTAGAGCTGCATTGGAAAATAAATCTGATAAGTCAACTGC
ATCTGCATATTTGTTACCAGTTTGTAATATTAATATTCAGGTTAATAAATAATCTGAGGGGAAGAGGAACTAAAACTATTTTTATTATTATTATTATTAATTTAATTTAATT
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CACAATCGGAATTTGATTTACCAAGGATTTCGATCATTTTTCCATGTCAGCGGGCGATTTGCATAGACATTTGCCAACCTGCTCACCTTGTCGTCCAGGTCTGCGACTATCAA
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AGATGGACGGATGGATAGGCATGTCAGGGAAATTTATTTAAATTAAAGCATACAATTATGCGTAGCCTCGTTTATCGGGTCGTTTGTGGGTCGTCTCTGGGATTTGGTGGAA
TTGGCCTCTAATTAAATGGACACTTGTTCTTTGGTCCATGCGGATTGTCGTTTCCAAGAAGGTAAGGGCTCCCATGGAGAGAGCACAAATTAATTTAATTGAGTGCAACAT
CCGTTGCTACGGAAATCTGACACATTTCTGGTAAAGTACGCTGAATGAATTCTTCTTTTTTTCTTTGCTGCGTACTGTGTGAGATGTAGTTCCTTGATTTAATGAATAACTG
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FIGURE SHEET 22

23/89

GCTTTTGTCTTGGCAGTCTATTTTAAAAGTTATCTTGACCATTGCAGAAAGCTATTAAATTTTGATACTAAAGCTTGGCATTTTCCAGAACAACTTTAATGATGCTGCATCG
TTATGTTCTTCTTGTGTATGTAGTAAAAATTCGGAAGAAGCCAGGGAGTCTGGTATATAAAATGCAGCTTACAAATAAACGGAAACACAGTATGTCTGTCAAAAGTAAATAT
AACCGAGTATGAATAAAATCCCATAATTTATTATTTTCCACCAGAAATATGAGCACTTTCGTTTGGACATTTATGCCGACATTATGTCTAATGAGGGTCAATTACACTTGCC
CAAACATATCGGGCACATTACGCATACGCAGCGTAAGCACGCAGGAGCAACAACTTTCGTCAGTGCCATTTGGCAGGGCTTTATCTAAAGCGGCGATTAATTGCAGTACATA
AATCGGGCTAATATGCAGAACAAACAAAAAAAAACTTCGGCTTCCCCCTAGCAGCTAACGTGGCCCCCAGTGGCGAATAAATCTCGTCGGCATCTTGCGGAATTAAAGAGAT
ACTTACGCACAAAGATGTTGCCAATCAGTGTGGCTGGCAGGCAGAAGACAATGACCAGGATGTCCGCAATGGCCTTTTCGTTGGAGAGGGGGGAATGTAAATTTTATTTCAA
ATTAATGGGGTTCATCCACGAGATTTACGGGGTCCACCCACCAGATTCACAATGAAGTAGTTCGTCACCGTCCGCATGCGAGGAGCCCGCAGGACGACGGCGATCACGAAGC
TATTCCCGATGAGTCCCACCAGGAAGACGACGATGTAGGCCACGCAGTAGACCATGGACATGGCCAGCGAGTGACGGTAGAGTGGGTCGAATCCGAAGTCCACGCTCCCGTC
CAGCTGCTCCCACCGGAGGGCACTGTCGTTGTACGACTTGGTGGCCGCAGCCGCCGAGATCAAGCTGGTGGTCGCCGGCGATAGGTTCAGCAAGTTGGAATAGTAGGTGGAT
GAAGTGGCGTCTGCGATGGCCAGCGACTTGCCCGCCAGGGATCCTCTCGCGATGCTGTTGTGGTGGCCGCCAAGGTGGCTAGCAGCGAACTGGCCGCCGGAGCCACCGTGG
CCGTGGCCGTAGTGAGAACCGTGCCCAGCAGAGTGTCCGTAATGGCGCTGTTATTCAGTTTAATGGCACTCGATGAGCCCAAGGAGCTGACAGCAGTCCCACCGCTACCACT
AGTGCCATTCAATTCGTTGAAACTCAAGAGGTTCTGCAAATCGACGAAATTATGCGTGAAATTATTGTAATCCCCGGCGAGGGCGGCGGCTTCCTCCATTGTCTCCGCGACC
ATTTTCCCCGGCCGCCATGGTCGGAATGGGCATGGGTACACTAGTCGTCGTACTGGGAACGTCGCCACTTGTATGGCTTTTATGCTTTCGCTTGCGAATCCGCCCGCTGGCTG
CCATCATCAAATCATCCGGCGTCTTGATTGGGCGGATGGCACTTTCACTGGCGCCTCGCTTTCGCTATCACTATCTGTAGACGTATCTCGAATCTTGAATCTGGTATCTCGC
TTGTTTTAGAAAAGGTCTATAAAAATGGCATCGTCACTTGGCATTTCGTTGGCTTGTGTAGGATATGCAGGAAGTTTCGTGGCTTTGGGTTAGAGAACAGTTTTTAATTAAC
ACCCATGTCCATACAATATCTCGTTTATCCGGGGATTGTTTTGCGTTTGCCCCGAAGTTGCACAATAAATGCAGTTTTCTAGAAACTCGCTTCTAGCGCCCAAGGACCCTTC
CGTTTTCGTTTTTTTTTTTTTTGATTGAAATCACCTACAAAAGTTTGTTGCCGTTTCGGCTGCGAATCCGAGTGCGGAATGCAATGCATTGCCTGGGTCGTTCGTCAGCTGG
TTGACGTTGCCTTGGCTGGCATTACGGAAAAGTCGGCGGCCCAAGGCCTCGTGTGCATATTTCAGATAAGGCCAGATGCTGGGTGCCTGGATAAATGCAGCTAGAGGGGATT
GGGGATCGGGCATTGGGCATTGGGCATTGGGCATTGGGCATCGGACATCGGGCAAAGGAGCCGAGAGCATCGGCTCAGGGACATGGTCACCGCCACAGTTGCAACACATGCG
CGTCGCTAATTAATTTTAATGCCCGTTCTGCCATTGTTTGGCTGTTGTTTTTGGCACAATTGAAAAGCCAGCGAGCGTGCACTTTGACCTCAAAAAATCGACACCAAACATC
GAACAAACGAGCAATTGAGCAACTCAATAGCAGCGCATAAAAAATTCCATTAAGCACAACTGCCAAGCGCACGCAGCACTCTTCGATTGAGTGCCAAAAAATTGCCAGTAAGC
ATTGAAACAATTGGTAACAAACGAAGCCAGTGCGACATTCTTTTGTGCGGTTCCATGGGAGTGTCCACATCAGACAAACTGGCGACTAAGGGCCCCTCGGCACACAATTCA
(SEQ ID NO: 43)

Exon: 13111..12362
Exon: 12281..12156
Exon: 1649..1001
Start ATG: 13111 (Reverse strand: CAT)

Transcript No. : CT18916
ATGGATGGCAGCCAGCGGGCGGATTCGCAAGCGAAAGCATAAAAGCCATACAAGTGGCGACGTTCCCAGTACGACGACTAGTGTACCCATGCCCATTCCGACCATGGCGCCGG
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TGGCACTAGTGGTAGCGGTGGGACTGCTGTCAGCTCCTTGGGCTCATCGAGTGCCATTAAACTGAATAACAGCGCCATTACGGACACTCTGCTGGGCACGGTTCTCACTACG
GCCACGGCCACGGTGGCTCCGGCCGGCCAGTTCGCGTGCTAGCCACCTTGGCGGCCACCAACAGCATCTGCGAGAGGATCCCTGGCGGGCAAGTCGCTGGCCATCGCAGACG
CCACTTCATCCACCTACTATTCCAACTTGCTGAACCTATCGCCGGCGACCACCAGCTTGATCTCGGCGGCTGCGGCCACCAAGTCGTACAACGACAGTGCCCTCCGGTGGGA
GCAGCTGGACGGGAGCGTGGACTTCGGATTCGACCCACTCTACCGTCACTCGCTGGCCATGTCCATGGTCTACTGCGTGGCCTACATCGTCGTCTTCCTGGTGGGACTCATC
TGCCAGCCACACTGATTGGCAACATCTTTGTGCGTAAGTATCTCTTTAATTCCGCAAGATGCCGACGAGATTTATTCGCCACTGGGGGCCACGTTCATTGCCATCTGGTGGC
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GGAGGTCTTCTCCGACGCCCTGGTCTCGGCCTACTCGCAGCCGCAGTTCCTCTGCCAGGAGGTGTGGCCCCCGGGCACGGATGGGAACCTCTACTTCCTGCTAGCCAACCTG
GTGGCCTGCTACCTGCTGCCCATGTCCCTGATCACGCTCTGCTACGTGCTCATCTGGATCAAGGTCTCCACGAGGTCCATCCCCGGCGAGTCCAAGGACGCGCAAATGGACC
GCATGCAGCAGAAGAGCAAGGTGAAGGTCATCAAGATGTTGGTGGCCGTGGTCATCCTGTTTGTTTTGTCCTGGCTGCCGCTCTATGTCATCTTTGCGCGGATCAAATTCGG
CTCGGACATCTCGCAGGAGGAGTTCGAGATCCTCAAGAAGGTGATGCCGGTGGCCCAGTGGCTGGGCTCCTCGAACAGCTGCATCAACCCCATACTCTACTCAGTGAACAAG
AAGTACCGACGCGGATTCGCGGCCATCATCAAGTCGCGCAGCTGCTGCGGACGCCTCAGGTTAGTTAAT
(SEQ ID NO: 44)

Start ATG: 1 (Reverse strand: CAT)

MMAASGRIRKRKHKSHTSGDVPSTTTSVPMPIPTMAPGKMVAETMEEAAALAGDYNNFTHNFVDLQNLLSFNELNGTSGSGGTAVSSLGSSSAIKLNNSAITDTLLGTVLTT
ATATVAPAASSLLATLAATTTASARGSLAGKSLAIADATSSTYYSNLLNLSPATTSLISAAAATKSYNDSALRWEQLDGSVDFGFDPLYRHSLAMSMVYCVAYIVVFLVGLI
GNSFVIAVVLRAPRMRTVTNYFIVNLAIADILVIVFCLPATLIGNIFVRKYLFNSARCRRDLFATGGHVHCHLVAPEADDKATCPHHDNRHMGNRAGDHHSLAALLRPGARR
GGLLRRPGLGLLAAAVPLPGGVAPGHGWEPLLPASQPGGLLPAAHVPDHALLRAHLDQGLHEVHPRRVQGRANGPHAAEEQGEGHQDVGGRGHPVCFVLAAALCHLCADQIR
LGHLAGGVRDPQEGDAGGPVAGLLEQLHQPHTLLSEQEVPTRIRGHHQVAQLLRTPQVS*
(SEQ ID NO: 45)

Name: Tachykinin receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384554
TGTTTGCAGAGCCCACAGCAACCAATATGTTTTCATTGTCTGCCCGGTTTGTCGCTCAATTTATTTGTGATGTTGACTTTCCAACAGTGACGTCAGTGGAGGCCACAGACAA
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GAATGAAAATGCGGGACATTCTTGAAGTCGTTGCCTTTATTCTGCTTTCACACATAATTATGAAATAAATATTAGCTTAAACCAAATTGACTACAACGTTATGCTCTATTAA
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TGGATTGAAACCTAGCTTCTGAGTGGTGGCAAAAAATCTTAATAGTTTTCGAAACACTTATTTCATTAGGATACCATATACTTAAATTAATTTCTCCAGTTTAAAGTTGAT
CTTGAATAGATTCAATTACCCATTTTGACACTTTGACATTTTTAATTTTTTAGAGTTAATTAAATGCCGTATAAATGTTATCTTAACTATAGATTGCGAAGTAGAAATAGGTTTG
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TGTCCGTGTTCCCCTTTAGAGAAACTCCGCGTCGCTAAAGGACGTGGGACCATGAATCGAGAACGCGGATCTTTTCCGGCTGGTGTGGGCCAGCTATCATACCTCCGACATG
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CGCAACTGTTGTGAAGCCGACGACCAACCGTGGACGACGGTTTTGCTGCGAGTTGTTGCGGTATGACTTGCAGCAGCATGTGAACCACTTAAAAGGCGGAAAGCGACTGGA
AATATAATAAAAATAAAAAATATCAAAGTAAGTAAATTAAAGCATAAGAAAATGTGTAAGATTTTTTAACATGAAATCTTAACATACCTTAATGTGCGAAAGACCTGCGATGA
GAAGAGGCAATAGATTAGTGGATTCGCCGCCGAGTTCAGCGGTGCCAGACTTTGGATGAAGGTGGCGATGGCAATGTTCGTCTGTGAGTGTGGAATCTGGCCAAAGACCTGC
AGCAGATCGAAGATGATATACGGCGACCAGCAGATGATGAACACAAACACGATGGTCAATGTCATCTTGACCGTTTTGACCTTTGCCCGTGGAATAATGCCCCTCGAGCTGG
CCCTCCTGGCAGGTGCAGCTCCAAAACCAGCACGTTCTGTTAAAATATAATTTAACAAATAAAATAAAATTATTTTTGGGAACTCCGATTTGGCAATATGCATAGCCAGAAGA

FIGURE SHEET 23

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TATCTTACCCGTGGGTACAAAAATGGAACCCTTTGCCCAAATCGTCTTTACGATGATCGCATAGCAGGCAGATATGATCAGCGCAGGAATGGCAAATAGAGTGGCCGACACC
AGGCTCATGTACACCTGCCAGGCGATCGGTGAACCCAACTCAATCCAGCATTGCGGATGTCCTTGGATGAGCTTCTCCTCGTACAAAACCAGGATGGGAAGCGAAAACAACG
CCGAGATGAGCCATGCGCCAGCCACCAGGTGACGGGCTCTTTTCCCTAAAAGCATAAAATTTAAATATATATTTAAGTGAAATATATTTCTAATTTAACTTAAATTTGTATA
TTTTTTTGGTTAATTCCCGAACTAAATTATCCAAGCAGTGTAAGCAGAAGCCACAAACAGCGCTCATCTTTGGCTAACAACATTTGGCAATTAGAAAACTTTTCATACGAC
GACTTAACTTACACGACTTTGAGAAGTTCATGGGGTGTGTGATGGCATCGTATCTGTCGATGCTCATGGCCACCAGCACGTAGGTGGACGAGTATGTGACGCAGACCTGCGA
GAAGCGGATGGCCTTGCAGGCCAGGTTGCCTGCCCGCCACGAAATCGTGATGCGCCATATGATGTCGGTGAGGACGTTGAGCAGTCCCACGCACAGATCTGGAAATAATGGA
CTGGGCATTAGAAGCAAGGGAAGAGGTCAGTCCCAATCCCAAAACTCACCTGCCAATGCCAGCTGTTTAATGAAGTAGTTCATCCGCGACTTGCGATTCTTGTTGATGAACA
TCACGAACAGAACAGCTGAATTGCCCAGAACGATGACGGTGAACAGGATCCAGAGCACAGCAAACTGTTCGGTCTGGAAGAGTGCAAAGAACAAAGTGTGGTCACATTTCAT
TAAACGCCTATCAAGTTCATTGTCAACAAAGTGTTAAGCACGGAAATCACGCATAAAACTCAATTTAATGCCATCCAAGCACACACACACACACACACGCCTTGTTTATGGCTC
TTTAAATAGCCATAAAAATGATAGAGCTATGAATTCAAGCTGGTTGGTGCGGCGGGCAGGATGTGCCGGCGGAAGTTTGCTTCTTCCAGTTCAGTACTAACAAGACTAGGAC
AACACGACATCCTGCACTCAAACACCCGTGGACGCTCACCCACACACCCAGACGTGATGGAAGACAGACAGCCACCGTTATTCCAGCAGGAAATTGCTGCCAAGATGAAGGA
CCTGCACTTCGAAAAATATTTCTTTCGACTTTTAAGGCAGTTTCACAGCTCAAAATGCGTGGCTTGGTATTTAATTTATAGAACTTATACTCCAGGCATTCGAAATTCAATT
CATAGCACTCAAATCTAAAATTGTAACAATTCTTTATATAGAAAACTAGTAGATAAAGAATAATGAACCCTTATTACTTTTACTTTTTTAACTGAACTGTTATTATTTTAAAA
ATATTTTAAACAGTGTGAAGTGCAGATATGACAGTGAGTAGTTCTGCTAGTTCTTAGCTTATTGCCGAAGAAAATGAAATATTCTTTATACGCCCGCATGCAGTTTATATAGC
AGAATATCGCATATATGCTAATATGACTAATGATCTCTTCATGGTATCTACAAAGTTTTTTGCTGCAAATTAAATTTGCTCTCAAGGCATCTCCCCCTATGCCCACGTCTAT
TGAAGTTAAGTTTGAATTATGGCCTCGGGGTCTTGCAGTCTGACGCCAACACCGATGTTGATGCGGACTTACTTAAGGGCAGGCCAAGTAAACTTGTCCCGAAAAAAAAGCT
GAAATCCTGACAGGCTTCGTCCTTGGAACTGCGCTCAGACTGAAGACGCCCCACCTTATTCTACAACTTTTTGTCCATACCAAACTTGCAGTATTCACTTTTTG
(SEQ ID NO: 46)
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Exon: 2688..2514
Exon: 2450..2253
Exon: 2061..1801
Exon: 1716..1431
Exon: 1339..1111
Exon: 1042..1001
Start ATG: 2688 (Reverse strand: CAT)
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Transcript No. : CT19191
ATGAAATGTGACCACACTTTGTTCTTTGCACTCTTCCAGACCGAACAGTTTGCTGTGCTCTGGATCCTGTTCACCGTCATCGTTCTGGGCAATTCAGCTGTTCTGTTCGTGA
TGTTCATCAACAAGAATCGCAAGTCGCGGATGAACTACTTCATTAAACAGCTGGCATTGGCAGATCTGTGCGTGGGACTGCTCAACGTCCTCACCGACATCATATGGCGCAT
CACGATTTCGTGGCGGGGCAGGCAACCTGGCCTGCAAGGCCATCCGCTTCTCGCAGGTCTGCGTCACATACTCGTCCACCTACGTGCTGGTGGCCATGAGCATCGACAGATAC
GATGCCATCACACACCCCATGAACTTCTCAAAGTCGTGGAAAAGAGCCCGTCACCTGGTGGCTGGCGCATGGCTCATCTCGGCGTTGTTTTCGCTTCCCATCCTGGTTTTGT
GCTGATCATATCTGCCTGCTATGCGATCATCGTAAAGACGATTTGGGCAAAGGGTTCCATTTTTGTACCCACGGAACGTGCTGGTTTTGGAGCTGCACCTGCCAGGAGGGCC
AGCTCGAGGGGCATTATTCCACGGGCAAAGGTCAAAACGGTCAAGATGACATTGACCATCGTGTTTGTTCATCATCTGCTGGTCGCCGTATATCATCTTCGATCTGCTGC
AGGTCTTTGGCCAGATTCCACACTCACAGACCAACATTGCCATCGCCACCTTCATCCAAAGTCTGGCACCGCTGAACTCGGCGGCGAATCCACTAATCTATTGCCTCTTCTC
ATCGCAGGTCTTTCGCACATTAAGTCGCTTTCCGCCTTTTAAGTGGTTCACATGCTGCTGCAAGTCATACCGCAACAACTCGCAGCAAAACCGCTGCCACACGGTTGGTCGT
CGGCTTCACAACAGTTGCGATTCGATGAGGACACTGACCACTTCGTTGACGGTTTCCCGAAGGTCCACCAACAAGACGAACGCCCGTGTGGTAATCTGCGAACGTCCCACCA
AGGTGGTTACCGTGCCAGCCATGTCGGAGCGACGCGGAGTTTCTCTAAAGGGGAACACGGACATCCTGTGA
(SEQ ID NO: 47)
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Start ATG: 1 (Reverse strand: CAT)
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MKCDHTLFFALFQTEQFAVLWILFTVIVLGNSAVLFVMFINKNRKSRMNYFIKQLALADLCVGLLNVLTDIIWRITISWRAGNLACKAIRFSQVCVTYSSTYVLVAMSIDRY
DAITHPMNFSKSWKRARHLVAGAWLISALFSLPILVLYEEKLIQGHPQCWIELGSPIAWQVYMSLVSATLFAIPALIISACYAIIVKTIWAKGSIFVPTERAGFGAAPARRA
SSRGIIPRAKVKTVKMTLTIVFVFIICWSPYIIFDLLQVFGQIPHSQTNIAIATFIQSLAPLNSAANPLIYCLFSSQVFRTLSRFPPFKWFTCCCKSYRNNSQQNRCHTVGR
RLHNSCDSMRTLTTSLTVSRRSTNKTNARVVICERPTKVVTVPAMSERRGVSLKGNTDIL*
(SEQ ID NO: 48)
```

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Name: Vasopressin receptor-like
Classification: G_protein_linked_receptor
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Celera Sequence No. : 142000013384294
TTCCAATGCGATTTAAGGTAATTGACTATAAGTACCCATGACGAACTTCTGGACAGTTCCCCAGTGGAAAAAAAAAACTGGATTTATTTCTTATCGCAAAACTTGCGATAAC
CAATTTGTATATGTTCATTCAGGGAGCGTGCCGATTTTTTAGTTTGCGAAATTGAGTTGTTATGTTTTCTGAGTCATTGTCGAGCGGGTTTTGGTAGCCGGGGATTAAATCT
GCTGTATCATCTTGGTCCAGCGTTTATTTCTATTTGCTTTTAATTTCACAATCAAAACAGCAATAATAAAACCGTGCCTTATCTTACGGACATATCTCCCCAAGCGTCGTCT
CGCTCTAATTTGGATTTTTCCTCTCTCTCTCGCTCTTTTCTTGCAGCTGGCGCCCGACGGTGGGAATTTCATCAGCTGTTGTTGTTGTTCATTTCACAGCAGCAGTCGGCCT
AATAAAAATGCAATTTTTATGGTTAAGAAAATAGTGCGCGAACGCCGTTGTGTTGCACATTGGAAATTGTGCAGAAGCCAGAAGAAAATGTGTCTTGGAAAATGAAAAGCA
CGAGCAGCAGTAGCACCAGCAGCAGCTATAACATTGAGCCAGTGATGTAATACAGAGCAAAAGTGAACGGCGGCAATTGGCATTGCAAAAAAGAAACAGATTATACAATTT
GTGTTGCTGCCGCACTGAACTAGGACAACAGCAGCAACAACAGCAGCAGCAACAACAACCACTAGTGATAAAGACCGGCTGGCAACAGTGCAGCGGCCACTTGCAGCAACAT
AATTTCAAAGTCGGAGCGTGGGAATCGCAAATCACGGCAGTGGCAGCAACAACAGCAACTGCAGCAACACTCGAGCACTCGTGGCTCTCCGGATCGCTCATTTCGCTCGCCG
TTCTCGCGCTGGCGTTTCTCCGTTTCGCTCGCACCCGCCTGTGGAGCAGTCGCGTATATTTGGAGGCGTTGGGGCGAACGCTCACGACAGTTGTGCTTGGACGCTTCGGAG
TGAAGATCGTGCTCGTCCGATCGGTGCGCGTGATAATACACGGCGAACAAAATTGAGTCAAGAGTCAGACGGTCGCAAGACAATTGACAAGACACGAAAAATCATAATAAA
CACAAGTGGAAAAGCAACTGCTTGAGAGCAAAAAAGAAATTGTTTTTTACAAATCTCGCACGTAAATTAGCAAGCGTTCGCAAGAAACAAACCGCATACAATACTGAACACA
AAAAAAAGGGTATTCAACAAAAAACCCAAAAATATTTGGCTGCAAATGTGAAGAGACGAGAGACAGCGGATATACTACCGAGTGAAATTTGTGTCATAAGCAGAGCCAAAACA
AAACCGAAAAGCCAAATTCAATAAAAGGCCATAAGTGACTGTGAACATGTAAAGTGATGTGTGGTAATCGAAAAACAGCATAAAGAATGGCCATAGACCTCCTGATCCTGGC
CCTGCTGCTCGTCTCGTTCCTGATCAACCTGCTGGCGCTGCTGTGTGCCTTTTGGATAACGCCTGGCTTGAGGACCACCGCCAATCGCTTTACGATCAACCTGCTGGCCATCAAT
CTCATTGGTTGCTGCATCTTGGCCCCCACTTTGTTCCTGGGACTGCCGGGAAAGTCTGCGGAGGCATCCACTTCCAACGCCGAGACCCTGGAGTTCTTCTCGAAGCCGGGAA
TGCCACCTACTGTCGCGAGTTGACCATCGATGAGCGCGGAGATGGTGGCTTGTCATCACGGAAACCGAGACACACGAAGAGAATCTCTCGGCCTTTGAGAGCTTACCCACG
GAGGCTCCCATTTTGCCGCCCGTCCAACTGAGATGTTGGTCCATAGACATGACTGCTGCGCTGGGAGCTCTGGCAGTACTGCTCGTGGTGGGGGGACACCTGGTGTGCCGTTA
CGGATCCCCTGCGCTACCACAGTCGCATTTCGGGCGTGAAAACCTGGATCTTCATAGCACTCACCTGGGTGGTGGGCATACTCTTTGGAGCCCTTTCCGGCTTCCGAGTTTT
GGACTTTGAGGCGGACGCCCTGTTCAGCAGACAACGCCGCCTGGCAGTCACGTACTTCAACATCAGCAGCACCAATAGTATTTTCGGAGTGGTGTACGCCAGTGTCTACTTC
ATCGTGATCATCCTCCTGCCCTTCGGCTTCGTGTGCGGAATGTACTGGAGGATATTCAGTGAGGCGCGCGGAAATGGGCTGCGCATGCGCCAGAATGGCTCTTCGCCGCTGC
TGCAGAGCGCCTTGAATCTGACGGCTGGCCAGCAGGCGGCTCAAGCCAACCAGTTCTCCAATAGCTTGTGTGTTCATCGGCATTCCATATCCTCGGCCAGTTCGCATGGCGG
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FIGURE SHEET 24

25/89

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CAACAGCAGCTTGGGGCTTGGGCGGTCTGCAAATGCAAATTGATCAGCGCCAACAGCCGAGGAGTTCGCCCAGTTGTCTCCGTCGGGACTCGGCCGCGAAAGTACTTTTGCCC
ACCATCTCGGATGATGGTGGCTCAGATGCGGAAAGTGGAGCCGGAGTTCAACTGATGCCCGTACAGGAGCACTCACTGTCAGATAGAAATCAGAACATTATGCTTACTCTGC
AAACAGCCAGTGGTGAAATAAAGAGGAACTACTCCGCCAGACAGCTGCCCCTGTTGGGCACTTCTTCGCAGGATCTGAGGGAGACTAATCGTCTGCAGGGCATACGCCAGGT
TTGCACCTGCAACATCAGCAGCAACAGCATCATCACCACCAGCAACATCATCCGCACTTCAGTTCGCCGCGCCACCAGCAACACGGCCACGCCCTCCAGATACCCGCCATTC
ATGCCTCCCCCAAGGCTCTGAGTTACATGAGCTCCTTGCGACACCGTTTGAGCAACGCCAGTTCGCTATTCAAATACCGTGAGGAGTCGAGAGCAGCCCGCATCAGCATCCT
GGTGGTGGTGATGTTTGTGGTCTCGTACCTGCCCTTCGGACTGCTGGTACTCCTGCAATCGCGACTGTCGGCTGCTAACTTTGGCGGATCCTCCCAGCTGGCCATCTTCATG
ATCCTGCTGGCCAATCTCAGTTCGCCATTCATCTTCGCCTACAGGAACAAGAGGGTGAGGCGAGGAGTCAAGCGGCTGTTTGGTCTGGATTCGTCGTCGGGCCTGCAGCGCA
ACTGCAGCAGCAGTGTAAAGACCAATGGCACCGCAGGTCCTGCTGCAAGTGGTGCACAATTGCAGCGCAACAGCAGCAAGTTGTCGCAGTACAGCAGCAACAGCTGCAAGTA
TCTCACCCCCCAGAGTTCCCTGGTCAGTGCCGGTGCATACGACCTTGACGTTAAGGCCCAACAGCAGCTGCAGCACCATCATCAATTTCGGTGGCGCCAGGGGCTCA
GCGGACTCCGATGAGCAGCCACCGGCAACACCACCACCTACTGTGGCAGTTGCTCCACCGCCCACACGACCGCAGCGCCCCAAGCTGCAGAGGGGCATCACCATCGTTGAGC
ACATAGCTATAACACCAACCATGCCCCAAAAGTTCCAGAATCGGCGCGCCAGGCTCTTCGACATGTTCTTCCGCAGCTCCAAGAAACTGCAGGCGGGCTGCCAGAGCCAGAG
TTTGCCCACTGAGGTCTAAACGGGGGGGTTATGATAACTATACATATAGGAAGGTAAACAAACACTAAACTTGCTTGCTGAAGAATTCTAAGAACAGTATTCGTAATTTGTAA
GTCTAGCAATTAACAAAGACAACTGTTGAATTTGAGTTTTAAGACCAGATCATGCTGTCCTAGAAGCTTCTCATGCCAAAAAACAAAACCACAAAGAAAGTCAAACTAGAA
AGTTTGAGATGCTTTAAATTAACAAAAAAAGAAAAGAAAAAAAACAAAAAACAAAACAAAGTACCTTTTAAAAAATAGAAAACTGTGTACAAGTCAAATTAACAAAGATTGAG
AGTGATGGGAGTTATAATCTTAGGGTGGATATCAAACTGAAAAGTGGAACCAAGCCAAGCCAAGTTGAGATCGTAATCAATGTACCTAAGCAACTTGCATATGAACATTTAA
TGTTTTTACTCAGATGAAATCACAGGAAAATAGCAAAGACAGCACAGCTTATTCGAACTTCCCCAACTAGTTTATTATTTATTGAAACAATTGTAAATATTTATTAGACATC
CACGCCGCAAAGCTTTAACTCCAAAAACATTCTGGCTAAACAAGAAGAGCGCATACATTCGATTCATAAGTTAATTAAGTCAATGTGCAAAGCATATGTGTATTCTAGAGT
TTAAGTTGTAGAGCCGAGTAGTCTTACACCGGCACCTAGTGCCGAGCAGTGCTTTTTCACCTGCCCAACTGGAGCGTCTGTTGCAGGCGGCATTTTCATATTGAAAATGCA
TTTTGGCCAGTGCACAGTTGGTTTTCCAGTTGGCCAGAATGTCAGTCAGCAGTTAGTTAGCCTTTGGTTAGCCAACGGCTATTGGGCCATTAAGTCAATTTGCTTTTTAGAA
CACCGCGGGCATTGCGTGCAGCTAAATACCTCATTAGTTATAATTTGAAGTGCGAGATGGATGGCGGCAATAGGTCAAAGGTCGGAGCCATCGGCACGGCCCATGCATAATG
CATGGAAAATGTTCGATTGCCCCTGGCATTTGTATCATTTGCTTTACTATGCTGCAGGCCAGAAAGCTTTATACCTTAAGTTCTCCTGCTTTGATTTCCCTTGGCTGCACAA
AAAGCCAACAAAAGCAACACACACTCACACAACACAAAAAAAACCTCGAATTTATATTTCTAAAGTTTATATTTTATAAAGAGTGTGTGCATAGGAAATATCTATAAATATTC
ATGCATGTGTG
(SEQ ID NO: 49)
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Exon: 1001..4051
Start ATG: 1431

Transcript No. : CT19320

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CTTTCGGAGTGAAGATCGTGCTCGTCCGATCGGTGCGCGTGATAAATACACGGCGAACAAAATTGAGTCAAGAGTCAGACGGTCGCAAGACAATTGACAAGACACGAAAAATC
ATAATAAACACAAGTGGAAAAGCAACTGCTTGAGAGCAAAAAAGAAATTGTTTTTTACAAATCTCGCACGTAAATTAGCAAGCGTTCGCAAGAAACAAACCGCATACAATAC
TGAACACAAAAAAAAGGGTATTCAACAAAAAACCAAAAATATTTGGCTGCAAATGTGAAGAGACGAGAGACAGCGGATATACTACCGAGTGAAATTTGTGTCATAAGCAGAG
ATCCTGGCCCTGCTGCTCGTCTCGTTCCTGATCAACCTGCTGGCGCTGTGTGCCTTTTGGATAACGCCTGGCTTGAGGACCACCGCCAATCGCTTTACGATCAACCTGCTGG
CCATCAATCTCATTGGTTGCTGCATCTTGGCCCCCACTTTGTTCCTGGGACTGCTGGGAAAGTCTGCGGAGGCATCCACTTCCAACGCCGAGACCCTGGAGTTCTTCTCGAA
AAGTGCAATGCCACCTACTGTCGCGAGTTGACCATCGATGAGCGCGGAGATGGTGGCTTTGTCATCACGGAAACCGAGACACACGAAGAGAATCTCTCGGCCTTTGAGAGCT
TACCCACGGAGGCTCCCATTTTGCCGCCCGTCCAACTGAGATGTTGGTCCATAGACATGACTGCTGCGCTGGGAGCTCTGGCAGTACTGCTCGTGGTGGGGGACACCTGGTG
TGCCGTTACGGATCCCCTGCGCTACCACAGTCGCATTTCGGGCGTGAAAACCTGGATCTTCATAGCACTCACCTGGGTGGTGGGCATACTCTTTGGAGCCCTTTCCGCCTTC
CGAGTTTTGGACTTTGAGGCGGACGCCCTGTTCAGCAGACAACGCCGCCTGGCAGTCACGTACTTCAACATCAGCAGCACCAATAGTATTTTCGGAGTGGTGTACGCCAGTG
GCCGCTGCTGCAGAGCGCCTTGAATCTGACGGCTGGCCTGGCCAGCAGGCGCTCAAGCCAACCAGTTCTCCAATAGCTTGTGTGTTCATCGGCATTCCATATCCTCGGCCAGTTCG
CATGGCGGCAACAGCAGCTTGGGCTTGGGCGGTCTGCAAATGCAAATTGATCAGCGCCAACAGCCGAGGAGTTCGCCCAGTTGTCTCCGTCGGGACTCGGCCGCGAAAGTAC
TTTTGCCCACCATCTCGGATGATGGTGGCTCAGATGCGGAAAGTGGAGCCGGAGTTCAACTGATGCCCGTACAGGAGCACTCACTGTCAGATAGAAATCAGAACATTATGCT
TACTCTGCAAACAGCCAGTGGTGAAATAAAGAGGAACTACTCCGCCAGACAGCTGCCCCTGTTGGGCACTTCTTCGCAGGATCTGAGGGAGACTAATCGTCTGCAGGGCATA
CGCCAGGTGCACAGTTCGCCCAATCTCCACAAGTACACGGAACTGCGCCAGGACTCGCTCAGTGAGGAGTGTGGTTCTCCGCATCTTTTGGGTCACGCCCAGCGGCAGCAGC
AGCAGCAATTGCACCTGCAACATCAGCAGCAACAGCATCATCACCACCAGCAACATCATCCGCACTTCAGTTCGCCGCGCCACCAGCAACACGGCCACGCCCTCCAGATACC
CGCCATTCATGCCTCCCCCAAGGCTCTGAGTTACATGAGCTCCTTGCGACACCGTTTGAGCAACGCCAGTTCGCTATTCAAATACCGTGAGGAGTCGAGAGCAGCCCGCATC
AGCATCCTGGTGGTGGTGATGTTTGTGGTCTCGTACCTGCCCTTCGGACTGCTGGTACTCCTGCAATCGCGACTGTCGGCTGCTAACTTTGGCGGATCCTCCCAGCTGGCCA
TCTTCATGATCCTGCTGGCCAATCTCAGTTCGCCATTCATCTTCGCCTACAGGAACAAGAGGGTGAGGCGAGGAGTCAAGCGGCTGTTTGGTCTGGATTCGTCGTCGGGCCT
GCAGCGCAACTGCAGCAGCAGTGTAAAGACCAATGGCACCGCAGGTCCTGCTGCAAGTGGTGCACAATTGCAGCGCAACAGCAGCAAGTTGTCGCAGTACAGCAGCAACAGC
TGCAAGTATCTCACCCCCCAGAGTTCCCTGGTCAGTGCCGGTGCATACGACCTTGACGTTAAGGCCCAACAGCAGCTGCAGCACCATCATCAATTTCGGTGGCGCCA
GGGGCTCAGCGGACTCCGATGAGCAGCCACCGGCAACACCACCACCTACTGTGGCAGTTGCTCCACCGCCCACACGACCGCAGCGCCCCAAGCTGCAGAGGGGCATCACCAT
CGTTGAGCACATAGCTATAACACCAACCATGCCCCAAAAGTTCCAGAATCGGCGCGCCAGGCTCTTCGACATGTTCTTCCGCAGCTCCAAGAAACTGCAGGCGGGCTGCCAG
AGCCAGAGTTTGCCCACTGAGGTCTAAACGGGGGGGTTATGATAACTATACATATAGGAAGGTAAACAAACACTAAACTTGCTTGCTGAAGAATTCTAAGAACAGTATTCGTA
ATTTGTAAGTCTAGCAATTAACAAAGACAACTGTTTGAATTTGAGTTTTAAGACCAGATCATGCTGTCCTAGAAGCTTCTCATGCCAAAAAACAAAACCACAAAGAAAGTCA
AACTAGAAAGTTTGAGATGCTTTAAAT
(SEQ ID NO: 50)
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Start ATG: 431

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MAIDLLILALLLVSFLINLLALCAFWITPGLRTTANRFTINLLAINLIGCCILAPTLFLGLPGKSAEASTSNAETLEFFSKPGNHQVILRRNGQLVEQDGVVVRRNISENGD
TVETFFKCNATYCRELTIDERGDGGFVITETETHEENLSAFESLPTEAPILPPVQLRCWSIDMTAALGALAVLLVVGDTWCAVTDPLRYHSRISGVKTWIFIALTWVVGILF
GALSAFRVLDFEADALFSRQRRLAVTYFNISSTNSIFGVVYASVYFIVIILLPFGFVCGMYWRIFSEARGNGLRMRQNGSSPLLQSALNLTAGQQAAQANQFSNSLCVHRHS
ISSASSHGGNSSLGLGGLQMQIDQRQQPRSSPSCLRRDSAAKVLLPTISDDGGSDAESGAGVQLMPVQEHSLSDRNQNIMLTLQTASGEIKRNYSARQLPLLGTSSQDLRET
NRLQGIRQVHSSPNLHKYTELRQDSLSEECGSPHLLGHAQRQQQQQLHLQHQQQQHHHHQQHHPHFSSPRHQQHGHALQIPAIHASPKALSYMSSLRHRLSNASSLFKYREE
SRAARISILVVVMFVVSYLPFGLLVLLQSRLSAANFGGSSQLAIFMILLANLSSPFIFAYRNKRVRRGVKRLFGLDSSSGLQRNCSSSVKTNGTAGPAASGAQLQRNSSKLS
QYSSNSCKYLTPQSSLVSQVPVHTTLTLRPNSSCSTIINFGGARGSADSDEQPPATPPPTVAVAPPPTRPQRPKLQRGITIVEHIAITPTMPQKFQNRRARLFDMFFRSSKK
LQAGCQSQSLPTEV*
(SEQ ID NO: 51)
```

Name: G-protein coupled receptor-like
Classification: G_protein_linked_receptor

FIGURE SHEET 25

Celera Sequence No. : 142000013384666
ATTCTATTGTCGTAGGCGTGGCAAAAGGTTTTTTGGTAAATCGATAGAAATGTACAAGAGAATGTAATTAATATGAAAAGGTAACAAAAAATTTTGCAAAAGTGTGGGCATG
GCAGTTTTGGTCGGTTTGTTGGCGTAAGGGCATTATCGGTATTTTCCTATTTTCAGCTATATGATGCAGTCGCCTAATTTTGATCAAACTATAACTAAAATTGTATATTGTC
AGAAACAACGAGCATGAATTTATAGTCAATTTATCTTTTTTATTATTTCTTATCTAAAGTTATATGCATATAGAATAAAAACAGATACGAGCTTCCTTAGAAGCGGACGGAAA
TAATGTCTCGAGATCTGGACCTTCATTAAGACAGACGAACATTAGGACAAGGCCAGGTCTACTCAGCTAGGGATCCTGATCAATGTATATGTATTTACTTTAAAGGGGCGTA
AACTTGTATTTTACATGTTACATACTTTCAAGCGAATCTAGTAAACCCTTTTAATTTACAAGTAACGAATATAAAAAGTTGAATGGTAGCGGGAGAAAATTAATTGTATAAT
ATAATATTATCTTTGTTAATCCAGAGTCTTGGCAACTTGTGCACACAATTTTTTTTTTTTTTTGGAAACTGAATCAGTTAATTGTGCCAAAATTTAGAGTGTAGATTTCTT
GGAAATCTCAATGAATTTTATGGTCAAGTTCCAAGAAGTGAAATGCTTAACAAACAACAAAAACAAAACACACAAAAGCAAACAAATTATGCAGAATTATCGGATGTATTTT
ATATGTATGTATGTACATACATATACAAAGAATAATAAATGGGTGGGTCTGTTGGCTTCTATGGAATTTCCAATTTAAGCTGCAATACATGTACATTTTAACGTCTTTCTGT
ACGCTCTCAAATAAAAAAACACAATTTTAGGATTAATAAAAAAACAGATATGTACGTCTTCTATTCCCATGAAGAAAAATATTCATATGATTTTTTGTTTGGCAGGAAAT
GCGAATAGTTATTGGATCGTTCACCGCATTTCTTTTGCTGTTATTGCAAAACTCAAATGCCGAAATTCCCGGTTGCGACTTCTTCGACACCGTAGATATTTCAAAAGCGCCA
AGATTCTCGAACGGATCGTACCTCTACGAAGGCTTGCTGATCCCCGCCCATTTGACAGCTGAATATGACTACAAGCTCCTGGCCGACGATTCGAAGGAGAAGGTGGCGAGCC
ACGTACGAGGATGTGCCTGCCACCTCAGGCCATGCATTCGGTTTTGTTGCCCCCAGTACCAAAAGATGCAAAAGAGCAAGTGCTACGGCGACATGTCGGAGGAC
CAAGCACGATCCCTTCGTGAACGTGACGCTCAGCGACGGGTCGGTGGTCAGGAGACACTTCAAGGAGGATCTGATCGTGCAGTCGGATCTGGCCAAGCCCGGATGTCCCCGG
ATGTGTACTTTCTGAATCACGAACTGCCGGGCAATGAATTCACTCTGTTTGAGGTTACTTTCCTGTGTTTCTGTCACTTCTGAAGATCGTAACCTTTTTTGAATCTCTGTAGAA
CGGCTCTCTTCTGCGTCACTGGGACAAAGTGGAACTGAGCAAGCCGGGAGTACTGCGTCCAGCATCTTTCATTTAAGGATGATAGTATCCGAATTGCACCCCACTTCTGTCC
ACTTTCGTCTGAGCACTCCAGAACGTGGAAGACCGTTGGTAAGCTGAATTCCCTGCTTGACTTTAAGGTTTTTAGTTAATGTCCATTTTCACAGCGATAGTGATATCCTTGA
TATGCATAATCCTAACGATCAGCGTGTACCTCTATGTTGAGAAGCTTCGCAACCTGCACGGAAAGTGTTTCATCTGCTACTTGGCCTCCTTGTTCCTGGGATATTTCTTCCT
GGTCCTCAACGTGTGGAAATACTCCTCCGGCTTCTGCGTTACAGCAGGTTTGCTTGTGGCGATTACAAGATAAAGGACGACCAATTTCACATTTCGATATCATGATCAGGGT
TCCTGGGCTACTTCTCCGTCATCGCCGCGTTCTTTTGGCTTTCTGTCATCAGTCTTACCCTCTGGAATTCATTTAGCGGCAACTCCAGCTGGTTGAACCGTTTCTTGCCACA
GAATCGGTTCCTTTCTTACAATTTATACGCCTGGGGCATGGCGCTGCTCCTGACTGCAATCACCTATATAGCTGACCAGGTGGTTAAGAACGAGAAGTTGAGACCCCGCGTG
GGCGTCGGCAAAAATTGTTGGATCTACAGTAAGTTACTATTCCTATAATAACAATTGCGGTGTAACTCGTTTTTTTTTTTAACCAACAGCTGGGGATATGACTGTCATGATCT
ACTTCTATGGCCCGATGCTACTGATAATTGTTTCAACATAACAATGTTTGTCCTGACGGCTTTTCGTATAATGAAAGTGAAGAAGGAAGCACAAAACTTTACTCAACAGCA
AAAAACAACCAATAGGCTCAATTCGGACAAGCAGACGTAATAATTTTACCATATTTTATACAGTTCTAAATCCAAAAGTTTAAATTTTAAATTATTTTCTATGGCTTTTAAA
GTTACGCCCTATTCCTGCGACTCTTTATCATCATGGGCTTGTCCTGGAGCTTGGAAATAATCTCGTTTTTGTTGAGCAAAAATCAGGCTTGGGCCAAGGCTTTTATGGTGGC
TGATTACTTCAATTGGTCACAGGGCACCGTCATATTTCTGCTATTTGTTCTGAGGCCCAGCACACTGAAGCTACTGAAGGAACGGTAAGTTATCGGTTCTTCCATAGGAGGT
GCAATTAACCTGGTTCTATCATCTGGCTGAGCAGGATTAAGGGTGGGAGGGATGAAGCCGGCGCCAGCGATGAACATATCTCACTTCAGAATACGAAAATTGACCCCAGTGT
TTTTTAATATATGGGTAATGTGAAAATACAGTTTATTAGTTCATTTGGTGTTGGAAACCTTCTATTTTGAATCACTAACAGGCAGCCTAATGATCGTGACCAAAGGCTGCTT
TGCTTGCTCATTATTGCTCACATATCGTATGCTCATATGGGCTACGAATATTTGCTACTTATCACTTTTCAAGTATCTTGATTTCTGCACGGTGTCTAAGCATATCTAAGTT
TTAATTAAATGTTGAATGTAATTGTCCTTTAAGTTATAACTTTTTGCAATAATAATCTATTCCAATCCATCCTAGACGTGCCATCAAAGCGAGATCAAAGCAACTACTACAT
GGGGATATGTACGAATCTTATAGGCATGAATACTCGGCATTTATATACCCTGGTCTATTATTATGGATGGAGGATAAAAACTCAGGAAAATACTTTTCGCATCAGCACTTAT
GTATGCTCACTCGTGATAATAATTTCGTAATAATTCGTACTGTTTTTACTGCCTCAACTTAATTCAAAGAACTACAAATGATTATATTATGACTTTTTATGACAATGACTAA
CTAAAAATAAAAATTTCTGAATATTTATAAACAACTTTAAAATGTTATTAACTTAGGATAATAATAATAACACAGTTTTAATTTATCAAGCACATCGTTAAAAAACAATAAA
TTACTTGAATATAAATTTAAAAAAAAAATGGAATATTGGTTTACATTAACGGTATGCAAAAAATCATAAAAAGTCATAGAACTGAACGATAGAGAAAATTACAAAAAAACGA
TCTAGTCGAGTTCCTCGACTATAAGATACTCATTTCTCAGCTAGTTCTTTCATTTAAAAAATTTCTCTTTCGTTTCGATAGTAATTGGCAAGAAAAAATAATAAAATACAACA
AATTAATGCATTTTTGAAAATTATGGGCGTGACTGATTTGGTCGGTTAGTGGACGTGTCAATATTATGAAGCAAACGTGGACACTACAAACTGAAATATATATATATATAT
(SEQ ID NO: 52)

Exon: 1001..1507
Exon: 1567..1703
Exon: 1756..1951
Exon: 2014..2268
Exon: 2329..2500
Exon: 2578..2772
Exon: 2835..2919
Start ATG: 1007

Transcript No. : CT20339
CAGGAAATGCGAATAGTTATTGGATCGTTCACCGCATTTCTTTTGCTGTTATTGCAAAACTCAAATGCCGAAATTCCCGGTTGCGACTTCTTCGACACCGTAGATATTTCAA
AAGCGCCAAGATTCTCGAACGGATCGTACCTCTACGAAGGCTTGCTGATCCCCGCCCATTTGACAGCTGAATATGACTACAAGCTCCTGGCCGACGATTCGAAGGAGAAGGT
GGCGAGCCACGTACGAGGATGTGCCTGCCACCTCAGGCCATGCATTCGGTTTTGTTGCCCCCAGTACCAAAAGATGCAAAAGAGCAAGTGCTACGGCGACATGTCGGAGGAC
GAGCTGAACAAGCACGATCCCTTCGTGAACGTGACGCTCAGCGACGGGTCGGTGGTCAGGAGACACTTCAAGGAGGATCTGATCGTGCAGTCGGATCTGGCCAAGCCCGGAT
GTCCCCGGATGTGTACTTTCTGAATCACGAACTGCCGGGCAATGAATTCACTCTGTTTGAGAACGGCTCTCTTCTGCGTCACTGGGACAAAGTGGAACTGAGCAAGCCGGGAGT
ACTGCGTCCAGCATCTTTCATTTAAGGATGATAGTATCCGAATTGCACCCCACTTCTGTCTGAGCACTCCAGAACGTGGTTGACCATTTTCACAGCGATAGTGATATCTA
TATCCTTGATATGCATAATCCTAACGATCAGCGTGTACCTCTATGTTGAGAAGCTTCGCAACCTGCACGGAAAGTGTTTCATCTGCTACTTGGCCTCCTTGTTCCTGGGATA
TTTCTTCCTGGTCCTCAACGTGTGGAAATACTCCTCCGGCTTCTGCGTTACAGCAGGTTCCTGGGCTACTTCTCCGTCATCGCCGCGTTCTTTTGGCTTTCTGTCATCAGT
CTTACCCTCTGGAATTCATTTAGCGGCAACTCCAGCTGGTTGAACCGTTTCTTGCCACAGAATCGGTTCCTTTCTTACAATTTATACGCCTGGGGCATGGCGCTGCTCCTGA
CTGCAATCACCTATATAGCTGACCAGGTGGTTAAGAACGAGAAGTTGAGACCCCGCGTGGGCGTCGGCAAAAATTGTTGGATCTACAGTAAGTTACTATTCCTATAATCTA
CTTCTATGGCCCGATGCTACTGATAATTGTTTCAACATAACAATGTTTGTCCTGACGGCTTTTCGTATAATGAAAGTGAAGAAGGAAGCACAAAACTTTACTCAACAGCAA
AAAACAACCAATAGGCTCAATTCGGACAAGCAGACTTACGCCCTATTCCTGCGACTCTTTATCATCATGGGCTTGTCCTGGAGCTTGGAAATAATCTCGTTTTTGTTGAGCA
AAAATCAGGCTTGGGCCAAGGCTTTTATGGTGGCTGATTACTTCAATTGGTCACAGGGCACCGTCATATTTCTGCTATTTGTTCTGAGGCCCAGCACACTGAAGCTACTGAA
GGAACGGATTAAGGGTGGGAGGGATGAAGCCGGCGCCAGCGATGAACATATCTCACTTCAGAATACGAAAATTGACCCCAGTGTTTTTTAA
(SEQ ID NO: 53)

Start ATG: 7

MRIVIGSFTAFLLLLLQNSNAEIPGCDFFDTVDISKAPRFSNGSYLYEGLLIPAHLTAEYDYKLLADDSKEKVASHVRGCACHLRPCIRFCCPQYQKMQKSKCYGDMSEDEL
NKHDPFVNVTLSDGSVVRRHFKEDLIVQSDLAKPGCPRMYFLNHELPGNEFTLFENGSLLRHWDKVELSKPGVLRPASFI*
(SEQ ID NO: 54)

Name: mth-like 3
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384666

FIGURE SHEET 26

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AATTAATGCATTTTTGAAAATTATGGGCGTGACTGATTTGGTCGGTTAGTGGACGTGTCAATATTATGAAGCAAACGTGGACACTACAAACTGAAATATATATATATATATC
ATTTCATTGCCCTTAAGTCTGAAAAACGGCTTTAAAATTGAGAAGTTACTTTAAGAGATATTCGAGGTATTCGGTGACAGCAGCGCACATTATCGACTGGCCAATGGGAATA
TTAGATTTGTAGAATAGGGTAATATGTAAACGTAAACCTTTCGATTGTATAAAGCATTCAATTCCTAATATGGATATGTCCGTTCACCAGCCTGTATTAACTTTGCGTGTTA
TTACTTAAATTTATCTTTCTATGTACATGCCAGAAACTGATAGAATGGCACGGTTACCGCCGATAGTCGCTGAGTATGGGGTATCTTATAGTCGAGCACATTCTCGTTCTCC
CTTGACATCGCATATATCGGTTGAGTTGTTCGCATTTTGGGATCAGTCATCTTAAAACTCTGGTCGCATAAACATGTTTTTTGTGTTAGTCGTTCCATTTGACCCTTGCGTA
AGTATTTATATTCAAAGTTTTTACGATTTTGGATCGTTAAGCATAAGAAGGACCACTCGAGTACGCGATTTGACCGTTTTTATACAATTTCGTCCTCTTAGACGAATAAATATT
GTGCCTGCCTTGTTTCTAAAAATGAACTTGCTTCAGCTTCGTAGAGAATGCTTAGTCATAACAGATGGATTTGTTGAATTTATTTTTAACAGTTGATAAGTTATACTTTTAT
AAAAAAAAAAAAAACAACTTACTCAGAATGCTATAGCACATGACTCAATTTTTTGTTTTTCATAAGTATTTAGATCAGTTTTCAGTTTTGCGGAGGTTATTTTGCTACTTTAT
TTCTAATTGTGAACACGTAACTTGGTTTAAAACCGTATATACTTACAGAATAGCATACATCATTTGAATTCAGTTGCCTATCATATTAATTTCCTTTGCAGAAAATGCGGAT
ATTGTTAATTGCAGTTCTTTTTCTGTTGATGCCAAAATCAAATGCCGAAATTCCCGGTTGCGACTTCTTCGACACCGTAGATATTTCAAAAGCGCCAAGATTCTCGAACGGA
TCGTACCTCTACGAAGGCTTGCTGATCCCCGCCCATTTGACAGCTGAATATGACTACAAGCTCCTGGCCGACGATTCGAAGGAGAAGGTGGCGAGCCACGTACGAGGATGTG
CCTGCCACCTCAGGCCATGCATCCGGTTTTGTTGCCCCCAGTACCAAAAGATGCAAAAGAGCAAGTGCTATGGCGACATGTCGGAGGACGAGCTGAACAAGCACGATCCCTT
CACGAACGTGACGCTCAGCGACGGGTCGGTGGTCAGGAGACACTTCAAGGAGGATCGTGATCGTGCAGTCGGATCTGGCCAAGCCCGGATGTCCCCGGATGTACTTTTGAAT
TCACTGGGACAAAGTGGAACTGAGCAAGCGGGAGTACTGCGTCCAGCATCTTTCATTTAAGGATGATAGTATCCGAATTGCACCCCACTTCTGTCCACTTTCGTCTGAGCAC
GATCAGCGTGTACCTCTATGTCGAGAAGCTTCGCAACCTGCACGGAAAGTGTTTCATCTGCTACTTGGCCTCTTTGTTCTTGGGCTATTTCTTCCTGGTCCTCAACGTGTGG
AAATACTCCTCCGGCTTCTGCGTTACAGCAGGTTTGCTTGTGGCGATTACAAGATAAAGGACGACTAATTTCACATTTCGATATCATGATCAGGGTTGCTGGGCTACTTCTC
CGTCATGGCCGCGTTCTTTTGGCTTTCTGTGATTGGAATCCACTTGCGGATTAAGTTTAGTCTAGCCTCTAACTGTTTGCACCGATTGCTGCCAGAAAATCCGTTCCGTGCA
TACAACTTATACGCCTGGGGTATACCGCTAATCATGACTGCAATCACCTATACAGCTGACCAGGTGGTTAAGAACGAGAAGTTGAGACCCCGCGTGGGCGTCGGCAAAAATT
GTTGGATCTACAGTAAGTTACTATTCCTATAATTACAATTACGGTGTAACTCGTTTGTTAACCAACAGCTGGCGATATGACTGTCATGATCTACTTCTATGGCCCGATGCT
GTTGCTAATCGCTTTCAACATAATAATGTTTGTCCTTTCGGCGATTTACATATATAACATAAAGAAAAATGTGAAAGGCCTTGTCCACAAGCAACAAACAAACCAACAGATA
AATGACCAACAAATGTAATTATATTATATTATAAGATAATAACTATAATGTCAAATGGCACTTTTTGTAATCTTTTATAGGTTTGCTATATTCCTGCGACTTTTCATCTTAA
TGGGTTTGTCGTGGAGCTTTGAGATATTATCCTTTTTGTTAACCAAACAGCAAGCTTGGGCTAGGGCTTTAATGGTGGCTGACTACTTTAATTGGTCCCAGGGTACCATCAT
ATTCGTGCTTTTTATTTTAAAGCCTAGCATTCTAAAACTTATAATAGCAGGGTAAGTAAAGTATTACAAATAACCTTGAAATTTGACCGTCTCATACGTATGAACAATCTTT
TGATTTAGGGGACGTCAAAACCTCCCAGGAAGTCACCATAATTCGAGATCAAAAGCAGCTCGATATAATTCAACTCATACGGCTTGTGAAGGATCAATTGCGGATCCAAACG
CTTACTGCTAAAAAAATGGAATTCAATAAGATGCAACGTCTCTGTTATTGATCACATTATTTTAATTTTCTATGGAGCAAAAGTTTAAAAAAAATATTTGTTATCAAGACAA
TAAATAATGTCTTGGAACATATAAAGCAAAATATATTAAAGGGTACAAAAAACAGGAAAAGTATGGGGCAATACAGCAAAATATTTTTCGGATCATCAACTTTTTTGTAAGA
CAAAATGTAGAAATATTTCTGGCACCGTTGTTTCAAACCAGGGTTTGAGTCAACAATGCTGGCCCACCACTGGCAAGTACCAAACGATTACAGAAAACTTTTTCTAATCGAT
TAAGCATCGGGGGTCATCGATGTTTCTCCACCACTACAATTTCATGTTGTTTTTTTAGTCGCGACTGTTTGACGTTTGTCGCTTTCCTCCGTTGCGAATATAATATATTACG
TAGCTCATTTTTATACAAACGGAATTACGAGCGCAACGACGACAGCAACACTAGTAGCACTAATCGTAAGCGCAGGGGCCAAAAATTAAATTGCGTTTGCGGCCGCAAAGAT
TTGATGACGTCGCATACGCCGTCTTCTAGGGCGTAAAAAGCAAAGCAAAGCAAACAAACGCGAAAGCGAAACGTGTAAACGGCGTAGAAGCGATAAACGCGACTCAAATACG
CAGCAGATAAAATACAATACGCGAGAAGAGAAAAGTCACGGGAAATATTGTTCATA
(SEQ ID NO: 55)

Exon: 1001..1492
Exon: 1552..1702
Exon: 1759..1935
Exon: 1998..2252
Exon: 2627..2640
Start ATG: 1001

Transcript No. : CT20351
ATGCGGATATTGTTAATTGCAGTTCTTTTTCTGTTGATGCCAAAATCAAATGCCGAAATTCCCGGTTGCGACTTCTTCGACACCGTAGATATTTCAAAAGCGCCAAGATTCT
CGAACGGATCGTACCTCTACGAAGGCTTGCTGATCCCCGCCCATTTGACAGCTGAATATGACTACAAGCTCCTGGCCGACGATTCGAAGGAGAAGGTGGCGAGCCACGTACG
AGGATGTGCCTGCCACCTCAGGCCATGCATCCGGTTTTGTTGCCCCCAGTACCAAAAGATGCAAAAGAGCAAGTGCTATGGCGACATGTCGGAGGACGAGCTGAACAAGCAC
GATCCCTTCGTGAACGTGACGCTCAGCGACGGGTCGGTGGTCAGGAGACACTTCAAGGAGGATCGTGATCGTGCAGTCGGATCTGGCCAAGCCCGGATGTCCCCGGATGTACT
TTTTGAATTCACGAACTGCCGGGCAATGAATTCACTCTGTTTGAGAACGGCTCTCTTCTGCGTCACTGGGACAAAGTGGAACTGAGCAAGCGGGAGTACTGCGTCCAGCATCT
TTCATTTAAGGATGATAGTATCCGAATTGCACCCCACTTCTGTCCACTTTCGTCTGAGCACTCCAGAACGTGGAAGACCGTTGCGATAGTGATATCCTTGATATGCATAATC
CTAACGATCAGCGTGTACCTCTATGTCGAGAAGCTTCGCAACCTGCACGGAAAGTGTTTCATCTGCTACTTGGCCTCTTTGTTCTTGGGCTATTTCTTCCTGGTCCTCAACG
TGTGGAAATACTCCTCCGGCTTCTGCGTTACAGCAGGGTTCCTGGGCTACTTCTCCGTTCCGTGCATACAACTTATACGCCTGGGGTATACCGCTAATCATGACTGCAATCA
CCTATACAGCTGACCAGGTGGTTAAGAACGAGAAGTTGAGACCCCGCGTGGGCGTCGGCAAAAATTGTTGGATCTACACAAGCTTGGGCTAG
(SEQ ID NO: 56)

Start ATG: 1

MRILLIAVLFLLMPKSNAEIPGCDFFDTVDISKAPRFSNGSYLYEGLLIPAHLTAEYDYKLLADDSKEKVASHVRGCACHLRPCIRFCCPQYQKMQKSKCYGDMSEDELNKH
DPFVNVTLSDGSVVRRHFKEDLIVQSDLAKPGCPRMYFLNHELPGNEFTLFENGSLLRHWDKVELSKREYCVQHLSFKDDSIRIAPHFCPLSSEHSRTWKTVAIVISLICII
LTISVYLYVEKLRNLHGKCFICYLASLFLGYFFLVLNVWKYSSGFCVTAGFLGYFSVMAAFFWLSVIGIHLRIKFSLASNCLHRLLPENPFRAYNLYAWGIPLIMTAITYTA
DQVVKNEKLRPRVGVGKNCWIYTSLG*
(SEQ ID NO: 57)

Name: mth-like 4
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384544
GATTGCCGTGGTCGTGCGCCGCGGGAGAAATGCCCTTTTCGTGTACGCAATTACTAGGCAAAAAGGTTTGGACGGCCCTTGCTTTATTAGGCCATAATTTACGCTGTCGAGC
GGCCATTAGAGCGGCATCCGCTGGCCAAGTTGGTCTATAAAAGCCCGGCGGCTGCAAGTGGCGTTTTCCATTCCACGTGAAAGGACACTCGCAGTCGGGCCGACGAGATGCT
GCGCCACCTGCTCCGCCACGAGAACAACAAGGTCTTCGTCCTGATCCTGCTCTACTGCGTCCTGGTCAGCATTCTGAAACTCTGCACGGCACAGCCGGATAGCTCTGTGGCC
GCCACGGATAATGGTATTTGATAAGGCATTGATAATATCATATTATTCGCTCTAATGGATTCCATTTACCATCCAGATATTACGCATCTTGGCGACGATTGTCAGGTGACG
CCCGTCATCCATGTGCTCCAGTATCCTGGATGTGTGCCCAAGCCGATTCCCTCGTTCGCCTGCGTGGGTCGCTGTGCCAGTTATATCCAGGTGGGTGTTGATATACTTGAAA
TATAAATTATAATTTGATATAATCTGATGACTTTAGGTTTCGGGCAGTAAGATCTGGCAAATGGAGCGTTCCTGCATGTGCTGCCAGGAGTCTGGTGAGCGGGAGGCAGCCG
TCTCGCTATTCTGTCCCAAAGTGAAGCCCGGCGAGCGTAAATTCAAGAAGGTCCTGACCAAGGCGCCATTGGAGTGCATGTGTCGGCCATGCACTTCCATTGAGGAGTCTGG
CATCATACCCACAGGAAATTGCCGGCTATTCGGACGAGGGTCCACTCAACAATCACTTCCGGCGCATTGCTCTGCAATAGATTCCCCCATCAGTTTAGCACTCATACCCATGC

FIGURE SHEET 27

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CCATTTGCTCATTAAAATAAATTAGAGTTGCCGTTTCTGCTTGTACACAGTGAAAAATGTGCCTCTGAAAGCTCATGCCAGTGAAAGGGAAACATCAGCAGATATATGATTA
TTTTAAATTGTAATTTATTTCCCAACTATCTCATGTCATTGCTACTAGTTCACTAAATGGTGTGTGTCCTGCTTCACAGGGTATGTATGTAGATGCGTAACTCCAAAGAAAA
CAAAGATAATCTTTACACTGCAACTGGATCTAACAATAGGAGTTTAACTACGGCATAATGCATATGACTCGCGCCGCCTACAAGTACTCGACGATATCGCATTTGATGGATA
TATTCGGACAGCTCTGGCCCACGGCACTGCGGCCCCGATAGTTGGGACTCTTCTCGGTGAGGAGTTTCCGGAAGATGGGCAAAATTGCCGTCTCGCCCTCGAGCAGTTCCGT
CTCGCTGCTGGCGCCGTAGATGCTGCTATCCTGCTTGCCGCGCTGCCTGCTCCGCTGCTTATCGGGCGCCACATTGGGCGAACTGTGGTGGTGGGCGGCGTGCTGGATGTTA
GAGCTCCGGCTGACCTTACGCGGCTGGACGCACGGCTGACTGTTGGGCGGCGGATCTCGTTCCCGTTCGCTGTCCGTCTCGCTCTGGCAAACGGTGCCCTTTTGCGGTTTTG
GCCGATGTTTGTTGCGGTTCTTCTCGGAGACGGACCGCTGGATGGGCGAGGTGGTGTTCGGGTCATAGGTCATCCCGTGGCCGCCATGATGTTCCGCACAGCGCTGCGGACT
GGCGTAGTTCCGCGGCGACTGGCGCTGCTTGGCGTGCGACAGCGTGTGCGTGTCCCAGAGGTCACTCTGTGAAACCACGAAATTGGACTTCAGAGCGGAGCCCATGCTGGTG
CGGCGATGGTCGGAGGCAGTGGGAGCTATTTTCGATTAGAAAATCGATAGTATTATAGTATTATAAGAGACGCGCAGAAAACTTACTCTTAATCACAGCCGGAGTACTGGGC
TTTGAGTGTGGACACATGTTGCTCAACTCCCGATTGCGATGTGGAGATGTTGGTGGAGGAGTTCCGGTGCGAGCTGCTGTACTTTGGCCGGGCGGTGGGCGTCTGGCTGCCAC
TGTCGTAGTGCCTGGAGGCGGTCGATTGACGCCTCTCCCGCATGCTGGAGCAGTCTCCTCCGCTCCGCTTGCCCGCCGTACTGGTGATGCTGCCTATATTATCATCGGTCTG
AGCGGACACCGAGTTTCTCTTCTCCAGATGGCGATGATGCTGCTGCTGCTGCTGTTGCTGTTGCATCTGCTGGTGTTGCTGCTGCTGCAGGTGCTGCTGGCTGCATCTGC
TGATGTTGCTGTAAGTGCTGCTGCAGTTGCTGCTGGATGGGCTGCATCATAGTTGGAGCAGGGGCATGCGAGTGGTGCTCTACAATCGATTGCTTTTTCTTTTTGCTGTTGG
AGAATATCCATAGATTAGAGTGTATTTAAGACCAAAATTTAAGAACTTACGGAGGAAGCGATGGCGCCATCACTGTAGACTGCACCGACACAAAGGAGTTATCCATCTCCAC
ATGAGTCGAGGTCACACTATCCACGGACGTCATCTCGGTAACTTCTATGACAAACGGGTTGCAATGCATGAACATATCTACGAAATCCCCCTCCTTAGCCACTCACCTGTGG
TGCTGGGCATCTCTCGACGCACCGGTGGAGCTGAGAGCCTAACAATGTCATCGTTCAGTATGGGCTCCAGTTCGGCTACCGACGTTGGAGCCACCTGTGCAGGTCACCCCATC
GATCCATTTGCGTGCCTCGGGTCCCAGCTTGCGGATTAAAGGCCTGCAGCTCGTTCTCCTTCTCCATCAGCGCCTTTCGGAATCGGCAGTTTGTGTTCTTTACATCTCGCAAT
CGTTGCTCCAGTTCGCACACCGAGGAATCCCGGCGTCCGTTTTTGGACATGGGTCTCAACGTGGCCCTAACGCGTTTGTCCACCACGCCCTGGGGATTCCGCTTCAGCTCCA
CCAACTGCAAAACGATTCGCATGAATATTAACCAAAGATTATACTACGCGGTCAACATCTAGGAAGGATCAACTCTACGGACAGTAATATAGGATAGTTAAAGATATTCCAA
CAGCAAGGAAGTGGGATTTGCCTACAAACCTTGCTGCTGCTCTTAGTGGGTTCTATATAGTTCAAGTTTATAGTTAGTCTGTAGTGTTATATAGCATTTTAAGATCTGTTTTC
GAGTACATGTTGTTTCTGTATCAAGGTGTATCAACGCTAGACGAAAGATCAGCTCAGCTGGCGGTAAAGTACGATCAGTCAGTTAAGAAGCTCTAACCACAACTGATCGGCCTATT
ACCGCCGACAAACAACATTCATATTACACGATTATTATATGTAACATATAACAGCTACAAAAACTACAAAACTTCCTTACTACCAGTCTTACTTTCGGTACGAACACCAAAC
ACAAAGTGGCTGTCGTACAAAAAATGATAAAAAACGAGAGTAAGACAAAAACTAAATCCTTTCGATCCGATAGCACCAGGGATATAGCCGCTCCGGCCAGACAAGTGATGAA
CACGTTATAAACGGAGAAACCAATATGCTTGGAATCGTTCAGAGCCGGTATAGAAACATGTCGAGTTTCCCAGGCCAAAAAGGCGCCAAAAACCTATTGAAAAAAATTATTG
CTTTATTATAATGATATCTTACAAATTAATGTTTATTATATACTCACCAACAACAGTCCCTTGTAGGCATAAATAATGCTAACGAATATGGTCATGTGCTCAGACTGGCAGT
ACTCGTTTTCGGGGATCACCAAGACATCATCAATATTCTCGTGATGCTGTAGTTAATAATAATCATTTTAGATTTTTCACTTCAAATATGTTCTATCAATGCACTCACCAAG
GGTTCCAACTGTTTAGTTTCGCGGTAAAAGGGATCGGCAATCTGCCAGGTGGTTATAATGGCTATATCAATGGCAAAAGCACGCCCACAACCATAAACAATTGATAGTCCT
TGATCACCTTCTTATTGAGCTTCAGATCGGTGAATATCGAATGCACCCGCCACGTCTTCGAGAACATGGCTCCAAAACTGAGACTGAATCCAGCCATCAAGATCCAGGCTCG
AGCTGTGCAGATATAGGGAAAAGCTGCCACACTACTTAATGTGGTATCGAGACCCAGGAAAATGATGCTCAAATAGGTCATCATACAGCCCACAATGATCAGATTGTTCAAA
TGGGGACTGGACATCTTGATGTATCTATAAAAACATCAATATTTTTATTAAACGAAATTGTTTAATATAGCATTGTTAAGCTCACCTTTGATTGCGATACTTAATGTTAAAGG
CCAGAAAAACTGTGGCAATAACTCACTCCAATGACCGAAGCACTAGCCGATACAATATATATGGTTGGATTGACCTGACTGTGCTCGATGTAGATCAAAGTGCGATCCTTGGG
AGGAGTTTCCCCACCCATTTGACTGGTTTTCCCAAGCTTAAATCCAAGTGTGACTTCTGTGAGTGGTATTCCCCGATCTTTTCCATTTGTCCCAGCTGAAACTGATTGATC
AGGATGTTGGCCTTGCGCTCGTTGTTGTAGAAACGCACGGGTCCCTTGAGAATGTAAAATATGTTTTAACTGCAAAAACTGGATTGTTTATCTATCTACCGTCACACCCTCA
AAGGATGTATTACGTAGAGCCTCAAGGAAGACACTCTCCCAGTCCTTCACGCGATAATCAAAATGTGTTAGCAGATCCTCTCGCTTTTCGGCCACATACTGAATGGCCAGGG
CAGCTGCCCAGATACCATCGTAGGTATAGCCATGAAAGCGGGAATATTCAGTGCCTCGCAGTCTGTCGTACTCCACAAGATACTCATCAGCAGTCTAGTAAAATATGAAATT
TATTACAAGAATTTTAATAGACTTTACTGGTACTAACAATGCCAGCCACTGTGATGTCACCACTGGTGGACAAGGGCAAAAGATCCACTAGAATGGCACCTTCCAAGGCTGT
AGCGATCTCCTCCACACTGCACTCGCTGTCCTGCGTGACATTCCACCAATCCGTGGAATAGGTAGCCATGATCAGCCATTGATAGGCTCTGCCATACATATCCAATCTGGAA
GGGAGTTTATTGCAATAATTTTAAATTGAGACTTAAGTTAGTATATCCAACTCACTTATAAGCCTCACAGAATGCCTTGCGTGCAAAGTGCTCGTTAAAGTTGCCCAGAATG
ATCCTCACGTGCCTTCTCGCGCAGTTTCTTCAATGATTCAGCCACATCGTTGACGAAGCTCTGCGTTTCCACCACCTCGACCTCCATGGCATCCAGGTCAGCCACCATGTGAT
TGTGGGGCAGCGAATAGCGTGGCTCATTCTGGTAGACAGTGCCCACTCTGGTCCAATTGAACTCCTTCAGCAAGGCCAGTCGCGGCGCATTAAAGGCATTCTCCGAGGGTAC
CACGCGAAAGAAATTCGGAAACGCACTTGGTGAACATGGGATGGGTGTCCGCGTGCTGAGCTGGGTGAGGTGCCAGTGCTTGCTGGCCTTGGCTATGGGATCGGTCACA
TGGGTGCACGCAGCGCCGAAGAGCATCACTTTATTGGGCACCCGAATGCATCATATCGAAGAAGGACTTTACGCCCACAGCAGCATTGCACTGGAAAGGAAACCAAAATTACA
TTCCAGAATATATGGAAATATGCATAGGTAAAGGTGTGATATTACAATATGAACCAATGAACATTAAAAAAAATACCTAATTGAACTTTAAAAACCACAAGTCCATCATCAG
AGATTCACTTAATGAAATCTTCAAGCTAAACCCTAACTCACCTGAGTGTCGTTCCACCACATGTGCAGCCTGTAGTTGGCCAGTATCTTTCCATGCTCATTAACGTGACCCA
AGGCGAGCTTTACACTGGGCATAACGCCCCGACCGGTGTAGGAGTTTTCCACGCCATCCCCGTACGGGAAGAATCCCGCTATGTAGACGTCCGATCTCTTGGCTGTCCTGCC
ACAGGCGGTGCTCCAAAGGAGCAGGAACAGCAGGCTGGCGAATGGAAACCAACTTGGCCGGAACATGTTGACCGCGTGGGCTGTAAAACGATTCTAAATGTGAATAGCGCAT
ATCGAGGACGTGAACTTGGAGCCAAGTTGTGGGTGGTGAATGGCAGTGGTTGGTTGCGGGTGAGCCAAGGCTGCCGAGGCAAGGCTGCGCCCAGTGGGTGTGTATTATTTTC
TACGTTCTACCTGTGTTTGCTGGCACTCGCATGCAATTTTACAGGACAGGTGGAGCAAGGCTAAGGCCAGTCCAGGCCAGCAAAATTGCTTCAAATTGCTGCAGCAATGCTG
GCACGTTTAGTAATTATAAAGCAATTTAATGATCTAAAGGATTCGTGCATTATTTAGTATGTATGCTCGTTAACGCGAAGGAGTATCTTCCAGGTGTTGCATCCTCTTAAATCTTA
TGTGTACATGTTTTTAGGAACCTACCAGCTTGCTTAGTCCCAGAACTGGCTTTTATTTCACTACCGATGCCATTTGAAACACTTATTTTACATCAAATCTCAGCCAACGAAG
AACTTTTGCAGTGCGAGGGTCCGAAAAATTATGTATCCCCCTGACTTGACATTTGTCTGACAGGAGGAATTCGAGGCAGGAAGTGCGCATGTCCTTAAACCGAAAGCTGTCA
CTGCTCCGCCTTGGCCTAGGCTTTCCAACCCCCGTAATTACCATAAACCCACTGCGCTTGTAAACATCCTGCAACAGGTGGTCCCATCAGCTGGTACTCCGGCAATTGTTGT
GCCCGTTGCCATGGACTACTGGGGTCGAAAAACGAAGTAGATAACTGCTCGGAAAATTACCAAATTGAAAATTGTGAGTAACCATAATGGAGGACTATGCGCCCAGCCGCTA
TAAAATGCTTGAGAAAATCGGCGAAGGGTCCCATGGCTGCGTGTTTAAGGCCATCGATCTGCAGCGCAACAAGGAGGTGGCCATCAAGAAGGTGGCCCTTAAGAACAAGTTC
GGAAACATAGCCCTAAATACTTTGAGGGAAATCAAGACCCTGCAGCTTTGCAAGTCTGAATATGTAGGTATACCATATATCTATTTTCATTTGTTAATTATGTAACTAATT
GTAGATTCTGGACATCATTGATATATATCCTGACCTAACTGGTCTCTCCTTGGTGCTGGAATACCAGCCGGACACTCTGTACAACCGCCTCAAGAGCGAGGTTAATCCCCTG
AGCCGCCAGCAGGTGCGTAAGTTTGCACACCAAATGTTCAAGGGGATTGCATATCTGCATGAAGCGGGTCTCATGCACCGGGATATTAAACCCGCCAATCTGCTTATCAGCG
ATACAGATATGCTTAAGATTGCCGATTTCGGACTGGCCCGTCGTACTTCCCTGAAGACGAGTCGCGCCTTTATTCGCCTCAGGTCTCAACCCGGTGGTATCGAGCGCCAGA
GATTCTATTTGGCAGCCAGAAGTATGGAACCGGAGTGGATATGTGGGCGGCAGGTTAGCCATGACTCTTTGATGGGTTTACATATATCCTTATGGCTGACATTATTGCTAT
(SEQ ID NO: 58)
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Exon: 6503..6410
Exon: 6016..5754
Exon: 5577..5096
Exon: 5034..4854
Exon: 4798..4580
Exon: 4524..4229
Exon: 4168..3805
Exon: 3742..3632
Exon: 3565..3341
Exon: 2916..2571
Exon: 2508..2403
Exon: 2345..1879
Exon: 1817..1001
Start ATG: 6002 (Reverse strand: CAT)
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FIGURE SHEET 28

Transcript No. : CT20836
AAAAGTTCTTCGTTGGCTGAGATTTGATGTAAAATAAGTGTTTCAAATGGCATCGGTAGTGAAATAAAAGCCAGTTCTGGGACTAAGCAAGCTGCCCACGCGGTCAACATGT
TCCGGCCAAGTTGGTTTCCATTCGCCAGCCTGCTGTTCCTGCTCCTTTGGAGCACCGCCTGTGGCAGGACAGCCAAGAGATCGGACGTCTACATAGCGGGATTCTTCCCGTA
CGGGGATGGCGTGGAAAACTCCTACACCGGTCGGGGCGTTATGCCCAGTGTAAAGCTCGCCTTGGGTCACGTTAATGAGCATGGAAAGATACTGGCCAACTACAGGCTGCAC
ATGTGGTGGAACGACACTCAGTGCATGCTGCTGTGGGCGTAAAGTCCTTCTTCGATATGATGCATTCGGGTCCCAATAAAGTGATGCTCTTCGGCGCTGCGTGCACCCATG
TGACCGATCCCATAGCCAAGGCCAGCAAGCACTGGCACCTCACCCAGCTCAGCTACGCGGACACCCATCCCATGTTCACCAAGGATGCGTTTCCGAATTTCTTTCGCGTGGT
ACCCTCGGAGAATGCCTTTAATGCGCCGCGACTGGCCTTGCTGAAGGAGTTCAATTGGACCAGAGTGGGCACTGTCTACCAGAATGAGCCACGCTATTCGCTGCCCCACAAT
CACATGGTGGCTGACCTGGATGCCATGGAGGTCGAGGTGGTGGAAACGCAGAGCTTCGTCAACGATGTGGCTGAATCATTGAAGAAACTGCGCGAGAAGGACGTGAGGATCA
TTCTGGGCAACTTTAACGAGCACTTTGCACGCAAGGCATTCTGTGAGGCTTATAAATTGGATATGTATGGCAGAGCCTATCAATGGCTGATCATGGCTACCTATTCCACGGA
TTGGTGGAATGTCACGCAGGACAGCGAGTGCAGTGTGGAGGAGATCGCTACAGCCTTGGAAGGTGCCATTCTAGTGGATCTTTTGCCCTTGTCCACCAGTGGTGACATCACA
GTGGCTGGCATTACTGCTGATGAGTATCTTGTGGAGTACGACAGACTGCGAGGCACTGAATATTCCCGCTTTCATGGCTATACCTACGATGGTATCTGGGCAGCTGCCCTGG
CCATTCAGTATGTGGCCGAAAAGCGAGAGGATCTGCTAACACATTTTGATTATCGCGTGAAGGACTGGGAGAGTGTCTTCCTTGAGGCTCTACGTAATACATCCTTCGAGGG
TGTGACGGGACCCGTGCGTTTCTACAACAACGAGCGCAAGGCCAACATCCTGATCAATCAGTTTCAGCTGGGACAAATCGGAAAAGATCGGGGAATACCACTCACGAAAGTCA
CACTTGGATTTAAGCTTGGGAAAACCAGTCAAATGGGTGGGGAAAAACTCCTCCCCAAGGATCGCACTTTGATCTACATCGAGCACAGTCAGGTCAATCCAACCATATATATTG
TATCGGCTAGTGCTTCGGTCATTGGAGTGATTATTGCCACAGTTTTTCTGGCCTTTAACATTAAGTATCGCAATCAAAGATCACATCAAGATGTCCAGTCCCATTTGAACAA
TCTGATCATTGTGGGCTGTATGATGACCTATTTGAGCATCATTTTCCTGGGTCTCGATACCACATTAAGTAGTGTGGCAGCTTTTCCCTATATCTGCACAGCTCGAGCCTGG
ATCTTGATGGCTGGATTCAGTCTCAGTTTTGGAGCCATGTTCTCGAAGACGTGGCGGGTGCATTCGATATTCACCGATCTGAAGCTCAATAAGAAGGTGATCAAGGACTATC
AATTGTTTATGGTTGTGGGCGTGCTTTTGGCCATTGATATAGCCATTATAACCACCTGGCAGATTGCCGATCCCTTTTACCGCGAAACTAAACAGTTGGAACCCTTGCATCA
CGAGAATATTGATGATGTCTTGGTGATCCCCGAAAACGAGTACTGCCAGTCTGAGCACATGACCATATTCGTTAGCATTATTTATGCCTACAAGGGACTGTTGTTGGTTTTT
GGCGCCTTTTTGGCCTGGGAAACTCGACATGTTTCTATACCGGCTCTGAACGATTCCAAGCATATTGGTTTTCTCCGTTTATAACGTGTTCATCACTTGTCTGGCCGGAGCGG
CTATATCCCTGGTGCTATCGGATCGAAAGGATTTAGTTTTTGTCTTACTCTCGTTTTTTATCATTTTTGTACGACAGCCACTTTGTGTTTGGTGTTCGTACCGAAATTGGT
GGAGCTGAAGCGGGAATCCCCAGGGCGTGGTGGACAAACGCGTTAGGGCCCACGTTGAGACCCATGTCCAAAAACGGACGCCGGGATTCCTCGGTGTGCGAACTGGAGCAACGA
TTGCGAGATGTAAAGAACACAAACTGCCGATTCCGAAAGGCGCTGATGGAGAAGGAGAACGAGCTGCAGGCCTTAATCCGCAAGCTGGGACCCGAGGCACGCAAATGGATCG
ATGGGGTGACCTGCACAGGTGGCTCCAACGTCGGTAGCGAACTGGAGCCCATACTGAACGATGACATTGTTAGGCTCTCAGCTCCACCGGTGCGTCGAGAGATGCCCAGCAC
CACAGAAGTTACCGAGATGACGTCCGTGGATAGTGTGACCTCGACTCATGTGGAGATGGATAACTCCTTTGTGTCGGTGCAGTCTACAGTGATGGCGCCATCGCTTCCTCCC
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(SEQ ID NO: 59)

Start ATG: 109 (Reverse strand: CAT)

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(SEQ ID NO: 60)

Name: GABA-B receptor like
Classification: G_protein_linked_receptor
Gene Symbol: BcDNA:GH07312
FlyBase ID: FBgn0027575

Celera Sequence No. : 142000013383823
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FIGURE SHEET 30

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TTTCGTTCCGTTTAAGGCCATCTCGTTTGACATAACCCCGTCATAAATTTCCAAGCCAAAGAGCATTTATGTGTGTTGGCTGGATCGCAAATGTCCCATCGCCGAACAAGCT
GAACATTTTCATGGAAATTGCCATATTATTAGCAGCTTCACATGGCCCCCACTATTCGTGCCAAGAATCCGCATGCTATCCATCCCCAAACTGCGCGCTTGATGGCAATTTA
AATTATGCTCAGCTGAACTACTCGCCCAACCGCAAACGGCAATAAAATTGCGAGGTATATGGTCTCATTCCGCACTTAAGTATCCATTTCCCCCTTACATGTATCCCAAATG
ATTCCCATCACATGCTGGTAGCTACAAATATAGTATCCTTTCCATGTAACATCTACAATGTAGCACAAATTTTGTGATATATGGATATAATCCCTTCATTGCATCATTAATA
TCTACGTGTCCTTCTCTTGAAACTCAGCCAAATGCCATTCCTGCTGGCGGTGAGGAAGGTGAGCGGAGACACCTCCACCCTGCACTGATCCTCATCCGCCAGCTGGACGCAG
TGGTCCTGCAGTAGTGTGGTCAGTGCAGCCTTCGTCTGGAGCAGGGTGCCGGATCAATGCGGGATCTCTGAAATCGAAAAAGACTGTAGTTCGTAGACAATCTGAAGTCTCACTGAAGTG
TCACTCACAAATGAATGGCCTGAACCGGCAACACCAGCACGGTGCCCAAATGCACCTTAAGTTCGCTGCTCGCTCCTGATTTCTGATCAGGAAGGGTGAATGTCTTGGTGCA
GCGCTTCTGCAGAGCCTGCATGGCCGGATGAAGACGCAGTGCCTCCAAGAGCGCAGCTTCGCTATAGCGAAGTTCACCCAGAGCCACTGGATCAATCAGATTGCCAGCGTGG
CGCTGGGCCACTTCATCCAATTCGATGTGTAACCGTCGCTGTGCATCCTCATTGAGGGCCAATCGTAGAGGGCGAAGGCGAGTAGCATCGCCGAGGTTTCGTAGCCCTCCA
GTAGGAGAGTGGTGGCATGTCCACGTAGCTCCTCCTTTTCCCAAGGCCTCTTTTGCTTTCCGCCAGCCATTGCAAGAGGTTGTCGCCACCACTTCGGGCTTCCACCAATTCCCT
GAACCAGTGCTGCAGGGGCAGGGGTACGTATCGTGTATAAGTGGATAGTGGATCAAAGGTTACACATTGGCGAGTTCCACATTACCAACCGGTGGCCAATGAGTCTACCCAAT
CGAGGCGTGTGCAACAGTGACATGGTCTCCAGCAAACTCCAAACGCTTGGCTGAAAGAGCGGAGCGAGCCATTCCAGCCAGCGACTTGGTTCATGAGCCACCCTCATGTGAA
TCCCCAGGCAATGTGCATCCAGACCGAAGATCGCGGAGGCAACCACTTGTAGCGTATAACGCGTGGCCAAGTCCTTGGCCTCGAAGCGTCCAAGGGGCACCTGATCCCGGAG
CAACTGACATGCTCTGGCCACATCGGCAAGGTCTGACGCACTCGGCTGGGTGCCGGATCAATGCGGGATCTCTGAAATCGAAAAAGACTGTAGTTCGTAGACAATCTGAAGTCTCACTGAAGTG
GGATTGTGGCTAGCCAGGACATCGCGCTGGTGGTCCACATAAACGGCGTTGTCCGCACAGTCGGCAAAGTTACGGCCCACCAGGATCTGGCGCAGCAACTCCTGGTCACGCA
TGTATCTTACGTATAGATTTCCTGGTAAATCTCTCCATATGAGCGGCGGCCCAGGGCAAAGTCCAACATATTCCCAACCAATGGCCAGCCAAAAGGTGCCTCCAGTCCCAGG
CGACGCCAGTGATTGCCCTGCCATTTCCAAAACAGGAGCGTGGCGGCCAATAGGATAAAATAGCCACCAGTGGCAGCATTATCGATGAGCATCTGAAAAGCTTGAAAGGCACAA
TCCCACTCAACTTGCATTCCCAGTTGAGTTGAATATCTCAAAGCAGCTGAGAGTGAACCACGTTGCGTGATTCCATGATTGCGCCTCATTAGCCACGTAATTGCTGTATATC
AATCAACTGACGGGTATGTTTCAATCACGCAAGATTCGAGACAGCTAGCATTGGGCTTTGAATTAATTTCTATAACCACTATGACTCAATATGTTTTCGGATAATAATCTTA
GTATTTCAACTTATATGCATTGTACACATCCATTCAGTTTTAATTTATTTAGTGCATTTCTTCTGTTCAAAATTTTGTTTTTTTTTTCTGTGCTTAACATTCAATTTGACAA
TCGTATCCATTTGCGAGTCAAATCAGATGTGTTTTGTGGATACCCTGTAACTTTCCATCTTGCAGATTACGGCCACTGTGGCAGCAAGCGGCGATTGATCAGCGGAGGAGGA
CCCTGCGAAGGAAGGAGGCATCTATACTGCATGCGGAGCGCATCCGTGAAGTCCCTGCGCCATCAGCAGATCAACGGAGGAGGTGGAACCCTAAGTGGAACTGGAGCTGGAA
ATGGCGAGTGCTGCAGCCGGGTGCACAGGATGCGCCAACAGATGCAGCTGCAGCAGCAAGGCTACGTGAGCGACAATGAATCCCGGCCGCAAGTCATTGTCGCAGCCCAGTCT
GCGTATCACGGAAGCGGGACTGCGGAGGTGAGTGCTTCAGGGTATTCTCATCCACATATGACCGACCGATTCGTGTGTCGATTTTCGCTTTCACGGTACCTTGCAGATCCAA
CGAAACCAAGAGTCTGGAGAGCAAGAAGCGTGTGGTCAAGATGCTGTTCGTCGTAGTGCTGGAGTTCTTCATCTGCTGGACGCCGCTGTATGTGATCAACACGATGACCATG
CTCCTTGGGCCGACGGTGTACGAGTACGTGGGCTATACCTCCATCAGTTTCCTCCAGCTACTGGCCTGCTGGCTACTCATCCAGCTGCTGCAATCCGATCACCTACTGCTTCATGAACG
CCAGCTTCCGGCGCGCCTTCGTGGCACCCTTTAAGGGGATTGCGGGTTGTGCGAGCGCCTGTGCGCTCCCTGCTGCTTCTGGCGGCGACGCTCCAAGAACGAGACGAATCTTTC
GGTGGCCGGTAACTCCATTGCGCTGGCCAACTCGGTCATGTCCAGCCACACGATCCTCGAGAGTCCGCGACTCTGAGCCAGCCGCCGCCGACGGCAGATGGCCGAGTCGGAG
GTGGAAGTGGCCAGATGGATAGGTGGGATGGGAGAGCGCTAATATGTGGATGGCAATGTAACTGCAATAGAAACTGTGGTTGTCAACGACATTCCGCCGCGTTCTGAATGTGT
ATGCTTAGAGTTGCGCTAAAGCGCTTTTATTCCGTGTGTGTTTATTCGACTTTGACCTCGCGTTCCATGTGTTTACACCTTAAGGTGGGTGCAACCAGTCATGCCAATCTAAAT
TGAGATCGCCACACGCTATGGGGAATGGGAAAGTGCTCAGCTGGATTAAGATTTTTAAACAAACAATAGGCTAAGAAATCAGCACAATGGTTTCACGACATGGTCACAGTATG
TCGTGAGCCAACAAAATGACTTCCAAATGGGGGGGGCGCTCCATAAAATTGTTTTAATTTATGGAAAATGGTATATGTGTTGGAAGGATTTGTTGGTTCAAATCTGGAGTTGGG
TCAAAAGTTGGTAAACAACTCATTTGTCACACATGTCGTATGAGTGATATTTACGCAAGCTATCCGACCATTGTGCTGCACTTTCTAATTTTATTTCCACACTTTACGTTCC
```

FIGURE SHEET 31

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AAAGATCAATCCCAAAAGTAAAAGGTATTCTGATCACGGTGCAGTGAAAGGTTTCAATGAATCAAGAAGCATTTGACAGCAAGCTGATTTTACAGGGTACACAGGGAAGTCC
CACTCTCAAAAGGATTCCCATCATTCAAAAATGGTTGTCAGACGGGAGCTTATGGAGTGGCAGACACTCCGAGGTCCAAAACTAAATTAAGAAACCCAATCGGGTGCCAAAAT
CCAATTTTAAGTAGACGAAAGTAGCTGGAAATGCCAATCGGATATATTCGGGCGGGATTAGCATTGTG
(SEQ ID NO: 61)

Exon: 89..105
Exon: 176..924
Exon: 1025..1252
Exon: 12710..12910
Exon: 12965..13303
Exon: 17202..17499
Exon: 17579..17996
Start ATG: 89

Transcript No. : CT21155
ATGTTGCCGCGCCTGTGCGCCGACGCTTGCCGTCAGTGCTTCGCGAAGATTGCGAGGCGCGACACACATCGCGGAACCCGAACTCCATACGGCTGTGCCGACACTCAATCCC
GACCTAAGCCCAATTTTTTGTTGCGTGAAGTTGACGAAGTGTGTTGTACTGCTGCAAGTGCAAGTCCCCGATTGCTAGTGCTATTCCGGGATCACAAACGAGCATCCTTCTT
CGGCCTCACGATTGACGCCTTCTACCACTACCTGCGCCAGGCGCTGCCGCTGGCCAAGGAGGCTGCGATCCACCTGAATGCCAGCAACGAGATCTCCGCTGTCGGTGACGGG
GTCACCATCACAGGGACACCCGGTGATCTTCTCAACTACAGCGGGCTGGAATTGGATCTCGGACTGGATTTGGATCTTAATCTGGACATGGACCTAGCCACTACTCCCAGCA
GTGCGCCGTGGTCGGGAACCTGCTGGTGGTGCTAACGCTCGTCCAGAATCGTCGCATGCGCACCATCACGAACGTTTTTCTGCTCAACCTGGCCATCTCGGACATCCTGCTC
GGCGTATTCTGCATGCCGGTGACCCTGGTCGGCAACTCTGCTAAGGCATTTCATATTCGGCGAGCTGCTCTGCAAGCTCATCCAGTTTGCTCAGGTCCCTATCCCCGTGACCG
AGCCCCATAATCGCTTGTCAAATGGCCACGAACCAGCACGACCTCGAGCGGATTCGCCAGCAGATCGTGTTGGCCAACATTCAGGAGCTGATAAAGAAGATGACACGTCGCT
GCTTCGACGTATGTATCGCTATGCCGGAAATGGAGTTGCGCTCCACGGAGCGCGACTGCCTGGCCAACTGTATGGATCGATTCATGGACTCGGTTCAGCTGCCTCGGTGGCC
GTTTCCTCCTGGACACTGGTGGCCATCTCTTGCGAGCGCTACTACGCCATTTGCCACCCGCTACGAGTCGCGCACCTGGCAGACGATCAACCACGCCAACAAGATCATCGCCA
TCATCTGGCTGGGCAGTCTGGTGTGCATGACGCCCATCGCCGCCTTTAGCCAGCTGATGCCGACCAGCCGACCAGGACTTCGCAAGTGCCGCGAGCAGTGGCCGGCGGATAG
CCTCAACTACGAGCGGGCATACAACCTGTTCCTGGACCTGGCCCTGCTGGTCCTTCCTCTGCTGGCTCTGAGCTTCACCTATCTTTTTATCACCCGCACCCTGTACGTGAGC
ATGCGCAACGAGCGAGCCATGAACTTTGGCAGCAGTGGGCCGGAGGTCACCACCTCCTCCTCTGCCGCTGTCGCAGAAGCCGGTAGCCAGCGACGCGCCAACGGAAGCCATT
GTCAGTCCCTCGACACCGATTGTGCCACACCAGCACAATCCTCACCAGCAGCACCACCACCATTCCCAGTACTACTATGATTACGGCCACTGTGGCAGCAAGCGGCGATTGAT
CAGCGGAGGAGGACCCTGCGAAGGAAGGAGGCATCTATACTGCATGCGGAGCGCATCCGTGAAGTCCCTGCGCCATCAGCAGATCAACGGAGGAGGTGGAACCCTAAGTGGA
ACTGGAGCTGGAAATGGCGAGTGCTGCAGCCGGGTGCACAGGATGCGCCAACAGATGCAGCTGCAGCAGCAAGGCTACGTGAGCGACAATGAATCCCGGCGCAAGTCATTGT
CGCAGCCCAGTCTGCGTATCACGGAAGCGGGACTGCGGAGATCCAACGAAACCAAGAGTCTGGAGAGCAAGAAGCGTGTGGTCAAGATGCTGTTCGTCCTAGTGCTGGAGTT
CTTCATCTGCTGGACGCCGCTGTATGTGATCAACACGATGACCATGCTCCTTGGGCCGACGGTGTACGAGTACGTGGGCTATACCTCCATCAGTTTCCTCCAGCTGCTGGCC
TACTCATCCAGCTGCTGCAATCCGATCACCTACTGCTTCATGAACGCCAGCTTCCGGCGCGCCTTCGTGGACACCTTTAAGGGGATGCGGGTGTGCGAGCGCCTGTGCGCTC
CCTGCTGCTTCTGGCGGCCGACGCTCCAAGAACGAGACGAATCTTTCGGTGGCCGGTAACTCCATTGCGCTGGCCAACTCGGTCATGTCCAGCCACACGATCCTCGAGAGTCC
GCGACTCTGA
(SEQ ID NO: 62)

Start ATG: 1

MLPRLCADACRQCFAKIARRDTHRGTRTPYGCADTQSRPKPNFLLREVDEVCCTAASASPRLLVLFRDHKRASFFGLTIDAFYHYLRQALPLAKEAAIHLNASNEISAVGDG
VTITGTPGDLLNYSGLELDLGLDLDLNLDMDLATTPSSSTLAPAVTVRTPGNRSVVRVSADVPIWVVPCYSAILLCAVVGNLLVVLTLVQNRRMRTITNVFLLNLAISDILL
GVFCMPVTLVGTLLRHFIFGELLCKLIQFAQVPIPVTEPHNRLSNGHEPARPRADSPADRVGQHSGADKEDDTSLLRRMYRYAGNGVALHGARLPGQLYGSIHGLGSAASVA
VSSWTLVAISCERYYAICHPLRSRTWQTINHANKIIAIIWLGSLVCMTPIAAFSQLMPTSRPGLRKCREQWPADSLNYERAYNLFLDLALLVLPLLALSFTYLFITRTLYVS
MRNERAMNFGSSGPEVTTSSSAAVAEAGSQRRANGSHCQSLDTIVPHQHNPHQQHHHHSQYYYDYGHCGSKRRLISGGGPCEGRRHLYCMRSASVKSLRHQQINGGGGTLSG
TGAGNGECCSRVHRMRQQMQLQQQGYVSDNESRRKSLSQPSLRITEAGLRRSNETKSLESKKRVVRMLFVLVLEFFICWTPLYVINTMTMLLGPTVYEYVGYTSISFLQLLA
YSSSCCNPITYCFMNASFRRAFVDTFKGMRVCERLCAPCCFWRRRSKNETNLSVAGNSIALANSVMSSHTILESPRL*
(SEQ ID NO: 63)

Name: GASTRIN/CHOLECYSTOKININ RECEPTOR like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384801
AGCTGTAAAGTACTACTACTACATATGTGTACATTCAAGTTTCGCTTACGAATGCAACGTTCCATTAAAGAAGCCACCAACTTTAAGATACACGCATATAACAACTCCTGAG
AATTGTGAAAACTGATCTACTTTGATGATCAACTTTCATTGCTGCTGATTGAATAATTGAGTAATGAGTAATTGGTATGCTGATAAACAGGAAAACCAAAATGTCAACAGTT
GATAAGGAACATTAAAACACAAATTAAGAGGACGGTAAGTCCTTCACTCGGACCTTTTCAGCTGAGCACCGTAAAGTGCTGAAGGGATTGCCCCCACACCCAGACCGCGCCC
ACTTCCACTTCCACTTTAAAATAATCATCATGGCCCTCTTTTTTGGCCAGGCTGCCGGTGGCTTTGGGCCTTAATTGTCGACTCAGTTGCTGTGCTGTGTACTCGGACA
AGGCGACGAACCGAGAGCCTTGCAGCTCCATAATGACAGGCGGATGGACTCGAACACTCGGACCCGGACCCGGACCCGAACCCGGACCCAGTCCACAGCCAGGACATAAGCG
GCTTGTGCTCCACTCAACTGTCGCCTTTCGGGAGCTGCTCCTAGCTTGCAATTAAAATACCCACTTGGGCCCTATAAATTGTGAACGTAGGAAGGCAGGCGGAAAAAAAAAA
AATATTCCAGCACTTTGGTGTATGGAGTGGGGTCCACTTAATTCCCAGGTACTCACCCAAAAGGATTCCAACTATAAAGACATACAGCGAGAGTGCTTAAGTTTTACTCTGT
TTATTTGCAGCAACCTTAGGAAGTTCAATTGAAACACCAATAGACTAGCGTCTGAGTTATTTTACGAGTACGATCATAATCACAAGTAGGTAAAAAAAATCCATATTCGCCT
TACTTAAAACAAAAAAAAAAAACCACACGCAGATCGCTTATCATACATATTTACACCGCATCTCGTTGATCCTGAATGGGTCCTTGGAGGCGAATCCTCTACAGCTTAGAGCT
GAGGACTGTTGACGGCGGCGGCGGCACTATTGGTGGTCACCACCGCATTGAGAAACTCGTGGCGTGAGCGACTCCGCCAGGTGCCCATACCCATGGCTAGGCCGGGATTGAG
ACTAATGTTGGTGTTGGCACTCGCATAGGCGCCCGGGCCTGCGCCCGCCTGGCTGGCGGAGAGTCCTCCACCAGCAGCACCACCGACGCCTCCGCTGGCACCTGCTCCACGA
CGCCCAGGGCAGACCCTTGAAGGTGTCGACAAAGGCGCGCCGGAAGCTGGCGTTCATGAAGCAGTAGGTGATCGGATTGCAGCAGCTGGATGAGTAGGCCAGCAGCTGGAGGA
AACTGATGGCCGTGTAGTCGACATACTCGTACACCACCGGTCCGATCAGCATGACCATCGTGTTGATCACGTACAGCGGAGTCCAGCAGATGAAAAACTCCAGCACCAGGAC
GAACAGCATCTTGACCACACGCTTCTTGCTCTCCAGGGTCTTGGCCTCGTTGGACCTGGATAGTGGATTGTGGATTGTGGAGAAATGGGAATAGGGAATAGGATTGGCAGAC
CGGTTATCGGACACGAATCCTACCTGCGAAGTGCCGCATCGTGGACGCGAATGCTGGGCGAGGAGGTCTTGGCCAGCGTCACCGTGGTCGTCGTGGTGGTGGTGATCACAGT
TGGAGCCGTTGGTCTCGTTGTCAAGGTGGTCGTTGCCATATTGGTTGATCCTCCGCCTGCGGATCCCTCTGAATTTCCATTATTATTGTTACTATTTTCTATGTGAAAAAAA
AAAAACATGTGAACACAAGCCAAATATAATCAAACAAATTAACGTTATTAGCAACGAACAAATAAAACAGTTGCCATAACTAATACATAGACGTAAAATAATT
AAATTTTCAATTGGTTTTAAGAGTCTCAAAAATAATATAGCATATTATGTTAAGTGGATTTGTACCTTCTTATCGAGCATTTCACCAACAATCTATATCTTTAAAGTATTA
TGCCATATTACATGTCATGTAACATTAAATAACTTATGAGTTATGATATTTAGATGCAAAATAATACTTGAATGCATTCATAAATGCTCTTAAAGTTGTTTGCATATTCATG
GCTTTTAAGGATTGAAAAAGGATTAGTTTCGTGCAGTTACCAACCATTATAGACTGCGGTGGCGGTCAGGACCAGGATGCAGTTACTACTGCTGCTGGTGCCCGGATTCGGT
GCGCTTCCGCCGGCCGTTGTAGCGGAAACAGGCAGCGATTGCTGCAGGATGCGTCCGCTGTCCTTGGCCATGCCTACGTACAGGGTACGCGTGATGAGGATGTAGGCCACGC
AGAGGACGAGAAGCGGCAGGACGAGCAGCAGGAAGTCCAGCAGGATGTTGTAGAAGAGCTCGTATCCCTGGTCGGGCCAAAACTCACGGCACTTGCAGTAGCCTGTAACGTA

FIGURE SHEET 32

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AGTTGGTATAACAACCAGACGGTGTCTGCTGGCCAGGTTGCTATGCACTCACCCGGTCGACTGGTGGGTATCAATTGACTAAAGACCGCTATGGGCGTCATGCAGAGGATGC
CGCCCAGCCAGATGAAGCCGATGATCTTGTAGGCGTGACTGATTGTCTGCCAGGATCGCGAGCGCAGTGGATGGCATATCGCGTAGTAGCGCTCACAGGATATGGCCACCAA
GGTCCAGGACGAAACGGCCACGGAGGCGGCTGAAATAAATAAATGAAAGCGGATTAACTTACAACAAACCGAACACAATGGACACACCCAGCAGCTCCTGTCGAGCGCCGTG
TCAAATCGCTTTCATTAGAAGGTCCTTCGCCCGCGTTCGTTGCATTTTAATTACACAATTTGCATATTGGGACCAGACGAACCGTACCAACCAGACGGACGGAGACATCGCT
CTTCGCACTTCTGCCTGTTCTTGTAGTATGACAAACACGATGCACGATGCAATTTGCAGAAAGTGCAATTCCCCAGCCACTCCTTTTCTTGTTGCCCGGTCTCC
TTTTCATGTAAGCCTGTTAGATGATTTCCCATTGTAAAGCAATTTGTACCCACACCCTGCCCATCCCTCATATTCTTTTGGGCTACCACTATCGATGGGGCTACACAAGTGC
AAGTCAATAGGGTGGACTGCTGTAGGTGAAAAACTCGACACCGAAAGAAAAAGACCCGATTCGAAAAATTGGTCAATTTTAGCGCAATTAAATGAGAAATAATTTCTAGTTT
TTCAATCGATTGTTTTATAGCACCAAATCATATATCTTAACCGTAAAGGCATCAAATAAATATGATAAACTGATCAAATGAAAGCATAATTTGCTTGTATGTATGCGTGTTT
TTGGAATTTATAGCTTACCAAAACACTTGTGAAATTTGCAAATATACATATTTGTTCATACACAATTTAGACTTCAATGCAATAAGCTGTAAGGTCTATGGTTTCAATTATT
AATACTCGGAAATTGTTGTGCTAGCAGATACATTTGTGGTTTGTTAGATATACATATTTGCTTATAAAGATATATATGTATGTACGTATTGCATTCAAAAGCAATAAGCAGT
AAGGTAAATTGGATCAAGGGACGAGTATTTAAGACAGCCTGTATATGTTCCCTTTACTTTAATGCGACACCTCATTCAGGCAATTAAGGTCCACCCTAATGTGCTTATCCCT
TCAGCCATCTGCAGCTGCATTGTATTATATTGGAATGGTATTTTCTCGCAAAATGATATGCAAGTTTTAGATTGATACGTACAATTGCAGTGATTACTACTTTAGTTACGAA
TGATGATAGGTGATGTAGTAGATATATATTTGCTACCAAAGATAGTTACACCTTAGAATCCTAAAAGAAATAAGTGTTTTGTAGTCGCAGTTCGTTTCTCTAGTTCAACACA
TCCAGCCAACCAAGGTCCACCCTAATGTGACTGCACTTCAGCTGCACTGTATTATATTACATTTTAGCTGCACAATTGTTTACTTTCTATTTTAATTATGCATGCAAACTAA
TATGAGCAGTAAAGATGGATTACCTCCACCTGTTCCGTTGGAGTGCATCCCGTCCAGGCAACCAAGGTCCACCCTAATGGGGTAGCCCTTGCCCTTCCAACTGCATTGTCAC
ATTGGTCTCGCCCTCTGTCGCGTTTGTTGAGTTAAACCCCTGAAATTGAAGTTTACTTTTGATTGACGGCGGTGTGTGATGCTCTAAGCCAGAAATGCTAGCATGTGTGCGC
TTAAACTTAAAACAAACAGCAGCATGGCATTTC
(SEQ ID NO: 64)
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Exon: 4080..4056
Exon: 2717..2517
Exon: 2454..2169
Exon: 1736..1001
Start ATG: 4080 (Reverse strand: CAT)

Transcript No. : CT21314
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ATGCACTCCAACGGAACAGGTGGAGCCGCCTCCGTGGCCCGTTTCGTCCTGGACCTTGGTGGCCATATCCTGTGAGCGCTACTACGCGATATGCCATCCACTGCGCTCGCGAT
CCTGGCAGACAATCAGTCACGCCTACAAGATCATCGGCTTCATCTGGCTGGGCGGCATCCTCTGCATGACGCCCATAGCGGTCTTTAGTCAATTGATACCCACCAGTCGACC
GGGCTACTGCAAGTGCCGTGAGTTTTGGCCCGACCAGGGATACGAGCTCTTCTACAACATCCTGCTGGACTTCCTGCTGCTCGTCCTGCCGCTTCTCGTCCTCTGCGTGGCC
TACATCCTCATCACGCGTACCCTGTACGTAGGCATGGCCAAGGACAGCGGACGCATCCTGCAGCAATCGCTGCCTGTTTCCGCTACAACGGCCGGCGGAAGCGCACCGAATC
CGGGCACCAGCAGCAGTAGTAACTGCATCCTGGTCCTGACCGCCACCGCAGTCTATAATGGTTGGCGGAGGATCAACCAATATGGCAACGACCACCTTGACAACGAGACCAA
CGGCTCCAACTGTGATCACCACCACCACGACGACCACGGTGACGCTGGCCAAGACCTCCTCGCCCAGCATTCGCGTCCACGATGCGGCACTTCGCAGGTAGGATTCGTGTCC
GATAACCGGTCTGCCAATCCTATTCCCTATTCCCATTTCTCCACAATCCACAATCCACTATCCAGGTCCAACGAGGCCAAGACCCTGGAGAGCAAGAAGCGTGTGGTCAAGA
TGCTGTTCGTCCTGGTGCTGGAGTTTTTCATCTGCTGGACTCCGCTGTACGTGATCAACAACGATGGTCATGCTGATCGGATCCGGTGGTGTACGAGTATGTCGACTACACGGC
CATCAGTTTCCTCCAGCTGCTGGCCTACTCATCCAGCTGCTGCAATCCGATCACCTACTGCTTCATGAACGCCAGCTTCCGGCGCCGCTTTGTCGACACCTTCAAGGGTCTG
CCCTGGCGTCGTGGAGCAGGTGCCAGCGGAGGCGTCGGTGGTGCTGCTGGTGGAGGACTCTCCGCCAGCCAGGCGGGCGCAGGCCCGGGCGCCTATGCGAGTGCCAACACCA
ACATTAGTCTCAATCCCGGCCTAGCCATGGGTATGGGCACCTGGCGGAGTCGCTCACGCCACGAGTTTCTCAATGCGGTGGTGACCACCAATAGTGCCGCCGCCGCCGTCAA
CAGTCCTCAGCTCTAA
(SEQ ID NO: 65)
```

Start ATG: 1 (Reverse strand: CAT)

```
MHSNGTGGAASVAVSSWTLVAISCERYYAICHPLRSRSWQTISHAYKIIGFIWLGGILCMTPIAVFSQLIPTSRPGYCKCREFWPDQGYELFYNILLDFLLLVLPLLVLCVA
YILITRTLYVGMAKDSGRILQQSLPVSATTAGGSAPNPGTSSSSNCILVLTATAVYNGWRRINQYGNDHLDNETNGSNCDHHHHDDHGDAGQDLLAQHSRPRCGTSQVGFVS
DNRSANPIPYSHFSTIHNPLSRSNEAKTLESKKRVVKMLFVLVLEFFICWTPLYVINTMVMLIGPVVYEYVDYTAISFLQLLAYSSSCCNPITYCFMNASFRRAFVDTFKGL
PWRRGAGASGGVGGAAGGGLSASQAGAGPGAYASANTNISLNPGLAMGMGTWRSRSRHEFLNAVVTTNSAAAAVNSPQL*
(SEQ ID NO: 66)
```

Name: GASTRIN/CHOLECYSTOKININ TYPE B Receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384546
```
CAAAATAAATGTATATAATTTCAAAATTGACATTTGCTAATGATAAGCCTCTGCCTCATGCCCATGCTTATGCTGAAATATGGACAAAATTCGGGCACAGAGCAAGAGATGC
GCAGAGCAGCTGCCATCCGGAATGGAATGGATTGGAATTTGGGCAGCAGATGGCGCTGTCGCAAAAGGAAGGAAGCTAAATTTCACTGGGCCCCAACCAAACGGAAATTTCC
ACCCACGGCTCAGAAATTGAAGCTGTTTATGGTAAATTAAACCAATTGAGTGGGATTACGTTTTGCGCACTACAACAACGCCACCAACCTCCGCATCAACTCCGCAATCTCC
GACACCCCGAAGTGTTTCCAACTGGGTTTCAATTTCACTGTCTGGACGAGCCTCGCGGCTAACGAAATTTATATACCCATACAATGCCATCAAAGCCACAAGGTGTTTATGGG
CTTAACTCCGGCCCTGATTCCGCCTACTTGGCTGCCTCGCCTCACAGATTTGGATTTGCATGTGCCACGATTTGGGGCATGCGGCTGAGAAGGCGGCTGAGCAGGCGGATAG
AAGACAAATAGCCAGCACGTTGCGGTTCATTTGGCTGTCACAAACAAATGCCGAATTGATGCAAATGTAAATGGATTCGATATCCAGGAACGCGTCGTCGGAATCCCAAGCAG
CAGTCAAGTGATGAATACACGGCTTAAAAGATACTGTATTAACTTACAGTAGCTTACCTTCAAAGCAAAAATTGTAGATTTCATTCTCTAGTAACGAGTTCATATCCATACC
TCTTTAATATTGGATACTATTTATTACCCAGTTTATTACTTAGTTTTTATTTCAGAATCAAAAACAAATATAAGCAAGCTTACCCCATTTAAGTACTTGGCAATTGCAAATG
TGCACATACCACTTTCTTTTCCATCCACAAACTGGCTTTCAAACTGCTGTTGGCCAACTCATAAATATGGCAGACAATAAATCTAGATTCTTTTTCAATTGCAGGGTTTGGC
AAACGATTGGCAATAATAGGAGTCATCAAAACGAGAGCAAATGTCATACAGCATGTCGTCTTATTCCGTGGCGTTAGTGCGACATTTGGAAACTAGGAGCCCACT
TAGACTAACAACGCCCGTGACCATTACCATGACGCTACTGCAGAGGCTTCAGGCCATGTCGGCCACCACGACCAGGACAATACTGGAGGGCAGCATCAGCAGTTTTGGTGGC
GGGACAAATGAGCCTCTGGCGAGCAAAATACCCGTTCTGGAGGAGTCAGCCTCACATGCCAGATATTTGAAATTCATTGCCGACGGGCTCATCGACGAGGGACTGGGCAGTG
CGGTGGGCAGTGGGAGCAGCATCGCCGTATCCGTTGAAGACGTGGTCGCCGGACAGGCGCAGGACATCCAGGCGAGCGAAGGATCCACCGACGACGCCGACGGCAGTAGCCA
GTCCTTGCCATTGTGCGTTCTAGCCATATCCGTTGGTCAGGACATGTGTGTCCTCAAATGTCTGGGTTTCATTAATTTGTCGCCATGAATCAGGTGGCTTTTTTCCCTTTTT
GCGCCATGGTTTCAATTTCATTGTGTGCATTTGCAGGAAGCTTCCAACTATAAGTTACTTAGATAATAATTTAACAAAGCATGAACTTCAACATCAAAACATTAGTGAGCA
ACACCCCCACCCCCCCCGCCCCTTTTTCCTTTTATTTCTTTGTTTGCTCCTTTTTGCCGAACGATTTTGTGCGATTTGACCGCGTTCGGCTTAACGAGTAGCTACCTCCTTTT
TTTGCGGCCATTAATTTGTCATCATTTATCATATTTTCCATCATTTTTGCGTGTCAAGCGCACAGAACTCATCTCGTTCGCCCACCGAACACTTCAGAGGGGGGCGTGGTTG
GTTGACTAAGTTAAATGCTAGATACGTGCGTAATTACATTAGAAATGTTAATAAGGGGCGAGCATAAAAATATTGTTGCCTACTTACGGGGGCGCCATTGGCATTTACTTTA
TGTGCGGCCATATAATTTGTCAAATTTATGAATTGGGCGCCACCTTCACATGAGATATGGCCACGTGGGCGTTTGAGGGATTTCCAGGTATCCAGGTAGCAAAGTACGTACG
TGTTTCAGTCGCAAATTCAAAAGCCCAACACCGCTGGCATTTAAAGAACCCAACATAAAACACTTGGAGAGAGGCGACAATGGTGTAACCTAACCCCGGGACATTCAATGTC
AAGGCGCAGACTATTAAAGCAGCCCCGGGAAAACGTCTTCCACTGTCATTGCCGTATTCCTTTCGCCTTGGAACCAACCAACGCACACCTGACATTTGTGGCTGCCACCGAG
```

FIGURE SHEET 33

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AATGAGGATGGGCATGGTGATGAGCATGGGGGGATGAGGCTCATTTAGCCTGCCAGGGACAGGCAATTTGGGACCTGACCCTGACTACTACGTGTATGCCATGTTGCCGTTTT
TATCTCAACTGCCTTGCGCCAGCATCTCTTTCATTATTGTTGGGCTCATTGTCATGTGCGTTTTCCGCACCATTTTCACCTTTTCCGCCTCGCTAGGCAGTTTAAATCATCA
CGGCAAATTAGACTTAATTACGAAACAACATGCATTCCCACTTAGGTCCCATGCTACCTAAAAACCTTGTGACCAAGCGGAGTAGCAGGTATCTATTTCAATGTTCTGGATA
AGCCATCTGGGCGACAGTTGTGCGACTTTTTCACGACTGGCCACTCAACTTACATTATTCATGTCACACGCATCGATAAAGTGGGTGACAAATTAAAGTCAGACTGCAGATC
AAGTACGAGGAAGAGCCGGGAAAGTGTTTCCTCACTTTTCCTATTAATTAGAGCTTTCCACGTTGGCTGCCTGCCGAAAGTGTCGACTCATAATTGTAATCAAACTTGACAC
CCAACAAGTTTCCTCCTTTCATTCCCGAGCACCCACTATATAATCGGCTTTTGGGTAACGCCTCAATAACATTTTCGTGTTGCCTCTGATCGGGTGTTTTGCCTTTGTACT
TTTTGGGCGCTTTAAGCTTGCTCCAAAAATGTAGACCTTTCGGGGCGTCAGTTTGTGGCCGTAATTAGGTTTGCGGGAGATGGTTTAATGTCCCAGTGAAATATGGCAAAAT
GGCGAGCGATTGTTAACGAGTTTAATAGATAAAGGTCGGATACACATAAAAAGAATATCCATGATTGATGCAGTTTAAGAAGTTCCCATCCAAAGTTCCTTCATTCAAAAGT
TTATCTGGCACATTAATCCGTTTAGACGGAAAGCAAAACTTTCATTTGCGATGTTGTGGTACGAAGAGTCAAGTTCCCGCAGATGTTATGGTTTTAAACATGAATTCCAACC
GCCCATTCGGTTGCGGTTATATCCGTGGAATGGCGTTATGTACGCCTGATTGTTTGGAAATCAGTGCGGACGGCCGATAAACGCATTTGCTGCTCCACATAGCGTATACGCC
GCGTGCACCTAATTGACTTAACGTTTTGCGGTGCCACGCAACGTTGATGATCGCTGGTGGAAGTTGCGGTGGCGTTAAGCTAATTATTAATTAACCCATTAAACAATGAAAT
CCACTCAGAGAAGCGCCTTTTCGTACATGAAACGGCGGTCACACGCGGCGTATGCGCAATGTGCGCACCAAAGTTTCCAACTCAAGTTGGACAGCAATCCGAAGTAACGATT
AGCGCTGCGAGCTCTGAGTGACTTGAAAGCTTAATGCACAAATTTAATTTGAGAACTTGGCACTCTCAATACCACTGGCACTCAGGCTTTAGGTTCATTCTGCCATTTTTGG
TTGACTGTGTGGCTTCCGCCTTGGTTCCTGCTAAGTTTTAACCTAGCATTTACTCCTCCTCCTTGCAGCATCATTACCAACTACTTTGTGGTCTCTCTGGCCGTCGCCGACA
TGCTGGTGGCCCTCTGTGCGATGACATTTAATGCTTCCGTCATGATCTCGGGCAAGTGGATGTTTGGTTCCGTGATGTGCGACATGTGGAACAGCTTCGACGTCTACTTCTC
CACCCGCCAGCATCATGCACCTCTGTTGCATATCGGTCGACAGGTGAGTCCCGGGTTTACTTTGTCATTGTGGAATAATTGAAGTTCCGAGTGCTACTGGGATGTCTTTTATA
CCTTCCTTTAAATGCCCATCAAATTGAATAGTTGCTTGACAGTTTCTAGTGACAATCTTTTTTCCCCTTTACCCGTAGATACTACGCCATTGTGCAGACTGCTGGACTATCCA
CTAATCATGACACAGCGACGCGTGTTCATCATGCTATTGATGGTGTGGCTATCGCCGGCGCTCCTCTCGTTCCTGCCCATCTGCTCGGGATGGTACACAACGACCGAGAACT
ACAAGTATCTCAAATCGAATCCGCATGTGAGTAGCTTACTTGAAGCCCTTAATTGGGACAATTAAATATTTGTACAATAGTGTATAACTCTATTATGGAGCCCACAGATTTG
ATGAGTAGGTCGATCCGGTGTATGCACCTACATTATTTATTCAATTTTCTTGCACATCAAACTAATAGAAAATTCTAATTTAGTTGAAACGGTATCGACTTTGCATGCATTT
TGCATGCCTTCGATGCCACGTGGGCGTCCATGTGGCAGTGGCAACCTTTGACTTTTCCCCCGACCCGCCTCAACGGAAATTGATTTATGTTTGTGTGGCTGAAGCAGTTTTA
CGCCTTTCAGGCTGCCAGCCGACAGGTAGCATATTTATTACTCCATTTTATTGGTTTCCTCCGCAAATACTTGGCAAACTCCTTGGCACCTCCTCCATCTACAAATATA
TACATTTATATATATATATATATATATGTTCTCTGCCCGTCAGCAGCTGCTGGTACTGATTCCCCCCGCCACTGCGGTTATCATTGCGCAATAAAATGCTGATGTAGAAA
TAAATGTAGGTAATTCCATTCCGGTTTTCTGCGCTCCCATTCAGGCTGACTTCAGCATAGGCTGTGCATAATTTTCGGCTCTACACCTGGAAGGACGCCTGAAACGCCTGAC
AGGCCTTTGCATACATTAGCATCCGCGGTGGGCTTTAATTAGTTTTACTTTGTTTATGCTAATAACTGTCAGCGCGAAGCCGGCAGAAATGTCCTGGCCGTAAATCTGTTTTA
TGTCTTCTGGTGGCCTTTTGTCATGGCAGCGCTGTAATGCACAGCGTAATTGAGTTTTTATTGTCGCACTTGGCATTGCAGTAATCGCATTGCCATTGCAATTGCCGTCGCA
ATAGCCGTTGCTCATACGCAACGTTGGCCGCCGCCAGCCGCAGTTGGCAATTGCCGAGCATTACGCTCCATTACGGTTCGCCACTGGCATCCGACTGCACTGCTCCAACGTT
CATTTTGATTTATTGATAGTCGCTAATTGAGTTGCCCATCAAATCGCAACGATTTCGATTCCGATTTCGATGCTCCCCTCACTCCATATTTCAGATATGCGAGTTCAAAGTG
AACAAGGCATACGCCATAGTCAGCTCGTGATGAGCTTCTGGATTCCCGGCATCGTAATGCGTGATGTACTACCGCATTTACCAGGAGGCCGACCGACAGGAGCGTCTGG
TGTACAGGTAATAGCTATTCGAGTGGCCCCTCCATTTGCCCGCTTCCAATTAACTCTAATTACTTACTGTGTGCGCCCAGATCCAAGGTGGCCGCTCTGCTGCTGGAGAAGC
ATCTGCAAATTAGCCAAATTCCCAAGCCCCGGCCGAGCATTCAGGTGGAGCAGTCGACCATCTCGACGATGCGGCGTGAGCGGAAGGCCGCCCGCACCCTGGGCATCATCAT
GAGCGCCTTCCTCATCTGCTGGCTGCCGTTCTTCCTCTGGTGCGTATACTTGATGGCTCAAATTGGGCAATTATCGCTAGCACTCTAAGGATCAAGTGCCGAGAAGTTTTTA
ATTAACTCGGGCTCATATCAAATAATTTGCACTTTCCATGCTACAGGTGGGCGGAAAGTGTGTATAAACAATTAACAATACAAGTATGTTTCCTTGGGATTGAAATATAAGA
AAGGCAATGTAGACTTAAGCAGTAGTTATTATGCACTATTCAAGTATCTATTCCACCTACTTAAAAGTAAAGAATCTAACACTTTCCCTTTCTCCAATTAAACCGCAGGTAC
ATCGTATCCTCGCTGTGCGATAGTTGCATCACTCCGCGCCTGCTCGTTGGCATCGTGTTTGGATCGGCTACTTCAACTCGGCCCTGAACCCCATTATTTATGCATACTTCA
TTCAATTTCGCTTTGTTCGGGCATCCAAAACTGAATTCTCTGCACCACCTTAGACTTAGTACAGGGCTTCGGCAACTGCTGCAATCGCAAAGGACAGGGCCAACGCCACCCA
TTGCACAGAAGCGGCGGCGGCCACCATTTCGACAACAGTATCGACTGGCAACGCGGAGGCGCCACCACCAGCGCCCACCGACGAGGCTCACGTTTAGCAATTATTTTGGTA
GCTATTGCATAGCATCACGGGTGCACTGAGAAAAACATGAACAATTTATCAAATATATTAAGTAACTTGGAGTAACTTAGTTCCAGTTACACGACTAACAAATAAGAAAAA
AGATATGTGAAAAAAGAACATTGTCTCCTCATTTTTTCTCAGTGCAGCTCAGTGTTCCGCGGAGAGCGTAGATAGCGTAGCGTTCATATTAGTTGATTGAAATGCTTCTTCAT
CCACATCTACTGGTTGCTAAGCAAACAAAATAGCTTTTCCTCTGCCTGAAGAACTGAAAACTCTGCACGTTCTTTGCTCTACAGCTCTACAGCTCTGCCTGCGCCTGCCTCT
GTCTCTCTATCAGTTTCATTCTCGAGGGTATCTTTCGGGCATGGTGAATGGGACAGTGAATGGGGGTTGCAATGCTTGGGCTTTCTAATCGCTTGAACACTCTGCTTTGGTA
TTACCATCGTATACTACCATTTGCCATATATAGTGCCATATACCATATATCATTTCTCTTTGCACGCATAGCTGGCGCTTACTGTGCTGATTCGTTGCCTATGGCCCAACAA
AAGCTAAGCCCGCCAAAGTATGCAACAGCAAAACAGAAAGCATAAAACGTAATATTTAAATTAAAACGGAACCTCTTCTTTGTATGTATGCCCAGCTACAACCAGCTACACC
TACACCTTCTCCACATTCATACAAGCGTAAATGCTGATGATGAAATGTTATTCTTTCTCTAAAAATTCTCCCTTTTATGCTGCACACTTCGACACACCAGCAACACCAACAC
CAACACACACACACACACTGAGGCACATGGACGGGTCCTTGTTCGTCCCTTTTTTATATGAATGCGCGGCCTTTCATTTCGTTTTAGCATTTTTGTGTGACATTCTGTTGTT
TGTTTTTTGTTTCTTTCCCTTTAGCCTTTGTTTTCTGTGTGAAACCAAATTGTCACAGACATGTGCCGCCAGCACCCGAAAAAAAAAAACACCATACCCCTGTCGATTGTGT
CGCCCGTCCCACGCGGCGTATGCTTAACCTTTGAGTGCTGTACAGTAGCGAGCTAACTCTATTAAATTACATAGCGTACTCTAACGGTAGCATGCGAGTTTATCTCATCTAC
GCCGACGGGGAACCAATGGAGCCCAACGGACCGGATCCGGATCCGCGCGAGCGATGGCCAACTGCGACTCCAGCTGCGCGGGTTTCTAATCGCTTGAACACTCTGCTTTGGTA
CCAGTATGCCGTCAATGTCACACCCACCACGGACGCCCACGATGCAGCAGCTGCATCCCCTGTACACCAACTAAACGAAAAACACATATGGCGTATACTTGATTTCAACTCCA
GTGCTTCACAATGTCTGTTCATGAGATGAGTGCGCAGTGCACAGCAAGTGTTCTCCAGAAAACCAGATTGCCAGCTTACAAATACAAATCACTCGATAAAAACATTCCTCAA
AATGGCTGCTAAGAGGGCTAAACAAGAATTTAACCACAAATAATAGCTAAAGCAACAGCCACAGCAACAATACGACAATCCCACAGATTAAATAAAGCCTTCAAGAGCAGCA
AATTGACGTGCAAAATAAATTGAAATCTTATAGAAGTATGTATTTCGACATACAATACATATTTAGGTGTCATGGAGTCAGGAATTTCATAACGAGATGTTTATAAATGCGC
ATGCAAATAGATATATGAATTTGAATGTTTGATATACGTATATAAAAAGATAGATGTTAACCCACAAAAAAAAAAATAATAAAATATGAAATATGCATTGATTGGTAATCTA
AAACGAATCGCAAATTAAAGCTACACTGTGCAACAGTGGTATGTAGTGAGAAAAAAAGTGTAGGTTCAAGGTCTGGTTGAAAGAAAAAAATTTTTAATCTGTTCAATTATTT
GAAATATTAACTTTAAATACGATCAAACTTATCTGGTCCTTTCACATTTTATTCGATTAGCGAATAAAGACTGACAATTTTATTTTATCAGTGACTTAAAAATGATTTAATT
AAAACATTATCCACATATTCAAAGTACTTAACCAGGCCTTAAATTCACTTTAACTCTCCAATAAACAAAGATAACTAATGTTAGTTGTAGCAGAGTGTTCGTATTGTTTGTA
AAACTCACTCTCAGTTCTGTTAGATGTAATGACAAAGCTTTGATTTGATTCGTTAAATACATTAAAATAATCTAGTTCATTGAAAAACAATCAAATTATATATGTCATAA
TACTTACATACATAGGTATTCATATTCATAAAGAATACATATAGGGCCTAAAGCGCACGACTAAC
(SEQ ID NO: 67)

Exon: 1001..1564
Exon: 4101..4298
Exon: 4447..4618
Exon: 5695..5831
Exon: 5905..6087
Exon: 6381..6534
Exon: 7983..8249
Start ATG: 1149

Transcript No. : CT21432
GGTTTGGCAAACGATTGGCAATAATAGGAGTCATCAAAACGAGAGCAAATGTCATACAGCATGTCGTCCTTATTCCGTGGCGTTAGTGCGACATTTGGAGTTGGAAACTAGG
AGCCCACTTAGACTAACAACGCCCGTGACCATTACCATGACGCTACTGCAGAGGCTTCAGGCCATGTCGGCCACCACGACCAGGACAATACTGGAGGGCAGCATCAGCAGTT
TTGGTGGCGGGACAAATGAGCCTCTGGCGAGCAAAATACCCGTTCTGGAGGAGTCAGCCTCACATGCCAGATATTTGAAATTCATTGCCGACGGGCTCATGGACGAGGGACT
GGGCAGTGCGGTGGGCAGTGGGAGCAGCATCGCCGTATCCGTTGAAGACGTGGTCGCCGGACAGGCGCAGGACATCCAGGCGAGCGAAGGATCCACCGACGACGCCGACGGC

FIGURE SHEET 34

AGTAGCCATTTGGCATTAGTCTTCGTCAAGTGTTTCATTATTGGTTTCATCATACTGGCCGCCATCCTGGGCAACATGCTGGTGATTGTGTCGGTCATGCGGCACCGGAAAT
TGCGCATCATTACCAACTACTTTGTGGTCTCTCTGGCCGTCGCCGACATGCTGGTGGCCCTCTGTGCGATGACATTTAATGCTTCCGTCATGATCTCGGGCAAGTGGATGTT
TGGTTCCGTGATGTGCGACATGTGGAACAGCTTCGACGTCTACTTCTCCACCGCCAGCATCATGCACCTCTGTTGCATATCGGTCGACAGATACTACGCCATTGTGCAGCCA
CTGGACTATCCACTAATCATGACACAGCGACGCGTGTTCATCATGCTATTGATGGTGGGCTATCGCCGGCGGCTCCTCTCGTTCCTGCCCATCTGCTCGGGATGGTACACAA
CGACCGAGAACTACAAGTATCTCAAATCGAATCCGCATATATGCCGAGTTCAAAGTGAACAAGGCATACGCCATAGTCAGCTCGTCGATGAGCTTCTGGATTCCCGGCATCGT
AATGCTGTCGATGTACTACCGCATTTACCAGGAGGCCGACCGACAGGAGCGTCTGGTGTACAGATCCAAGGTGGCCGCTCTGCTGCTGGAGAAGCATCTGCAAATTAGCCAA
ATTCCCAAGCCCCGGCCGAGCATTCAGGTGGAGCAGTCGACCATCTCGACGATGCGGCGTGAGCGGAAGGCCGCCCGCACCCTGGGCATCATCATGAGCGCCTTCCTCATCT
GCTGGCTGCCGTTCTTCCTCTGGTACATCGTATCCTCGCTGTGCGATAGTTGCATCACTCCGCGCCTGCTCGTTGGCATCCTGTTTTGGATCGGCTACTTCAACTCGGCCCT
GAACCCCATTATTTATGCATACTTCAACCGCGACTTCAGGGCCGCCTTCAAGAAGACCCTCAAGAGTCTGTTTCCCTACGCTTTCTACTTCTGTCGACGTGGCAGGGGGCGA
GACGATGACCGGGATCTGGAGTTCGGCGGGTCCCAGCCGACGGGGGAACCAATGGAGCCCAACGGACCGGATCCGGATCCGCCGAGATGGCCAACTGCGTCAACTCCACGGCCT
CGTCGGAGATACACATGAGCGTGATGCGTGCCCGCCAGTATGCCGTCAATGTCACACCCACCACGGACGCCCAGATGCAGCAGCTGCATCCCCTGTACACCAACTAA
(SEQ ID NO: 68)

Start ATG: 149

MTLLQRLQAMSATTTRTILEGSISSFGGGTNEPLASKIPVLEESASHARYLKFIADGLIDEGLGSAVGSGSSIAVSVEDVVAGQAQDIQASEGSTDDADGSSHLALVFVKCF
IIGFIILAAILGNMLVIVSVMRHRKLRIITNYFVVSLAVADMLVALCAMTFNASVMISGKWMFGSVMCDMWNSFDVYFSTASIMHLCCISVDRYYAIVQPLDYPLIMTQRRV
FIMLLMVWLSPALLSFLPICSGWYTTTENYKYLKSNPHICEFKVNKAYAIVSSSMSFWIPGIVMLSMYYRIYQEADRQERLVYRSKVAALLLEKHLQISQIPKPRPSIQVEQ
STISTMRRERKAARTLGIIMSAFLICWLPFFLWYIVSSLCDSCITPRLLVGILFWIGYFNSALNPIIYAYFNRDFRAAFKKTLKSLFPYAFYFCRRGRGRDDDRDLEFGGPS
RRGTNGAQRTGSGSAEMANCVNSTASSEIHMSVMRARQYAVNVTPTTDAQMQQLHPLYTN*
(SEQ ID NO: 69)

Name: 5-HT1A/Ocr-like receptor
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384515
CTGGACGCCGGACACGAAAGCAGATCACCTGCCGTACAGTGCCAAGATCATCGAACGCATTTACAATGAGGAGATCGGTGATGGCGGTGGCCACAGTGCACGGAGGATAAAC
ATGCTGGAGTTCAGTCAGTATCTGGAGCAGTACCTGTGGCCACACTACCAACGTGAAACCGCCACCCATGCCCACCTTATGTCCATCGTTATAATGGCCAACGAGAAGTTCC
GGGAGCGCGTCGAAGTTTGGACCGTGTTTGAAAAGCTCCCGGATCAGTATCCAGCCTTCTTTCGCCACGTGCTAGAGAGCTGTTTGCCGAGCAAAAAGGCAAAGGAGGCTAG
TAGCACGCTAAGGGAGCGGACAGCGCTGTTGATGTTCATTAACCACTGCTTTAACAGCATGGAGATAGAGCTGTGCAGAGAACAGGCCAAACGACTAGTCTCCTTGTCCATG
TGGCATTGCCTGCAGCCTCGTAAGTTCTTCTTCGCAACTCTTCACATCTATCAAAGTGATCAAAAATGTATTTGCTTGCAGGCCGTCGCGAACAAGAGCTTCGAGAAGTTCC
CTCGAAAGCATTCCCGCCGAAGGCGAGGTGCCGCGCAACGTGGTTCACTACTGTGTGAGCGCTTCCTAGAGTTTATTATCGACTTGGAGGCACTTTTGCCGACTCGACGCTTCT
TCAACACGGTTTTAGACGACTGTCATCTGATTGTGCGGGCTCTTCTGTCACCCTTGGTTCGTCGCGAGGAGGGAAAACTGTTTGGTCAGGTAGGTGTCAGACTTCTCATTTA
ATAACTATCTCGTACAGCATAAATTAGTTAAAATTAAGTACAAATCTCAATGTTGGACATTGCTAAACTACGAAACACTTATATTAGTGTGGACGGTGGCTCCTCAGTAAT
CGTTGCCGTTCATATAATGCAGCTCATCGCCCCAGTCGTTTGCCGACGGTGGCTCATTGTAGCAGCAGGTCTTTTTCAGCAGAAATGTCACATGTCGCTGGCGCAGCACGCA
TATGTATAGCAACAGCGGCGTCTGCAGGGCGTTAACTACGATGTGGGCGTAAAGCAGGCCTTCCATCTGCAACCAGGACATTATGAGGAATAGCCAGGCTATAGACATTACT
AACAGCATCAGCGAGAACATGATAAAACTGCAAGGAAGATAATGTTTTCATATACTTATATGTAATGCCTAGATGCCGATCTACTTACTTGGCTTTCAATTTGTGCGCAATG
CGGCCGTATACCGTCCTGCGGTTAATCAACTTCCTGGTGGTCACATAGAAGAATATGTTTACCAAATGGTACAAGCAATTGGAGCAAAGAATATGCATATGCCTAGCCAGC
CGATCGTCTCTTGCTCGCCCACCATGTGCTCCTGTTTGTAGGATTCGGCGTCGAGGAAGAAATGTGCGAAGACAGCCAGTGCAGCCATCGTTGCTGTGCATCCCCAAGCATA
CGCAGAATAATAGCAGTACTTCCTGCCGTCCGTGACTCGCAGGAAGGACGTTCCTCAAATGTAAAAACCGAAACTGTTCAGCCAGAAGAAAAGCTGCC
AAGAGGCTGAAGCACAGGATAATGTCCGCCACAATGAAGCTCACATGGCTGGTCAGCTCGGTGAAAATTCTGACAAGGTCTGCTGCCTGGCTTACCATAAGGCACATGGCTA
TCGTTGTCACAATGTTACCAACCAGATCTCTGCTGAATGGATTGAAAATTAACGCATGAAGCAAGTCAAATTCAAACTATTGCTCACCTGAGAGTAGGAAGTATAAAATAGA
TGATGGCGATGACCAGCAGGATAACAAGCGAGATGCCATGGAAAATTGGGTTTAAGATTTTGCGGAGCAGAAAGTTTGAGTCACTCCACTTGATCTCCTTGCGGGCCAAGCA
CAATACAATCCCTTATCGTAGTCATGGTATAGCGGTTCCAGACTGCCGGCAATATCCTCCTCATAATCCGATTGTATTCCATGACGCTCCTCTGCTTCGTTTTCGGCATTGG
TGTAATGCCTTAGCCTCCCATCATCCAGTAACACTAGCTTATCAGAGCTCTAGAAAATATAAAAATATCTATAAGTATCTAAAAGTTTCTATGCAAAGAACTTCAAACTCAC
GCCAGCATAGTGGTATATTGGCCACATCTGCATGGATCCACAATTTGGAATCCCGATGACGAATTTGAACTTAACGGGCCTGTTTTGCTCTCCTCCATAGCTGGTGAACATC
GGCTGGAAGTAGTCTGCAAATGGAAACGGACGATAAATAGAGAACACAGACCGTGGAAAATCATAAAGGCAGTTCAAGTTAACGCTGCTTTTGTTGCGGCTGGTGGATCAGA
GGGGAGCCAGATTTTCTTTTCTCTCTGCGAATATAAATATTTACGCTTCTGGGCAAAGAACTTGAGCTGTTCCATGCGCCTTCATCAGCTGGTTTTGCAATTTGTGCAGATT
GGTTCTTCTTCAATTATCGGAGTTCGGATACATTTTTTTCCACTCAGCCATTCATATGTTAATCATAGCTAAGCACACGGAAATTAGATTGCATGTTGCGATTATGTGCCCT
ATGGCCGATCCATGGTCATAAATGTTTTATCCAGTTTTAGTTGTCGAGCTAGAATATCGATATAGATGCTAGAGTACGCTTTTCTATTTCCCACAATTGTTGCGATTGTTT
GTCAAACATTCACCCAAGGCAATATACTATATTCACCATTAGCTCCACAAACATTAATTACCAGGGCTCGCATTTATGGGGAACAGAAGCATCTTATATTACCTTACTA
ATGGATTTTTTGCCTCATTTTACTTCCAAGAGATAATAATTCCCGATTTGGGAATCCCTCATCAAGTGGCTACTTTATAGTTTAAACAGAAACATGCCCCACAGCATAAATCA
TATTTCTCATCAGGATTGGGGCCACCCTCTGTTTGTTTAAGAACTTTCTTGGGGGAGTGCGAACTGTGGAGTTGGGGATATTTAGCTGTTGGCTTCGTTCCACTGATCCAC
TGATAGCCAACAAATGGGCCATTTAATGTTGGGCATACATATGTTGCATGCCAGAAGGGAAAATCCATAAAGTTGAATGGCCAACCAACTTCGTTGTGGTTGTTATGGCAAC
GACCAGCACTAGGTTGGGATCGGAAGATAGGGCTGTTGATGATCCGGCGCTAGTGACATGACTGGTT
(SEQ ID NO: 70)

Exon: 2651..2621
Exon: 2477..2353
Exon: 2289..2119
Exon: 2061..1880
Exon: 1824..1321
Exon: 1259..1001
Start ATG: 2651 (Reverse strand: CAT)

Transcript No. : CT21585
ATGGAACAGCTCAAGTTCTTTGCCCAGAAGCACTACTTCCAGCCGATGTTCACCAGCTATGGAGGAGAGCAAAACAGGCCCGTTAAGTTCAAATTCGTCATCGGGATTCCAA
ATTGTGGATCCATGCAGATGTGGCCAATATACCACTATGCTGGCAGCTCTGATAAGCTAGTGTTACTGGATGATGGGAGGCTAAGGCATTACACCAATGCCGAAAACGAAGC
AGAGGAGCGTCATGGAATACAATCGGATTATGAGGAGGATATTGCCGGCAGTCTGGAACCGCTATACCATGACTACGATAAGGGATTGTATTGCATTGACAAGGCCACTTCC
AGTACTGGAGAGGAAAATGTGCTATTCGCCAACATTTGCTTGGCCCGCAAGGAGATCAAGTGGAGTGACTCAAACTTTCTGCTCCGCAAAATCTTAAACCCAATTTTCCATG
GCATCTCGCTTGTTATCCTGCTGGTCATCGCCATCATCTATTTTATACTTCCTACTCTCAGCAGAGATCTGGTTGGTAACATTGTGACAACGATAGCCATGTGCCTTATGGT

36/89

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AAGCCAGGCAGCAGACCTTGTCAGAATTTTCACCGAGCTGACCAGCCATGTGAGCTTCATTGTGGCGGACATTATCCTGTGCTTCAGCCTCTTGGCAGCTTTCTTCTGGCTG
AACAGTTTCGGTTTTTACATTTGGAAGACCTTTCGTTCGAGGAACGTCTTCCTGCGAGTCACGGACGGCAGGAAGTACTGCTATTATTCTGCGTATGCTTGGGGATGCACAG
CAACGATGGCTGCACTGGCTGTCTTCGCACATTTCTTCCTCGACGCCGAATCCTACAAACAGGAGCACATGTGGGCGAGCAAGAGACGATCGGCTGGCTAGGCATATGCAT
ATTCTTTGCTCCAATTGCTTGTACCATTTTTGGTAAACATATTCTTCTATGTGACCACCAGGAAGTTGATTAACCGCAGGTATACGGCCGCATTGCGCACAAATTGAAA
GCCAATTTTATCATGTTCTCGCTGATGCTGTTAGTAATGTCTATAGCCTGGCTATTCCTCATAATGTCCTGGTTGCAGATGGAAGGCCTGCTTTACGCCCACATCGTAGTTA
ACGCCCTGCAGACGCCGCTGTTGCTATACATATGCGTGCTGCGCCAGCGACATGTGACATTTCTGCTGAAAAAGACCTGCTGCTACAATGAGCCACCGTCGGCAAACGACTG
GGGCGATGAGCTGCATTATATGAACGGCAACGATTACTGA
(SEQ ID NO: 71)

Start ATG: 1 (Reverse strand: CAT)

MEQLKFFAQKHYFQPMFTSYGGEQNRPVKFKFVIGIPNCGSMQMWPIYHYAGSSDKLVLLDDGRLRHYTNAENEAEERHGIQSDYEEDIAGSLEPLYHDYDKGLYCIDKATS
STGEENVLFANICLARKEIKWSDSNFLLRKILNPIFHGISLVILLVIAIIYFILPTLSRDLVGNIVTTIAMCLMVSQAADLVRIFTELTSHVSFIVADIILCFSLLAAFFWL
NSFGFYIWKTFRSRNVFLRVTDGRKYCYYSAYAWGCTATMAALAVFAHFFLDAESYKQEHMVGEQETIGWLGICIFFAPIACTILVNIFFYVTTRKLINRRTVYGRIAHKLK
ANFIMFSLMLLVMSIAWLFLIMSWLQMEGLLYAHIVVNALQTPLLLYICVLRQRHVTFLLKKTCCYNEPPSANDWGDELHYMNGNDY*
(SEQ ID NO: 72)

Name: mth-like 5
Classification: G_protein_linked_receptor


Celera Sequence No. : 142000013383774
GCTGTTCGCACGGCATTTTTGGGCCAGCAAACAGGATGCGGAAAACCGGAAGCTGGGAACTGGAAATGGGCAAGAATCTGGTTTTTGGCTGCCATTCAATTAGGTATCGGTC
AGCCCAATTCAACTGCTGCTAACTGGCAACTGGAGATTTGGCGATTGCAGCTGCCCATTGTCAACACTTCAATTAACGCAATAGCAGGTAAAAAGGGGACATCTTTTCATCG
AGATCTCGACCTTGTTTTGCTATCCTTGCAAACAATTGATGGTATGTCGTAAGTTTGTGCGAATAAAATGGTTTTGGAAATATATATATATATATTGTTTATTAGTTTATGGCC
CCAAAAAATGCTACAACACAATATTGAAACCGTTGTTATCTGAAGGGAATGCAACGATTCGAGCTTCATATTGAGAAGGTCCTGTTTTCTCTCTGTTCCTGCATAGTTCCTC
TTTCATTTCGCATCTTTTTCCACTGGCCGCAGTCTCGCAGGATATGCTAACTAAGGACTATGCCACCATATTCGACAATTTGTTGGGCACCAAGTTAATATGCATTGATGCG
CTTAGGATAACAATTACGTTTAGGTTAACTAGCATAAATCTATAATCATCACATTATGGCACAATGTATGTTATGTAGTATATATATATCGTATATATATAGAGAGACTGATAT
ACATAGATATCGATTGATATAACAAATTAAATTTTCAGCTAACCGCACGCTTCAACTGAATCACTTTTGATTCAATCATCTCACTTGTGATTCCGCGTGATTTGCTGGCAAA
TTTAAAGCCCTCTTCTCGTGTTTCATGAGAAGTTTCATGATATCATCTATCACTCCTCTCATGGAGTTTAAAACCATAAATATTTTATTATAAATATTCACTATTCACGCTA
CGTATTGTTACGCGCATGTCGACGTCTATAGCGATATCCCGTTATCAGTTCTCGAACCGTCTTTCGGTACTTATCGGAAAGTACACAGTATAGAAAAAAATTGGATGCCGCA
TGTAGGGAGGCCAATAGGTTACACACATTTCCCGCCACCACCTGAGTGCCAATTTGAATTTCCATATACTGATTGACTATCAAATAGATCGCCCAAGGCAATTGGCAAACTA
TGAACATTAACACCACCGCAATAAGTGTGATCGTCACGCGATTTTCCTGCGATACGCTGCCTTTTAGTCCAGAATTTGATTGCGCTAAGGATTCAGAATTTATACAACATA
TCATCATCATCATCGTTTCGAATAACTCACTTTTGTGCGCCTTATGCTGCTGGCATTGGTCAGGTCACCACGCAGATTCTTGGACCGATGAACCAATAGAATGAGAATG
GAGTTGAAGGTGGCCAATAGAAGTAGGGGGAATACCACGAAGACCAGCAGGGTGAACAGGTTCCACAGATAGCTGTATAGCTCATCATAGCCCAGTTCCGAAAGACCATGAT
TGTAATAGGTCACCTAAAACATATAGATAGATACATAGAATACATACATAGATTTCCATTAAGAACAACCTTTTAAGCAATGGAATATCCCAAGCGACTAAGTAAAAGCATG
TCTTACAAAACCCAAAGCACTGATATCATTTTAAGTTATCACCGAATTTATCATAGTCATGGCGCTTGTACACCGCTCGTGATTTTCACTGGTTAACAATTTTCTCATGTTT
TTTTCTCCAGGGAAATCGACGGTATTTCCAACATTATTTTACTCACATTTTGACAGTATTCCGTTACGTTAAATGCGAATGCATCCGTATTGTTGATGTTGTGATTCTCAGC
GTCACAAATCCAGATGACTGCCACGGGTGGCGGCGGCATGGGCGAGATGTTGGCCACCGTTTGGTTGCACGGCTGGTAGGCGTCATCAATCTGCCTAGTACCAATCGTAATTGTA
TGCTCGAATGCCGTCGATAGTGTGGACAGCAAACAGAAGATGGCCACCGCCTGGCAATGTAGAATATAAAGTTGCATATGGAAATGGATTCTATTGTTACATACGCCTATTTC
AGCCAACTCACCTGCTATCACCTTTTTGGCCAGCGATTCCGTGCAGAATGTTTGCCTCTTGAGCGGATAGCGTATCGCAATGAATCTCTCGATGGTGAAGCACACGGCTATG
TAAATTGAGATGTAACCTGTCCGGTAAAAACAGAGAAAGCAATTGTGAATGGGGGCGTGGCAGTACAATACGAACGCAATCAAAGATGCACTGCAAATATTTTGGGAAAATC
CAATCCAAAAAGGATATATATACATATATATTTATTCAGGTTAAGTGTCTAATATAGATTGGTAAATTAAATTCAAACTTCGGTTAGACTGTGCCTTTTTTCCGTGTACTCT
GGAATTATAAAATAAACGCAGCTCCGCTGTTAATACCCCAAACCATCCATTTTTGACCGCACCACCAATTTATTTGCCGCGCGGGCTGTCAATTTATTCAAAACGCAGCGCAC
TCTAAGCGATTGACGTCCGTGCTGTGCTGATGAGGTTGCTGCGGGAGGGTGGGATATTCAAGGGGGTGAGGGGGGTGAAAAGTGGGGTGGGAAAGCGGAAAACGGTTCGGA
AAAACGCTATCGCATGGCAGTGAGCCTCAGCTGACCGCTGGCATTTCGCAGAAAGCGCTGCTTACTATACCTCGTAAATTGGCAGAGCTCAATGAAATTGATGCACAACAGA
AACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACAGCCGCAGGTGCAATTCGAATTGATGGGCCCATCGCTGGAATCCGGTTGATACGGGGGGAAATGGGGGAT
ACATTGGATCCGGGGATCCAGACGAGGCTAACCCGGGGAACTGGGGAATTTATGGAATCCGCACCATTCCACTTAGTGCTCTCCAAACGTTGCATTCGAACTGTTTTTGCTTT
TTTGCCCCCGGCAGCAATTGTTTTCACCGCATGATATGTACGCTTTTCTTATTGTAGTTTTGCGGGAATAATGTTAAATATAAAAACACCCTTTTGGTAAATTTTTTCAAAT
TGAAAGCTTATTTAAGCATAAAATACTCGTGTTTCGATTTAAAGAACACTAATCGAGTTACTTTCGGTCTCACAACCTTATTTATTGCATACTTTGCGACTGCTTTGAATTA
TTGAATTATTACTCCATTGCTACTTAATTCTAATTTGGTCAGTACTCACCGAAACTGTCGCACAGCCAGACAAAATAGCCATAGAGCTGCCAGTAGAGCTTGAAATGATACT
TGGGATAGTCATAGTGCTGGAGTGACAGGATTAACTGGCACGTCAGGTAGGCAATATCCGTAATGGCCAGTGCCGTTAGATATATGTTCGTCGTGCATCTCATGCGCTTTCT
AAAAATACCGTCAAGAATATCGAAAAGAATTGCAAATGGTGTTGATTCTGTTGGGCACTCGACGCATTTGGAAATCAGGCCAAACCATTTCGGTGGACAATGCAAAAACGCT
CTTGGGCATTTTCCGAAATGCGCACAAATGTCGGCACAGTCATAAAGCCAAAAGATGAACAATAAAAACTAACTGTTAGCATTTAGTTTTCTCCCTGGCATCGCCCGCAGCT
CTGATAGTTAAATTCTCTTGTATTCCCGTAAAACAAAATAAAATAACGTAATGAAAATATTTAATTAAAAAGCCATTCATGCCGTCAACGCTCAATGTTAAGCTAGTTGCTT
TGAAAAGTTGTAAATATGGTTTAAAATAATAAAGTTCATGCTATAAATATCAATAAATTTTGTTTAGCAAATAAATGAATTTGCTAAGATCTTAGCAAGGAACACAGTTTAT
CTTTTTTTTTTCACGTTTTCCTGGGAAATGGACATATGGTGTCATAGCAGTCAGCCTAACGCACAGAGCACTTGCAACTGTCGCATATTTTCCGGCAGACATAAAAAACACAC
CCATCCACACAGCATATCGCCTATCTGTGTGCGTTTTTGCATTTGGCACATAAAATGGCTCTTATTGTTTCAGTTACTGTTATTGTTGTTGCACTTGTACCCAACGTAGTTG
TTGCTGTTGTTATTGTTATCGTTGTTGGCTGTGTGGAAATGATTTTAAAGTGCAGCGGTGGCTACAATTAAATGTCGTGTTTAATGCGCTGCGTACCTGCTCGCCGCTTCAT
CCATGTTCCACTTATTTCACACACACAGACACACACACACACGCCACACACGCACACACGGACACGCATGCATGCAGTTGGATGCACAGAGAGAAAATCGTGCAAGTTAGCTGGCATTTTAAATGGAAA
ATTGTAACTTAAAACTAGTTTAAAACAAGCTCAAACGAATAAGTTGAAGTTTGGAATAAAATTAATTTGAAAAGGCTCATATATTTTATATGCATTGCATACTTTTTAGTAC
TTAACCAAATGCATGAAAATCCAATTAGTCGCTTTTGCATACCTAATAACTTAACATTCTTAACGTGGCAGCTAAAACTTCTTTCAAATGCCATCATCAGCTAAATGATTCA
TATTTAATTCGAAAATCTTGTGACCCTGCTGCATG
(SEQ ID NO: 73)

Exon: 4299..3858
Exon: 2816..2700
Exon: 2625..2338
Exon: 2177..1951
```

FIGURE SHEET 36

Exon: 1693..1490
Exon: 1189..1001
Start ATG: 4299 (Reverse strand: CAT)

Transcript No. : CT21642
ATGACTGTGCCGACATTTGTGCGCATTTCGGAAAATGCCCAAGGCCCCGCGCCCATCACATCAACCGCCTGGAATTTTCCACCCCCTCTGCGCACAACCCCACCGATCGTTT
GGCTTTCAGGCAATTTGCTATTTCAATTGGTGTTGCACTTGGCAGCGTTTTTGCATTGTCCACCGAAATGGTTTGGCCTGATTTCCAAATGCGTCGAGTGCCCAACAGAATC
AACACCATTTGCAATTCTTTTCGATATTCTTGACGGTATTTTTAGAAAGCGCATGAGATGCACGACGAACATATATCTAACGGCACTGGCCATTACGGATATTGCCTACCTG
ACGTGCCAGTTAATCCTGTCACTCCAGCACTATGACTATCCCAAGTATCATTTCAAGCTCTACTGGCAGCTCTATGGCTATTTTGTCTGGCTGTCGCGACAGTTTCGGTTACA
TCTCAATTTACATAGCCGTGTGCTTCACCATCGAGAGATTCATTGCGATACGCTATCCGCTCAAGAGGCAAACATTCTGCACGGAATCGCTGGCCAAAAAGGTGATAGCAGC
GGTGGCCATCTTCTGTTTGCTGTCCACACTATCGACGGCATTCGAGCATACAATTACGATTGGTACTAGGCAGATTGATGACGCCTACCAGCCGTGCAACCAAACGGTGGCC
CGACGTCCGGCAGCTCTAATCAGCTCGTCGACTGGGGCAGTGGCAGTGGTGATGGTGAGGAGCCAGAGAACATTCCACGACATCGCCGTCACTGGCAGTCATCTGGATTTGTGAC
GCTGCCCACACTGAGAAAAAACGCTGGAGGAGCAGGATCAGAAGGTGGCAGACGCGGCCCAGAGGTCAGGGGTCACAGAGAGTTTGCTGCAATTGTGGCGTCGCAAGCGCAGC
GCTGAGAATCACAACATCAACAATACGGATGCATTCGCATTTAACGTAACGGAATACTGTCAAATGTGACCTATTACAATCATGGTCTTTCGGAACTGGGCTATGATGAGC
TATACAGCTATCTGTGGAACCTGTTCACCCTGCTGGTCTTCGTGGTATTCCCCCTACTTCTATTGGCCACCTTCAACTCCATTCTCATTCTATTGGTTCATCGGTCCAAGAA
TCTGCGTGGTGACCTGACCAATGCCAGCAGCATAAGGCGCACAAAATACCGAAAGACGGTTCGAGAACTGATAACGGGATATCGCTATAGACGTCGACATGCGCGTAACAAT
ACGAGTCTCTATGTGCCGCATACAACGACTACACTGACCCAAATAAATGGCGATCATTATGGTAGTAATTATGGCGGAGCCGGAAGTCGTCGAAATCGTAATACGGGTCGCC
TGATAGCGTGA
(SEQ ID NO: 74)

Start ATG: 1 (Reverse strand: CAT)

MTVPTFVRISENAQGPAPITSTAWNFPPPLRTTPPIVWLSGNLLFQLVLHLAAFLHCPPKWFGLISKCVECPTESTPFAILFDILDGIFRKRMRCTTNIYLTALAITDIAYL
TCQLILSLQHYDYPKYHFKLYWQLYGYFVWLCDSFGYISIYIAVCFTIERFIAIRYPLKRQTFCTESLAKKVIAAVAIFCLLSTLSTAFEHTITIGTRQIDDAYQPCNQTVA
NISPMPPPPVAVTPPLATPPLPTPATIWQSPDSAMESTTSGSSNQLVDWGSGSGDGEPENIPRHRRHWQSSGFVTLPTLRKTLEEQDQKVADAAQRSGVTESLLQLWRRKRS
AENHNINNTDAFAFNVTEYCQNVTYYNHGLSELGYDELYSYLWNLFTLLVFVVFPLLLLATFNSILILLVHRSKNLRGDLTNASSIRRTKYRKTVRELITGYRYRRRHARNN
TSLYVPHTTTTLTQINGDHYGSNYGGAGSRRNRNTGRLIA*
(SEQ ID NO: 75)

Name: TRH receptor like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384839
ATAAATGGCCGAATTTGCAAGTCAGTTCCACTTGCTCTTTAAAAAGCGAATCTCACCGAAATTTAAGCAAAATTTATCACCGACCAATGTGAAATTCCACTAATAATTTTTC
AGCGGTGTTGATGGCTTTATTGACATCGCCAGAAATGATTCGAGCTGTAGCAGCGAAAATTTAATCAAAGACCTAACCCACGAACCTGGACGTTCTCACATAGAAAATGAAA
ACGAAAGCTGAAAGACAGATGGATCGTTCGATGTGAGCTCTTTTTACACTTGGCTTACACGACGACTGCGGCGTCGGTAAAATTAATATACCAAACAATTACACGGCCCGGC
AAAACAATTTTAAGCCCAGTTAATGCCGTCGCACAGTGGCTGCAAGCCACGCAAATTCGCCGCGAAAAATTGCCCACAATTGCCAGTGGCCGAGAAATGAAAGCGCTCAAAT
TTGCATACTCGTACTGTCAAATGAAGCGTAGCAAAAGGAAAATTGCTACACATACTAATTGGAAAAGAAATGCAAAACCAATGCAAATGAAAATAATGACAGGGCGCGGTTT
CTTATTTGGACATATAAACCATACGTAGAATGATAAGAATAATAAAAACAAGTATGTTGGACACAATTGATAAGGAATCTTTAGTACTTTCTCACCTAAAAAAGGTGATAT
ATATTTGAATTCATGTTGTCATGATAGCTACTCGAACCACTGTGCGTTGGCTACAGTCTGCTGATGCTCACAGTGTTTGAAAGTTAAGACTTTTGCTTTCCTTCCCCCGACT
TGGTTTTTGCTTTTGGAAAGACCAAGCAAATGGATAAACAAGAGTTCAAGAGGTTGTCAGCCCCGCCCCTTTGCGCACATGAGGCAAGAAAGAAAAGAAAGTTATTACAAAA
GAAAAGCTCGTATGAGCGGGACTTACCACCTCCATTGTTGGCACTGGAGCAGTGTTTGGACGTGAGCCCGTGTTGGATGCGAGAGTTGGGCAGTCCGCAGCCGGGTC
ATCACGCCGTACTTGATGGGCTTGAAGTGGAAGAACGAGGGCGAGTAGCCGGAACCGGCCGCGACTCAGGGAACTGAACTGCTCGCGGTCCTCCACGTACAGGCCCTCCT
TGCCCATGGCCGCCAGTTGCCTGCCCTTGGGCATGAACATCACCAAGAAGACCGTGGCGGATGTGGCTACCAGACCGAAGGCCACGCAAGCGTCCTTGTGCCGCTCGGCCAC
GGCCAGGCCGCATAGCATCCATCCCAGCCAGATGGGGATGGCTCCTCCGATGGCCAGCCCAATGTAGGTGGCCTCACGGTAGTTGTCCCTGATGCGGCGCGACTTGATGGCT
AGCACGGCGATGAAGACGATCAGAAAGACAATGTAGATCAGCGAGAAGAGCAGCTCCGAGAACTGCGTCTTGCAGAGCGGTATTAGTACGGTGCTAACCGCCGCTATCCGGG
TGTAGATCTCCGGAGTCCCGTCCAGCGTTGTGTAGGACGTGGGGTAAAACAGTGCCGAGTAGTTGGTCTGTGTGAGGCCACCGTGGTGCTAAGGAAGCCACTGCCCATCACAGG
CACACTGGTGGTGTATACCTCCGGTGGTTGGGTGAGCAGCCACTGCCCTCCGATCGCTACCTGGATGAGCAGCGCAAAGAGGAGCAGCAATCCCTGGTATGGAGCCGGCAGA
TACACCCCTCCATTTAGACTAATCAGAAATACGCATTTGACCAGCAGGGCGGCAAAGACCAGGGCGTAGGCCACGCCCACTCCGAAGCGGATGGCCCCGCAACTGATCAACG
AGGGCTGTGCGGTGATGATGGCCCCCAAACTAGCGCAGCCGGCGAACAGACCGAGAAGCAGCATCTGGCCCAGAAAGAGGTGCCTACGCGACGGGGACGTCCGCCAGGCCTTGAA
GAGCACAAAGATCTCGAACGCTGCCATCATGAGCATGGTGAGGGTGGCCAGGACTAGCACCGGCACCACCCACGGCTCCTTGCCGTAGTCCCGCGAAGGGCAAGTGGGTGGAC
ACTATACTGGGCGGTGTGCTGTTGGAGCTGCTCCCGGGAGTCACCCGTCCAGTGGTGCCGGCTGCTCGCGCCTTCGCCCCTGAACTCCGACGGGGCGTGGCTGGTGTGGTGG
TGGACGTGGTGCTGCTAGAACTGCTGGCCGATAGTGTGGGTACCACAAAGAATTCCGTCGACATTTCGAGACGGGCAGCACTGGAGACATTGCCACCCGGAAAATTGAGATC
CGGCTACTCGGCTTAAGCACCTGGTAGGCGTTGCGATCCGATTCCTGGCTGGTCACCAGGCCACCCGCCCAAATGTTGTTGCCATTAACGCTGAGGCTGCGCGACGCCG
GCGTGGTGGCGATCAACTGCATGATCAGCAGCAGGATCAGCAGCAGGTGGCGTCTACCGGCCATTGGATGTGGTGACCTTCGATGCCCTGGACCTCTGACAATATAATCAAA
CGCGGCACATCTCTTGCAAACGCACACTAACCACGCACTCGCGATCGCGATTGTTCAGGTTCGTAAATTCTTCAGTCCTCGCAGGCCCTAGATCATGAATTCTTCTTCTCGA
TTCTCGCGCTAAAACGTCCGCTCGCTCCGATCGACCAACTGCAACTGACTGGCGGCTCTGCAAGTTGGGCTTTGGACCGGCTTAGTCGTTTGAGACCAGTTTGACGGCAGCC
AAGTCGAACTAACACTTGTTTGAGTTCGATGTGCGTTTGCTAACCCGGCTAACGTTACAGGAACGCAACATGATGCGTGGGAGGCAGTTGGGGTTTGGGGCGCTTTATATG
ATTTTTTGCAATGTAGAGTATTGCACGAGCATTTACTAAAGCATCCTTTGAATTTGATACAACATTCGTTACTCGATCTTCTGGCTTTAAGGTTTAGTATATAGCTTCAACA
ACTAATGTTCTAAATAGCTCAATGTCTTGCTGAAGGGCTATTGATTTCCTCTCGAAAGCTATGGTACTTAATTTCCTATTTAGAGCCAGTAAGAACTCAATTTATCTTTAGC
TTCCGTGCTAATCCGCTGGAACATATACTTTAACACAACATTTACATACGTAAGTTTTTTTTCCATTTGATAATTATTCCAATTAGATTTCATATTGCGGGATATTAACATT
CGTTCTGCATATGCGGAATTTCGGTTTATGGGCTCTGATGCTCGAGTTGGCTGGTAGGAAAGTGCTATGGGCCATTATCTATTAGCCAACCGCTTTACGGTCTCCTCGCGG
AGCCTCTCTCCTCGAAAACGAGCCAACAAAAGGCCAAATAGCGAAATCCGAGCACAAAAGGTGATTGTAAATCAAAGAGCGCTAATGGTATATCGATATACAAAGTGTTGA
GGCGGGAAAGGCATCGCCAATAGCGTTAGAAACGGCAATAGCAATAGCAACCCGCTCTGATTCCTTAGGTCTTATTGTATTCGGCGCGCGCTTTCAGTCAACCGCAGTTAGA
ATTCAGATCACCTGAATGAGTGGGCA
(SEQ ID NO: 76)

Exon: 2946..1001
Start ATG: 2752 (Reverse strand: CAT)

FIGURE SHEET 37

Transcript No. : CT22117
TCGATCGGAGCGAGCGGACGTTTTAGCGCGAGAATCGAGAAGAAGAATTCATGATCTAGGGCCTGCGAGGACTGAAGAATTTACGAACCTGAACAATCGCGATCGCGAGTGC
GTGGTTAGTGTGCGTTTGCAAGAGATGTGCCGCGTTTGATTATATTGTCAGAGGTCCAGGGCATCGAAGGTCACCACATCCAATGGCCGGTAGACGCCACCTGCTGCTGATC
CTGCTGCGTGATCTCATGCAGTTGATCGCCCACCACGCCGGCGTCGCGCGAGCCTCAGCGTTAATGGCAACAACATTTGGCGGCGGGTGCGCCTGGTGACCAGCCAGGAATCGGATC
GCAACGCCTACCAGGTGCTTAAGCCGAGTAGCCGTAATGCCACCAGCACCACCACTACTACCAGCACGACTACAAGTACTACAAGTAGCACCACTAGTACCACTACTCCGGC
AGCTCCTCAGACCCAGCCGATCTGCCAAACAATTGGATCTCAATTTTCCGGGTGGCAATGTCTCCAGTGCTGCCCGTCTCGAAATGTCGACGGAATTCTTTGTGGTACCCACA
CTATCGGCCAGCAGTTCTAGCAGCACCACGTCCACCACCACACCAGCCACGCCCCGTCGGAGTTCAGGGGCGAAGGCGCGAGCAGCCGGCACCACTGGACGGGTGACTCCCG
GGAGCAGCTCCAACAGCACCACCGCCCAGTAGTGTCCACCCACTTGCCCTTCGCGGGACTACGCAAGGAGCCGTGGGTGGTGCCGGTGCTAGTCCTGGCCACCCTCACCAT
GCTCATGATGGCAGCGTTCGAGATCTTTGTGCTCTTCAAGGCCTGGCGGACGTCCCCGTCGCGTAGGCACCTCTTTCTGGGCCAGATGCTGCTTCTCGGTCTGTTCGCCTGC
GCTAGTTTGGGGGGCCATCATCACCGCACAGCCCTCGTTGATCAGTTGCGGGGCCATCCGCTTCGGAGTGGGCGTGGCCTACGCCCTGGTCTTTGCCGCCCTGCTGGTCAAAT
GCGTATTTCTGATTAGTCTAAATGGAGGGGTGTATCTGCCGGCTCCATACCAGGGATTGCTGCTCCTCTTTGCGCTGCTCATCCAGGTAGCGATCGGAGGGCAGTGGCTGCT
CACCCAACCACCGGAGGTATACACCACCAGTGTGCCTGTGATGGGCAGTGGCTTCCTTAGCACCACGGTGGCCTCACAGACCAACTACTCGGCACTGTTTTACCCCACGTCC
TACACAACGCTGGACGGGACTCCGGAGATCTACACCCGGATAGCGGCGGTTAGCACCGTACTAATACCGCTCTGCAAGACGCAGTTCTCGGAGCTGCTCTTCTCGCTGATCT
ACATTGTCTTTCTGATCGTCTTCATCGCCGTGCTAGCCATCAAGTCGCGCCGGCATCAGGGACAACTACCGTGAGGCCACCTACATTGGGCTGGCCATCGGAGGAGCGCATCCC
CATCTGGCTGGGATGGATGCTATGCGGCCTGGCCGTGGCCGAGCGGCACAAGGACGCTTGCGTGGCCTTCGGTCTGGTAGCCACATCCGCCACGGTCTTCTTGGTGATGTTC
ATGCCCAAGGGCAGGCAACTGGCGGCCATGGGCAAGGAGGGCCTGTACGTGGAGGACCGCGAGGAGCAGTTCAGTTCCCTGAGTCGCGCCGGTTCCGGCTACTCGCCCTCGT
TCTTCCACTTCAAGCCCATCAAGTACGGCGTGATGAGCGGCTGCGGACTGCCCAACTCTGCATCCAACACGGGCCAGGGACTCAGCTCCAAACACTGCTCCAGTGCCAACAA
TGGAGGTGGTAAGTCCCGCTCATCAGAGCTTTTCCCCTCCAAATTTGTCACATTTTCTGCCCGAGGCGGTCGGACCCAACTCAAGCTAGATACAGTTCCATTTCGGCCCCAT
TCCTCTGCCCTTGTCAGCTGTCAGCCTCTGTTAATTTTGTAA
(SEQ ID NO: 77)

Start ATG: 195 (Reverse strand: CAT)

MAGRRHLLLILLLIMQLIATTPASRSLSVNGNNIWRRVRLVTSQESDRNAYQVLKPSSRNATSTTTTTSTTTSTTSSTTSTTTPAAPQTQRSAKQLDLNFPGGNVSSAARLE
MSTEFFVVPTLSASSSSSTTSTTTPATPRRSSGAKARAAGTTGRVTPGSSSNSTPPSIVSTHLPFAGLRKEPWVVPVLVLATLTMLMMAAFEIFVLFKAWRTSPSRRHLFLG
QMLLLGLFACASLGAIITAQPSLISCGAIRFGVGVAYALVFAALLVKCVFLISLNGGVYLPAPYQGLLLLFALLIQVAIGGQWLLTQPPEVYTTSVPVMGSGFLSTTVASQT
NYSALFYPTSYTTLDGTPEIYTRIAAVSTVLIPLCKTQFSELLFSLIYIVFLIVFIAVLAIKSRGIRDNYREATYIGLAIGGAIPIWLGWMLCGLAVAERHKDACVAFGLVA
TSATVFLVMFMPKGRQLAAMGKEGLYVEDREEQFSSLSRAGSGYSPSFFHFKPIKYGVMSGCGLPNSASNTGQGLSSKHCSSANNGGGKSRSYELFPSKFVTFSARGGRTQL
KLDTVPFRPHSSALVSCQPLLIL*
(SEQ ID NO: 78)

Name: Metabotropic glutamate receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384617
AAATTTGTATAACTTTCAGTTCTTATACTCAGTTATTCCATTAATCTCTAATCCCACGACATTTAAATACACATACAAATTTTTTATACAAAGTTTGCTTTATTGACTATTT
TTGAAGCACATTTACCATATCTGTATTATTAAAATACTTAGCATAGATTACAGAATTTTCAGCTTATTCCATGAAATACTGTTTGTCAAACAAACAGATTTCATCAGTTTTT
GTTTTTATAATCCTTTTTTTTTGGGAAAGATTCTCATATATTTACAATTATAATTTAAAATAGTCTCTACTTTAGCTTACTACATATTCAATTAAATCTCAGGAGGCTGACT
TTTCCGCGGACTTTTATGGTGGCTCTGACCCAACTGGATGCATCCTGCGCCTTTCCTCGCAGAAAAGTATTTTATTTCACATTTTACGGGCGTCTTGGCTGGCTGTCTTACC
TCTGGCTAAGATGCTTATTTTATACAAATCCGACTTTTGCGATTTTAATTGCATAAATCAGCTTAGTTATTTAATTGGTTTATTAATCTACGGGAGAAGCAACCATTTTATT
TTAGGTAAGCACTAAGAAAAAGATTGGATCTTAAGATTCCGATATTATTATATATCTTTATTTACTTAGTAAAAGGATGGGGATTTACGTATATTTATTTAAGAGGGTATA
TTGGCAGTAAAAATATTTATTCAAATTGTGGGTTGTACAGTTTATATTAATTATTAATATGTTATTAGCTGTCAAGGCAATAAGAAAATGTAATCCATTTCAGCCCCCTTCAG
TTAAATATATTGCTAACATATCGATGTGCCGGTTGTACAGACTCATTTTCAAATCTTTGAATTTTAATTCTGATCTCGGTTTTTATTACGTAGACACATATTAATACTGCTTA
GTCTTAAGTTCTTCATTCATATTTGGATAAGAAAGGATTATAAAATCATTTAAATGCATACTATAATATTGGCTTATTTAAAGGAAATTCCTACTTAAACTGGGTTACAAAT
CTGTCTGCTGCACTGCGCCCGATCCTCTTCTCGCGGTGGTGCAAAATGCCTCCTGCTGCTCGGTCAAACATAATCAAATTCTCCGGCGGAGCTGTCACTTTGCCATTGGA
ATTGCATGATTTCTGTGTCCCCGTGGTTCCGGTCTTTTCCGCTGTCGTGGTCGAGGATGTGGTGGTCGATGAATTGTTGTTACCCGCATTCAGTGGCAGCAGTGGAGGAATC
TGCGGATTGCTGGTCAACAGGCGCTTGGAGCCCACCCCTCTTTTTACTGCCCTGTTTGGTGAAAACACTGGGCTCCAGCTGGAGTTGAGCGTTGATATCCTGCTTATTCATAC
AGGTAAAGGCCTTGAAGAAGCTCTTCCGGAAGTTCTCACTTAGGAAGGCATAAAGTATGGGATTCACCGCCGAATTCGAGTAAACCAGTGCCCCCAGAAGTAGGAAAATGAG
TATTTCCAGTCGGGAGAGGTCCCTTTGCGCGGGATTCGAGTGAATCAGGGCCACCTTGGAGATCCAGTGGTGTGTAAATAAAAAATCGAATATACTTTATAATTAATTACCT
GAGAAATCCAGTGAGGGAGCCAACATAGAATGTATACACTTATCACCTGCGGATTGAAAAGAAGGTGGGAATCTACAAATGAATTGAACTGATTATTTCGGCATTATTACCG
TCAGTACCAGTCGAGTGACCTTCCTGTGAGCCCGCCTCTTCTCCTTGGACTTCGTTCCTGGTTTGGGACCCACCGATCGCAGTTTCCTTATAACCAAGTAGTAGAAACTCAG
GATAAAGCACAGCGGTGTGGCGAATCCTAGGAAAAATGTGTACAGTATGAAGGTGGTGCCCGAATGCTTCTTGTACGCATCTGGCCACCATTATGTTGCACGAGTAATTGATG
CCATCCTCCTGCTCCACAGTGCTGGCATAAAGGATCACGGGCAGCATGAGGACCGCTGAAGTTGACCAGGCAATCGCTGAGACCACTTTGGCAATATGCAGAGTTCGATATC
GTGGCGAGGAAATCGGGTGGCATACCGCTATATATCGATCCGCGGACATGATGAGCAGAAAAATCGACGAGGTGAAGGAGGTGATGGATGTGCTCACCGTAGGCTTTGCA
CATAAACTCCCCGAATCGCCAGCTGCAAATTCGCATTGTGTACAGCAGAAAGGGTATTCCAATCAGGAAGCACTCGTCGCCACCGCCAGATTCAGGATATATATATTCGTG
ACCGTTTGCATTTTGGAAAAGCGCAACACCACGTAGATCACCAGGGTGTTGCCAAATAATCCGATAATGCACACAAATCCGTAGAGCACCACAGTGAACAAGTCAGCAAAGG
AATTCCGCGTGGCTATGCAATGTTGATAGGTGGGCAAATCAGTGCCATAAAGGGACTCCTCTGGCTGAATTGTGGAACTACCACTAATCCATCTATGGTTCAGTTCCGTGGT
ATATAAGCTCTCGTTCGTGTTATACCAATTTGTGGCATTTGCCTCTGAATCGGCTGTCATTTCCCCTTTCACAAACTGGAGGACATCCATCATCAGCCACGTAAACATATTT
CCACCTAAGCGCTGTCCAGTTCAAATTTAATTATTTTAAATAGGTTTTACGCGTTGTTGCTCCCCGCTCGTTTTGTTCTTGCATTTTGGCGTTGCTGCAAAATACATTTTGT
TATTACGTGAAATATTTTCAGACACAGTTGTTTTGGCCAAACTTGATTAGTTACTAATTGAAATACTGTGGTGCTATTAAAGAAAAAAACCTAAAACCTTCACTAGTCTAGT
CAATATTTTTTATTCCAACGTAAGTTTAAAATGTACTGTAACAATTGGTGATAAGTATTCAAATGGAATTAAGTTAAGTCTACAAGTTTTATAAGATATTTTAATATAACTA
GATTGCAGCTCTTTAATGCATAGTGTATATTTTTAATATATTATGAGTTTACTTTTAAGTGGCAGTCAATTTTATTTGCTGTCTTAACATCTTTGAATCGTATGTACCCCAT
TCGTAATGCCACTTCACATACAGATTCTTTTGCAACTTTACTACAACTTTTACTGACTTTCTGAGAAATCCCCTCGAAAATTGAAAACTTTCCTGAACAACTTGTAGAAAAA
CAAACCTTTAAAAATACGACGTATGAAATAAATCGTCTGTTTCCTGCTTTTGAAAAGTGAGTTACCACAAATTTGGTTTGTAAGGCGAAGGAAATTAACATTTATATTTAAA
TTAAATTGCTCACAGCTTGACACGTCCAACAAACAAGAAACAAGAACTTTTTTATATTCTGACCTAACTCGACACTTTCTGTAAATAAATTAGGCGTAAGGAAAAGCTGGGC
AGCATTTATGCAAATATCAGGTGAAAATATTTGTCTTCTCGGAAGTCGGAAAACTCCAGCTATACAGATCCCCATGGTTTTGTATTAGGAGATTGAAATTTAAGCCGATTTG
TTTGTGCATTCCATGCACATCAAATATTGTTGACTGAGCCAAAACACATGTG
(SEQ ID NO: 79)

Exon: 2524..1679
Exon: 1510..1001
Start ATG: 2524 (Reverse strand: CAT)

Transcript No. : CT22465

39/89

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ATGACAGCCGATTCAGAGGCAAATGCCACAAATTGGTATAACACGAACGAGAGCTTATATACCACGGAACTGAACCATAGATGGATTAGTGGTAGTTCCACAATTCAGCCAG
AGGAGTCCCTTTATGGCACTGATTTGCCCACCTATCAACATTGCATAGCCACGCGGAATTCCTTTGCTGACTTGTTCACTGTGGTGCTCTACGGATTTGTGTGCATTATCGG
ATTATTTGGCAACACCCTGGTGATCTACGTGGTGTTGCGCTTTTCCAAAATGCAAACGGTCACGAATATATATATCCTGAATCTGGCGGTGGCAGACGAGTGCTTCCTGATT
GGAATACCCTTTCTGCTCGTACACAATGCGAATTTGCAGCTGGCGATTCGGGGAGTTTATGTGCAAAGCCTACATGGTGAGCACATCCATCACCTCCTTCACCTCGTCGATTT
TTCTGCTCATCATGTCCGCGGATCGATATATAGCGGTATGCCACCCGATTTCCTCGGCCACGATATCGAACTCTGCATATTGCCAAAGTGGTCTCAGCGATTGCCTGGTCAAC
TTCAGCGGTCCTCATGCTGCCCGTGATCCTTTATGCCAGCACTGTGGAGCAGGAGGATGGCATCAATTACTCGTGCAACATAATGTGGCCAGATGCGTACAAGAAGCATTCG
GGCACCACCTTCATACTGTACACATTTTTCCTAGGATTCGCCACACCGCTGTGCTTTATCCTGAGTTTCTACTACTTGGTTATAAGGAAACTGCGATCGGTGGGTCCCAAAC
CAGGAACGAAGTCCAAGGAGAAGAGGCGGGCTCACAGGAAGGTCACTCGACTGGTACTGACGGTGGCCCTGATTCACTCGAATCCCGCGCAAAGGGACCTCTCCCGACTGGA
AATACTCATTTTCCTACTTCTGGGGGCACTGGTTTACTCGAATTCGGCGGTGAATCCCATACTTTATGCCTTCCTAAGTGAGAACTTCCGGAAGAGCTTCTTCAAGGCCTTT
ACCTGTATGAATAAGCAGGATATCAACGCTCAACTCCAGCTGGAGCCCAGTGTTTCACCAAACAGGGCAGTAAAAAGAGGGGTGGCTCCAAGCGCCTGTTGACCAGCAATC
CGCAGATTCCTCCACTGCTGCCACTGAATGCGGGTAACAACAATTCATCGACCACCACATCCTCGACCACGACAGCGGAAAAGACCGGAACCACGGGGGACACAGAAATCATG
CAATTCCAATGGCAAAGTGACAGCTCCGCCGGAGAATTTGATTATATGTTTGAGCGAGCAGCAGGAGGCATTTTGCACCACCGCGAGAAGAGGATCGGGCGCAGTGCAGCAG
ACAGATTTGTAA
(SEQ ID NO: 80)
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Start ATG: 1 (Reverse strand: CAT)

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MTADSEANATNWYNTNESLYTTELNHRWISGSSTIQPEESLYGTDLPTYQHCIATRNSFADLFTVVLYGFVCIIGLFGNTLVIYVVLRFSKMQTVTNIYILNLAVADECFLI
GIPFLLYTMRICSWRFGEFMCKAYMVSTSITSFTSSIFLLIMSADRYIAVCHPISSPRYRTLHIAKVVSAIAWSTSAVLMLPVILYASTVEQEDGINYSCNIMWPDAYKKHS
GTTFILYTFFLGFATPLCFILSFYYLVIRKLRSVGPKPGTKSKEKRRAHRKVTRLVLTVALIHSNPAQRDLSRLEILIFLLLGALVYSNSAVNPILYAFLSENFRKSFFKAF
TCMNKQDINAQLQLEPSVFTKQGSKKRGGSKRLLTSNPQIPPLLPLNAGNNNSSTTTSSTTTAEKTGTTGTQKSCNSNGKVTAPPENLIICLSEQQEAFCTTARRGSGAVQQ
TDL*
(SEQ ID NO: 81)
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Name: Somatostatin receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384531
```
AGCATGCGGCTGAACAAAAAAAACTCGAGGAATGGCCGCAATTTCGGTGAGCCCATATAAACAACATAACATATAGTTTTCCCATCCATCTACGCTGTCTGCGCCACTGGCC
AAGTCCAAGTTGTCTTGACGGCCCGGCAAAAAGCAACATCCAAGGAAAATGTTGCCATTTTAGATGCGCCGCCCGCTGAGCGGAAAAGTCGCGCGGAAATTACTAAATCGAT
ACGTGCTGCGTATCAGATTTTCCATGGGTTCTGCATGCAAAAATACCTTGAAATCCTTGCCTGCAGTCGCACACATACACGTATTGCCATCTTTGTACAGACAAGCTTGACT
AAGTCGAACTTTACTATGTTATTCTACTAAAAGGTTTTAAAGCAAATGATCTATACTATACTATACTATTAACTTCAATAGAATTCCTATTTTCTCTGGCTAGCAAACAAAT
TTGGATCATAAAAAGATTTTCATGGCATTTATGAGATACGTAGATTGTGTGGCTCAACCTTTTATCTATATTATTTCCATAAATTTAAGCACCAATGGAAATGTTTATCTCC
AAAGCTTAGGAAAATTTGGAAGTATATATAATAAAAACCTTTTATGTCTGCAAATAAGAGATATTACGTGTATACTGAGTTTCGCTTGAGTTTCGGAGTTAAGAGGCTTCCC
TATAGACTGTTTGAAAATCCTATAATGCCTTGGCATTTCTAAAAGGTCAACTGAAAGCAGTGGAATTGCTGGTGGGCGAGGTTCGTCTCCTAAGTGGCAAAATGATCCAGAA
TCGGAAGCAAACCCTGACGATGAAATAAACTATACGAGAAACTGGAGAACAATTACACATGGACTGTGGGTGCAATTAGGGACCACACCTTTTCGCTGCCGACGCGTCTAA
AGTTAATGAATATGTTAATAATATGTTATGCGCGTGCAAATTTGTTCAGGGCTTGAGGGGTTTTCTGTGTTTCTGTTTTCCAGGCGAGTCCAGTCCAATCCAATCTATCGCC
TGATGGACATGGTGTTCGTGGGGAACTGTGGCTTCTGGCCGGCGCTGAAGAAGCGTTGGCAGGTGAGGCGCCAGAAGGCCGCCCGGAAGTCGACGCTGTAGAAGGCGTAGAT
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CACTGGTGTTCCCGCTAGTCGATGTCGTGGTTACGCCCGCCTGGTGATGATAATGAGGATGGTGGTGATGGCTTCGCAGTCTCTCGCGGTCCCCGCTCCCCATGCGAATGCGT
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TAAGCAGATGGCTTTAAGCTGATTTAAGACTACATACCCAAATGCCATGCGGCCATTGTTCTATCAACTGCACGATGTGCTAATCTCTCTAAACATAAAACTGAATTTCAGA
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(SEQ ID NO: 82)
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Exon: 6448..5911
Exon: 4171..4069
Exon: 3988..3863
Exon: 3132..2949
Exon: 1945..1001
Start ATG: 6448 (Reverse strand: CAT)
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GGATGCAGTGGCTCTCACCGAACCCGGACCCACGGCGCCCGTGACCACCATTTAATTTACTACAACGAGTCGGCGGCGGCCGCCGAATGGGCGCACTTCTACGATCTGGTGCTC
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CACAGCTCGGTGGGCCAGCGCCAGAGACAGGCCACATCGCGAACGTTCTCCAACCAGACGATAGCCAAGGAGCTCCAAGACATGATGCTCAGCGACAGCGACAATTGTGCGG
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(SEQ ID NO: 83)
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Start ATG: 1 (Reverse strand: CAT)
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SWQGIILIAVFATFIVVTVIGNTLVILAILTTRRLRTITNCFVMSLAVADLLVGIFVMPPAVAVHLIGSWQLGWVLCDIWISLDVLLCTASILSLCAISVDRYLAVTRPLTY
SRKRRSKRLALIMILIVWLLALAITCPPMLGWYEPGRRDLRECRYNQNEGYVIFSAMGSFFIPMAVMIYVYARISCVIASRHDNMTDISVHNKKFKRYTAADVENELSEQEQ
HSSVGQRQRQATSRTFSNQTIAKELQDMMLSDSDNCAAMGAGGAGGGGGGGGASSATGGTHCQSLLALPSGGVGGSMGCAKNGCYELTRPSSLKRASTASTTITTMTSGMGPGS
SLLDAQWQSQPPGQTGQVQTHSLSQPPRTHSFRHSHGERDRERLRSHHHHPHYHHQAGVTTTSTSGNTSANTNSKSLSNRITSLKKENKTTQTLSIVVGGFIACWLPFFINY
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(SEQ ID NO: 84)
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Name: Octopamine receptor-like
Classification: G_protein_linked_receptor
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Celera Sequence No. : 142000013384651
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41/89

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ACCCTATATATACTTCACATACATGGACCTACAGGCACGAGTACCACTCACCGATATGGCTATTATCAGAGATGAGTTCTTTGATTGTGATGAAATGATTTACATCAGCGAC
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(SEQ ID NO: 85)

Exon: 1001..1673
Exon: 1849..2025
Exon: 2087..2338
Exon: 2403..2836
Start ATG: 1001


Transcript No. : CT22963
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(SEQ ID NO: 86)

Start ATG: 1

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RFKPYIYFTYMDLQARVPLTDMAIIRDEFFDCDEMIYISDFNYFLEEVSIQIFNKCGLIVWFQDGKFWVTVDLFMEKQDYCLYRHNFDSDFPKSMWIIRHRCTSHISPGSLE
ILIITMICFVLTIAVYLYIKKLRNVTGKCIVCCIVSRFIQCLIMILDHLNLLNGICSPAGYSSHFFRMASNLWLSVISYHTWKVLTSLNRVDPNYRFLRYNAFVWSTAAIMT
GSIYIVNQIWENDPSKWNWLPLVGFIRCSVKDWHPSVWIYISGPSLALSTFNVAMFALTAIYIRKVKGGINKFTNEEEGRINCINFDSQT*
(SEQ ID NO: 87)

Name: mth-like 7
Classification: G_protein_linked_receptor


Celera Sequence No. : 142000013384621
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FIGURE SHEET 41

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```
CCGTGCGACTCCTTCCGATCACACAGAGCAAGGTGTGGGCCACGAAGAGGTTGCAGGCCACGATTACAATGCACAGCAGGGTACCTGGAATACATCGATGGTCAAACCAATA
TTTGAAATGTAACCAATTTGATAGGAACTTACCGAAGACCATAAAGAGCACCGCATACGTCTTGTTCCACACGCCCGGCGCATCGCGATATCGTATACACTTAAGCTGGTCC
GGATTGGATTCATCGATGTATGCACCAAAACCAACGAATGGCAGGAACGTGATCACCACGGCGATCATCAGAATGCTGTTGATGCTCTTGCGAATGAGCTCGTAGGTAATGT
GCTATGGCGGAGAGAGATTTGTGAATATTTAATGAATGAGTTGGCAATGTTTGTGATTTCGTGTGCACTTGTATCATTTCTTAAAATTAAATTACACTAAGAATAAAAATGC
ATAGAAAATGTTATTTATTATACATATATTGCAATCAAGTTCATACCTTGTGGTAGATAAAGGGTCTGGCTAGGGCCATCCATCTTTCTGCCGCCATAACTGCTGCAATGCA
TCCAGAACTGAGCCCGAAAAATCGCCAAACCACGAGTCCCACGCAATCCACTCGGATGAACGACTGCAGGACTTCCTTTGAGAGATACATTTTCAGCAGCGTCGTGGTCAGC
ATGCCCAGTAGAGCCACCAGATTGTTGGTCGCCAGGCATCTGAAATAGTTGAGAGCTCCGTAAATTTCGGATAGCTTAGCTTTATGGCATTTCGAAGCTCATAAATCGGAAA
GTAAATGCTTTTCCTTGCCATTAGCGCCCAAATTGCCTACAGTTCGTTGGGTTCTTTAATAAGCTACGAATATAAGTTGGGTATAAGATCGATAAAATGTAATAACGAATTG
CTTTTTAATTAATTGCCACTTTTATAAACCGAAACTTTCAATCAAGATACCTCAAAGCTGCTCCATATGGTTGTACAACTATCGATTTTGGTTATCTAAGACGTGACTCGGTC
CTTAAACGCTTTGATTCGAACGCCGACCAATAGCAATGAATAATTATTTTGGTTCGCAAAATGCTCAATTATAAAAAGGAAATATCTATTATATGGATATTTAAAAATTTAA
TTCATTTTTTTGAATGTTTATATTATAAAGGATGCTCCTCAAATTTCTCCATTGAATATTGTGTATATTCACTTTATATTCGTTCATATATTTAACATTTGTATATTTATAC
TAATATAAACTAAAGTACAGATCCCTGTATTTTTATCTACTTAGTGAAATATGTGACTGTCAATGGTGACTTAGATTAAGTGTTTCCTTTTATTGGTATCATAAAATATTGC
ATTTGTGGGGCACGAATGTGTTTCGATTTGATTGTTTTTGGGGCGCCGTTGACACAGGAAACTCATTTGTCTCCGTGTGAAATGAAACTATATGAATGTAGGGCTTTTTTCC
AATGGAAATATATGTATATATATATAAAACACACGCTTGGAATAGAACACAAAAATGGGATTGACAATTCCCGGGGATTGGCCTAACAGTCCGTGCATCGTTAGGCATCGCA
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TAACACGATGTTTAAAATATCAACAAAGTCTATTATGAGTATTCGTATTGAGAAGCGAATATTTTACAAGAAATTATTATTATTAATATTAAAAGGAATTTGGTGAA
ATACACAAGTTTTATTTCACTCATATTTACAAAGGAATAGATTATCATTTTTGAGTATTATTATATCTACCAGTTTTTTGCACCTAAGCAAAGTTAATTTAAATACATATTC
ATATAAATCTTTTCCCCAGTATGCACATTTGCCAATCAAGTCAACCACCGATCGCCGTCTTCAGTTACACCATAAAGCTTTTAATGCATTCGCAATTGGCTGCATTCCCACG
ATAAAACAGCAAAAACCATGCCAAGCAAAACAATTCAAACTATGCAAATCAGACCCGCCATAGACGAATAACCAAAGTGGCCCAGTTGAGAGCAGGTTGAATAAA
CTTACATAGCCATGAACTGGACACAAACAGTGGCAAACATTAACTGCATGAAATGAGTAGCTACACGCTGAGAAAATATGCAAAATGTCAGCTCAATAATATTATTAACAAT
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TGAAAAGGGCCAGCGAATTGCCAAAAACGCCCAGAACCATGATAATAACACCAATAATCAGGCGATTTCGATTTGCATAGAGCGCTTTCGGAGGCGCCACAGTAGTTGAGTT
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GCCGACCGTGCCGAGCAGAGCACTCGTCGGCTGCTGCCCATAGCTCCAAGCTATCCAAGCCATCATATACACGTGGGGGTGGTTGGTAGGGGCCAGTTCGGAGCGGAGGCCAGT
TCGGCTGGCGCCGCCGCCGGTCGGATCGCATCGGATGTAGCATACAGCACATAGACACCCCCAAGCGAAGCGGCCACCCACATCCACGCCCAGCGATGGCGACCACCCCATC
GAAAATTCACAGCTCGTGCCAGCGCCTTTGCCTTTTGGACGTGTGCGAACGGTCGGAATAGCACGACGAATTTTATTGTTTTATACTCTCTCCACCTGCGGCTCACTTTAAT
TTCACTTTCAACTGGATGTAATATTAATTATGCAGTTTTTAAGCTTCCATTTGATTTTATACAGTTGACTAAATTAGAATAAAATAATATACTCAAAAGTTTACTTCAGCAA
TATATTTACTCATGTTTCTTTGCTCATTGAAAAATTAACAAAACAAAAAAACAGCTATTTCATAGATAGATTAATTATTATTATTAAGAGTCTTCAGATTCGTCATCTTTAGT
ATATGGTGTGTCATTTGAAAACCTATTTTTGGAGGAATATATGAACTGAAATCTGCGTATACTTTAATTACTGTAATGTATTAAAGTATTGTTTCTTTTATACAAAAAGTCTA
AAAAATATAAGCAAACAAATTATTTTACTGAAAATTTGTTTTTTATGCCACTTTTAAGAAATTTTGCGAATTAAACATATATTTTTAAAGCTAGGAGCCTGGTAATTATAGTA
GTTTAGCTTTAACTCTTTGCTGAAAATATTTCCAACTAATTTATTTGTTTTCAACAGAATGCATTACGAAAGATAAAAATTAAATTTGCAGTTACTAAGCGTTGCAGTTGCA
CCTTTTCTTATTCTTATCTTCTTAGTATATAGTACTGTTTTGTTGGGCAAAAATGTTTATTGTTTAGTTTCAACTGCC
(SEQ ID NO: 88)


Exon: 5238..4765
Exon: 2391..2175
Exon: 2017..1825
Exon: 1764..1409
Exon: 1267..1001
Start ATG: 4970 (Reverse strand: CAT)


Transcript No. : CT23019
ACTGCGGACGCGCTCCTCGGATCGAATCGAATCGCCTTCGAATTGGTCGGTCGTTGGTTGATCAAGTGTCGCGTGCGCTAATCATTAATTAAGTGTCTTAGGAAAAAAGTCC
CAATTTGGCTATCGAAACGGGTTTCCATCTACCAGTGCATTTGCGAGCTGCCTTGCCTTTGCGGCAGGCTCATTTATGAAAAAGAAATATCGTTTGCGGCCAGTTAGATTTT
CACCTGAATCACCTGCAATCGAACGCAATTATCATACCGGCAAAATGGAAACCCACAACACCTGTGCTCGACCTGTTGATGCCGCACAACTCAACTACTGTGGCGCCTCCGAA
AGCGCTCTATGCAAATCGAAATCGCCTGATTATTGGTGTTATTATCATGGTTCTGGGCGTTTTGGCAATTCGCTGGCCCTTTTCATTTTGGCGCGCAAGAAGCTCAACAAA
AACAGCAAATACACGCTCATGCTGCGATGCCTGGCGACCAACAATCTGGTGGCTCTACTGGGCATGCTGACCACGACGCTGCTGAAAATGTATCTCTCAAAGGAAGTCCTGC
ACCCTTTATCTACCACAAGCACATTACCTACGAGCTCATTCGCAAGAGCATCAACAGCATTCTGATGATCGCCGTGGTGATCACGTTCCTGCCATTCGTTGGTTTTGGTGCA
TACATCGATGAATCCAATCCGGACCAGCTTAAGTGTATACGATATCGCGATGCGCCGGGCGTGTGGAACAAGACGTATGCGGTGCTCTTTATGGTCTTCGGTACCCTGCTGT
GCATTGTAATCGTGGCCTGCAACCTCTTCGTGGCCCACACCTTGCTCTGTGTGATCGGAAGGAGTCGCACGGCCAAGCGGCATATGCACTACGACCTGGTTCCAGGGACAA
AAACAGTGCCATCAGCATCGATCCCGAGAGCAGCAGCGGCACCACCCTCTACCAGACGCAGCTGAGCACCGGAAGCGGAAACAGCCATCGCAGTGTACAGCCGGCAAGGCAG
TACAGGCACAGCGTTAGCGTCACAATGGCGGCCACCGACTCCTCGCCAGTCGAGATCAAGTTCGCCAAACTAATGGCGTTCCTCAGCATCTCGTTCGTCATCTGCTGGATGC
CACAGATGATCGCCATCCCGTTGGCTATAGCTCCAAATCGGGTGCCCGCATCGAACAAGTTCTTCATCATCGCCGATGTTCTTACGGCGCTGCACTTCACCTCGGATCCGTA
TGTCTATGTGCTGAGTCGCTCCAAGTCCATCAACTGGTCCTTGCTGGGATGCATTAAGCGCTGGAGGAGCGGATGGCGTCCGGGCGGACTTCGTCGTTCCCAGAGCGACCAG
AGCCGCATGCGTACGACGATGACGGAGGCGAATACTCTGGAATTCAACTGA
(SEQ ID NO: 89)


Start ATG: 269 (Reverse strand: CAT)


METTTPVLDLLMPHNSTTVAPPKALYANRNRLIIGVIIMVLGVFGNSLALFILARKKLNKNSKYTLMLRCLATNNLVALLGMLTTTLLKMYLSKEVLQSFIRVDCVGLVVWR
FFGLSSGCIAAVMAAERWMALARPFIYHKHITYELIRKSINSILMIAVVITFLPFVGFGAYIDESNPDQLKCIRYRDAPGVWNKTYAVLFMVFGTLLCIVIVACNLFVAHTL
LCVIGRSRTAKRHMHYDLVSRDKNSAISIDPESSSGTTLYQTQLSTGSGNSHRSVQPARQYRHSVSVTMAATDSSPVEIKFAKLMAFLSISFVICWMPQMIAIPLAIAPNRV
PASNKFFIIADVLTALHFTSDPYVYVLSRSKSINWSLLGCIKRWRSGWRPGGLRRSQSDQSRMRTTMTEANTLEFN*
(SEQ ID NO: 90)


Name: Prostaglandin receptor-like
```

FIGURE SHEET 42

Classification: G_protein_linked_receptor

Celera Sequence No. : 142000012711419
TACACTCATGAATATTCAAACAAAACTCTTCAACTTGTCTGGCATATATCCATAGACAATTACGCGGGTATGTATGCTGGGTTTTGTGTTCTTAAAATCGTATATCTGCTGC
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TAAAAGAAAGTTTCTATGAACGTTTGAAATCAAAATTAGGTCCGATTTTGCGTAGTTTTCGACAAAGTGTCACCGTCAAAAGGGCTTCGACTGGCATATCCCTCAAAGGGTT
AACATGCTTTTCTTTGGTCTTCTTATGGCCTACCCCCTTCATATGTCTGCTTTTCATTGATATATTCTGCGGAACAACAAAAGAAGTATTATTCTATATTGGGATATGCTTT
AGAGTTTTGGTTTGTAGGGTTTTCTAGTCTCGGTAAATGTGTATATCTTATGCTTAATTTATTTTATTAGCTATCATATCATATACTTTGCATGGTTATCATAGATTGGTTA
TTAACATTAAAATATTTATTGTCTAAAACATTTCGCCCCGCTTAGTGCCACTCTAGACCTATGTATGCATCCCAAATCGGATTGCTTGTTTTCCCCCCCAACGATTCTAACT
ATAGCACACACCTTTGGCTACTTACAGATAACTCTTCCCTGTCCACCGATTAAATTTTGAATTTAATAAGTGTTTGATTCTAATACTTTGCTGATGGTCGAAATCCAGCAGA
TATTCCATTAAGCGGAGCACTTTCGTTGGGTATGTATAGAAAACTTATGGGCCTAAGGAGGTGTAAGGGGTTTGGGAATGGAAAAGTTTGCAAGGCGCCAGACTCTCGGGGC
TCTGAAGTGTCTGGTCCTTTGCGCAAGTGCAGTGCAAAATGGAAATCTATCAGGGATTTAACTCAACCACCAGCAGCTTAACCACTTCAGATCCCCAAACCATCTTAGGTCA
TGTGCAGATCCCCCTTGAGGATCCGCGTAAAGGTCTTCTTGAACTGCTGATTGGCCAGAGCGTAGCAAAAGGATTCATCGGGCTGTTGGCGTAGCAGAGGAAGTACGAGAA
CATGTAGAGGTGTTCATTGATGCAGGGCGGATGCCGGCAGAATCCCTCGACGAGGGCCAACACATGGTAGGGTGTCCAGCAGGCCACGAAGCAGCCCAAAATGAACGAGATC
GTGCGAAACGCTTTGCGAGCACGATTCTCCGACTTGGACTTCTGCCGTCCACCCACTCCAAGGATCAGGGGTAGAGCCTTCTTGCTCTTGAAGTGCTTTCCTATCGAATGAA
TGAATGCCCTTTTGCTGGAGTTTCGGCTGGCCGCCAAACTCTTCTCCTCCCTGTTGGCATCGTCATCCCCCGCGTTCTTTTTGGTGGCACCAACACCGTCTTGTTCCCCGCC
TCCACCCACACCGCCCGTACTGCTGGTGGTGCCCGAGGTGGAGGGCATCTTGTTGGTATTACTGTCCGAGGTTTCTCGCTCCTCAATCCTTTCCAGTGGCACCGGTGGTGTT
ACACCCGCCGCCGACTGGGGCGTTCCCGTTTGTGGCGTTGAAGTCTTTACCTTGGGTGAGAGTGGCATTGGTGGCATCGGGGAATAGAGTATGGCATCCTTGCTGCTGGTCT
CCATAGGACTGGAGGCCCGGCGATGGGGACAGTCCGCAGCTAGCTTTCCGGGCACATCCAACAGGCAGATGGCCTCAATGCAGCTCTCCCGCCTCACCTTAGCAAAGTCCTC
GGACTCTGGTTTTGGCTGGGAGTTTGACTGAGGCTCTGGTTCAGGTTCGATTTTGGTGGATTTCGGCGTGCGGGCGGTGGTGGAGGCAGGACTGGTGGTTTCCCCTGGACGC
TGTCATTCGGGGAGGTCGTCGAGTTGGCCGTCACACTGGCCAGCATGGCGGAGCTCTCGTCCATATAGCGTAGCTCCGAGTTCGTCATCAGGTCATAGGTCAGGGCCAGTTC
ACTGTTACCGGAACTATTCCCAAAGGGACGATCCGAGTAGTCATCGGAGAGCGGGGTGGGGCACTGAAAGGCGTCGGGAGGTGGCAAAATGGTCTGCACCAGACCCTGATGC
TCTGGGACAGTGTGGAGCAGGATGTGCGCTTGGGCCTGTCCAGCGGTGGGTTCGGCTGGTTTTGGTGGTGCTGGTGGTGCGGTTGTTGCTGGTTCTCGGTGGTGGTGCAGGGA
GCGCATCTCTTCCTTGCTCTGCGCCCGCTGTAACGGACTCTGGTTGTGATGGTCGCTGTTGGTGGTGGTGGTGGTACTGGTGCATGGCCTCGATCGACTTGGAGTTAGTGGTGCTC
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GCTGGGGCCTGGTTGACGGATGATTCCTCATCGGAATCGAAGGCAGGACTGCTGGATCTCTCCAGGTCCTTTTCCGCATCCACGGCTGCCTCACGTTTTTTCGCCTCCTCCTGGAT
TTTTGCTGCCGACGCTCTCCTCTGTTCCGGTGTCATCTTCTCCACTTCCTCGGTGGCCACGGCCAGAGGATTTGCCTGACCGGAACCACTTAATCTCTTAATCACTGTGGTG
CAGGCACTATCCAAATCGGTTTGATCTCCCGCAAGTTCCACTTTGGTCTTTAGGATTTTCTCCTCAATCACACCAATGCCAGCTGCATGACCTGCCATTCCGGACATCGCTC
CAGCACTCAGTGCCACCATGGATTGCATTTTCCGTTGCTTCGCCTCACTGCGCTTTTGCATATCATAGGCTGTTTTGTAGATCCCGGCATATAAGACAAAAAGCACAATTAG
TGTGGTCCAATAGTAGCCAATGATTAGGGCCGTATTAAAGATCGGATCCTTGAGAAACTGAACGGCGCACTGGCCAGGAAGTAGATCCCGCTTGCCGGTGAAGTGCTCCCAT
CCAAAAATCGAGATGAAGAAGAGCAGAGCGGGAATGATCCAAGTGATTGTGACCATATATATCACTCTGGTTCTCGTCCTCCAACTCCGGTACTTGGCGGCAATCTTCACAG
AGCAGTAGCGATCTATCGTGATCAACAGCACCGTGTACTGGGACACCAGACACACAGTATAGTCGACGGAAAGCCAGAGATCGCAGAGCATCGGACCCAGGTCCCAATAACC
CTTGAGCACGTATATCGTGTAGAAGGGCATCGAAACGGTTCCTGAAATATGGGTTTATAGTACAATTAATAATTTTTTTTTTTGAATTTAAGGTAAAATAGTTACTACCTA
TTAGCATATCCGTGGCTGCTAGGGAGGCAATAAAGTAGTTGCTGGGCTGCCGAATATTCCTGTCCACGATGAAGGCCAGTAGCACCAGGATATTACCGCCCACCGTAAGAAT
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CGCCATAGATCTTGGCCGCCTCCAACAGACGTTTGCACTCCGTGTGCGTCAGGACTCGCTTGAAAATGAAGCTGCACAGCTTATCCCGCTCCCTTCTAAGGCTCCTGGAAGT
GCGAAAGTAAATATATGCTTAATTAGAGTTGACATAAAACTATCTCTATCTCTATCTCTATCTCTATCTCTATCTCTATCTCTAAACTAATGTCCTTGAAAACAAATTCTAA
CTTGATGGTATAGATGGAGTCGCTGGAGTTGCCATTCAGGCCAGTCAGCTCCTCCTCGCCCGCCGACTTGTTAAGCGACCGCATCCTTAACCGCTCCGCCCTCTTCCCGCTC
TGGCCACGTCCCGCTCCCTGCTCCCCGCACTTCGCCTCTGCGCTCCACAACCTCTGCGGTTTTTATGGTAATTTCAAGTTGTTCCTCCTTAATGTGCTGTCGACGGCGGTTG
TCTCGGAATGCTTACATTGCCTCCATGGAATGCCAAGACTTGTCTCCGGTCAGGTGCAGCATCTGCAAGAGGCAACAAAAGCAGCCACAGTCTTGGTTAGCACTTGAAAAAA
TATAGAGGTTATTAATATTATATGATAATAATAATATATATGCATATAAAATATGATATAATAATATGCATATAAAATATGATATAATTTATATATGTATACATAATATGA
TAAAAAGTCTGAATTTCAGAATTCTGCCACGAAGTCGTTTTCCATCCAAAAATTAATTGTTTTTTAATCGAATTTTTGGTAATAATAATCCGAATAAGGAATGGAATATTTCG
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GACAAAAAAAATATTTTTCCGTTTTAGTTGCGCGACCATTTTTAGCCAAATAATAGTAAAAAATCTATTTGAAAAATACATTGTCTTCATTAGATGGTGGAAAATAATGAAA
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CAAGTTTAAACTAATTTTGCAACCGTTAACTGGCAACCGGCGACTGGCGATGCAATTTGCTTGTGGCAGTTGCTTC
(SEQ ID NO: 91)

Exon: 4340..4237
Exon: 4024..3582
Exon: 3513..1001
Start ATG: 4340 (Reverse strand: CAT)

Transcript No. : CT23924
ATGCGGTCGCTTAACCAAGTCGGCGGGCGAGGAGGAGCTGACTGGCCTGAATGGCAACTCCAGCGACTCCATCTATACCATCAAGAACAAGTGGATCACCGACTGGAGCCTTA
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TTCCTGGCCAGGTTAATGAACAGCTGCAATGGTACAGGAACTTCGATGTGACAATACGAACCTTCGTTGGCTGTTAGAAATCAATCCTCTGATGGCGGTTCCACCATGTCG
GGATCCAGTTCCGACTCGGAGATTCTTGGTCCTGTTTTGCCACCATTTGCACTGTGGCAGACGATCCTGATAGCCATATGCCTGGCGATCTGTATCATTCTTACGGTGGGCG
GTAATATCCTGGTGCTACTGGCCTTCATCGTGGACAGGAATATTCGGCAGCCCAGCAACTACTTTATTGCCTCCCTAGCAGCCACGGATATGCTAATAGGACGCGTTTCGAT
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GAGATCAAACCGATTTGGATAGTGCCTGCACCACAGTGATTAAGAGATTAAGTGGTTCCGGTCAGGCAAATCCTCTGGCCGTGGCCACCGAGGAAGTGGAGAAGATGACACC
GGAACAGGAGGAGAGCGTCGGCACGCAAAAATCCAGGAGGAGCGCGAAAAAACGTGAGGCAGCCGTGGATGCGGAAAAGAGCGAGAGATCCAGCAGTCCTGCCTTCGATTCCGAT
GAGGAATCATCCGTCAACCAGGCCCAGCAGTTGATCACCCAGCAGAAATTGAACAACATGAGGAAGCGGTCATCGATTGGTCTGGTCTTTGGGGCACAGGCCGCCCTGCTGG
GCGGGCGCAGAGCAAGGAAGAGATGCGCTCCCTGCACCACCACCAGAACCAGCAACAACCGCACCACCAGCACCACCAAAACCAGCCGAACCCACCGCTGGACAGGCCCAAG
CGCACATCCTGCTCCACACTGTCCCAGATAGCCGAGCATGATCGTTTGGTCGACCTGTCCGCTCCTCCAACATTACTCAACACCAGTGATCCCCTGTCCCCGTGGACTTGG

FIGURE SHEET 43

44/89

CACCCATCGAGGTCCCTAGCGATCAAGTGCATCAGGGTCTGGTCAGACCATTTTGCCACCTCCCGACGCCTTTCAGTGCCCCACCCCGCTCTCCGATGACTACTCGGATCG
TCCCTTTGGGAATAGTTCCGGTAACAGTGAACTGGCCCTGACCTATGACCTGATGACGAACTCGGAGCTACGCTATATGGACGAGAGCTCCGCCATGCTGGCCAGTGTGACG
GCCAACTCGACGACCTCCCCGAATGACAGCGTCCAGGGGAAACCACCAGTCCTGCCTCCACCACCGCCCGCACGCCGAAATCCACCAAAATCGAACCTGAACCAGAGCCTCA
GTCAAACTCCCAGCCAAAACCAGAGTCCCAGCCAAAGCCTGAGCCTCAACCTGAATCCGAATCACAACCAGAGTCAGAGTCAGAGTATCGAGGAGGCGGTGGCCATTGAAAA
ACGTCTTCTCGTCTCGTACACAGGAATCGAGGACTTTGCTAAGGTGAGGCGGGAGAGCTGCATTGAGGCCATCTGCCTGTTGGATGTGCCCGGAAAGCTAGCTGCGGACTGT
CCCCATCGCCGGGCCTCCAGTCCTATGGAGACCAGCAGCAAGGATGCCATACTCTATTCCCCGATGCCACCAATGCCACTCTCACCCAAGGTAAAGACTTCAACGCCACAAA
CGGGAACGCCCCAGTCGGCGGCGGGTGTAACACCACCGGTGCCACTGGAAAGGATTGAGGAGCGAGAAACCTCGGACAGTAATACCAACAAGATGCCCTCCACCTCGGGCAC
CACCAGCAGTACGGGCGGTGTGGGTGGAGGCGGGGAACAAGACGGTGTTGGTGCCACCAAAAAGAACGCGGGGGATGACGATCCCAACAGGGAGGAGGAAGAGTTGGCGGCC
AGCCGAAACTCCAGCAAAAGGGCATTCATTCATTCGATAGGAAAGCACTTCAAGAGCAAGAAGGCTCTACCCCTGATCCTTGGAGTGGGTGGACGGCAGAAGTCCAAGTCGG
AGAATCGTGCTCGCAAAGCGTTTCGCACGATCTCGTTCATTTTGGGCTGCTTCGTGGCCTGCTGGACACCCTACCATGTGTTGGCCCTCGTCGAGGGATTCTGCCGGCATCC
GCCCTGCATCAATGAACACCTCTACATGTTCTCGTACTTCCTCTGCTACGCCAACAGCCCGATGAATCCTTTTTGCTACGCTCTGGCCAATCAGCAGTTCAAGAAGACCTTT
ACGCGGATCCTCAAGGGGGGATCTGCACATGACCTAA
(SEQ ID NO: 92)

Start ATG: 1 (Reverse strand: CAT)

MRSLNKSAGEEELTGLNGNSSDSIYTIKNKWITDWSLRRERDKLCSFIFKRVLTHTECKRLLEAAKIYGESSDFNSWPVNEQLQWYRNFDVNNTNLLLAVRNQSSDGGSTMS
GSSSDSEILGPVLPPFALWQTILIAICLAICIILTVGGNILVLLAFIVDRNIRQPSNYFIASLAATDMLIGTVSMPFYTIYVLKGYWDLGPMLCDLWLSVDYTVCLVSQYTV
LLITIDRYCSVKIAAKYRSWRTRTRVIYMVTITWIIPALLFFISIFGWEHFTGKRDLLPGQCAVQFLKDPIFNTALIIGYYWTTLIVLFVLYAGIYKTAYDMQKRSEAKQRK
MQSMVALSAGAMSGMAGHAAGIGVIEEKILKTKVELAGDQTDLDSACTTVIKRLSGSGQANPLAVATEEVEKMTPEQRRASAAKIQEEAKKREAAVDAEKSERSSSPAFDSD
EESSVNQAQQLITQQKLNNMRKRSSIGLVFGAQAALLATRGKGNLQKSTTNSKSIEAMHQYHHHQQHHHNQSPLQRAQSKEEMRSLHHHQNQQQPHHQHNQNQPNPPLDRPK
RTSCSTLSQIAEHDRLVDLSAPPTLLNTSDPLSPVDLAPIEVPSDQVHQGLVQTILPPPDAFQCPTPLSDDYSDRPFGNSSGNSELALTYDLMTNSELRYMDESSAMLASVT
ANSTTSPNDSVQGKPPVLPPPPPARRNPPKSNLNQSLSQTPSQNQSPSQSLSLNLNPNHNQSQSQSIEEAVAIEKRLLVSYTGIEDFAKVRRESCIEAICLLDVPGKLAADC
PHRRASSPMETSSKDAILYSPMPPMPLSPKVKTSTPQTGTPQSAAGVTPPVPLERIEERETSDSNTNKMPSTSGTTSSTGGVGGGGEQDGVGATKKNAGDDDANREEKSLAA
SRNSSKRAFIHSIGKHFKSKKALPLILGVGGRQKSKSENRARKAFRTISFILGCFVACWTPYHVLALVEGFCRHPPCINEHLYMFSYFLCYANSPMNPFCYALANQQFKKTF
TRILKGDLHMT*
(SEQ ID NO: 93)

Name: Muscarinic Acetylcholine receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384504
GACATACGCAGGCGGAGAATTGATTTGATTTCTGTTATTGTTGCTTATCACTATCGATTTCGATTATTCAAAGTCCCTTTTTGCCCTGCGGCGAACGGCGATTGCCCTCAGT
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CATTAATTATTACTCATAGAGCTGTCCTATGACTTATCGACTTTAAGCCAATTGGAGAGGGGGGAGTAAGGCTGGCAGGGCAACCCGATCAAAACGAAAAATCAAAGTGTGG
GTATCATTGTGTATTTCGTAAATTAGAAGGCCAATTTGGTGGCAATTCCTGTTTGTGATACAATTCCTGGCCGCCATTGTACCCGTGGTACTTCTAGGAATTCATTAAATGT
ATCCAATTTGCTGTCAAGGTAATTTACTTGGTGAACAATTAAGTTCAAGTAGCTATGTTTAGTCATTTCAAAGTTATGTCTTTACAATTTATTTTTATATAAATACTAAGTGC
TATTCTTAATTAAGCATCTGCACTTAAGGTTTTCTCTATAAGGAGCCTATTCAAATAGTTTTCATTAATGTTTTCATTCTTTCCCTTTCTCGATTGCAGCTCCAACTTCCGG
CGCTTTGGTGGCGTAAAATGTTTGCCACCAATATCCGTTCGGTTGCCGTAGAAATCGTCCTGGTGGCGCCGTGAGCTCTCGTCCTTTTCCTTTCGCGAGTCCTGAATCCCCG
TTTATTTTTTTTTTTGCGATCTGCCGTTGCATATGCGGAGGGCTAATTAGCATGCGGCATTTCCAGCAATCAGAGTAGAGCGCACAATAGGAATAATAACGCGGAATGGAGA
GGATGTGTATGCCTCGCTAGGTGCCTACAACGACAGCGGTGGCGACGATTGGAGCAGCTCGGAGCACCTGGTCCTGTGTGGGAGGAGGATGAGACGCAGCGAACGACTGCTAAT
GCCACCAGTCGGCATAATCAACTGCATGTGGCCAGGTGGAATGCCACCGGCAATGCGACCATCAGCGCGACCTTCGAGGACGTACCCTTCGATGCGAACAACTACTGGGCCC
TATTGGCCCTCGTCCTCGTCCTGGGAACAGCGGCCGGGAACATCCTTGTCTGCCTGGCCATCGCCTGGGAGCGCCGGCTGCAGAATGTGACCAACTACTTCCTTATGTCGCT
GGCCATCACCGATCTCATGGTCGCCGTGCTGGTCATGCCCGCTGGGCATCCTTACGCTGGTGAAAGGTGAGTCCTTTGTCCCATTCAAAGTCCGGAACAGAGGTATTTTTTGC
AGCCACCTTTTGTTGAGGGACTCAATGGACACTTGAGTAAGTCACTTGTGCGCCAGGATTGGCTTGTGCGGCTAATCTTAGTTGGAAAAGTTCCTTTTCCATAATTTCATAG
TTTACTCTAACGAAAATGAGTTGGTGGAAAACTTGATGAAAATTAATATTAATTACTTGGGGCAAGGGAAAAAAGAGTGAGAAGTTTTGATAGTTGTTAAATTTTTAAGGCT
TTTAAAAAGTGACGAAGAAGATGCAAGGAAACGCAAAGATGTAGGGAATATACAAAATTATTTTAAATCTTAAGATTTCTTATATTTGCAATTTAAATGCGGTAAATGCGAA
TCAATTGAATAATGTACAGGGAATTGTGAAAAAATATGGATATTTACGGATTCCTTTTGCTGCAACTCAATCCGAATGATAATCTCTCCAAGTGGAAGAGTATAATAATCAA
AGCCAGCGACAGAAACGTGGCAAAGACATTCAGGCCAGGACCTCCTGCGATGTCGCCAACACGAGGCACGAGTTGCATTTAATGAAGCTGCTCAGTGGGAATGGCGTTGGCGG
CTCCATCGTTAGACAATTTAATAAGCGCGGCGCCTTTGTAGCCAGCCTGGCCAGGACGAACCGCTGGCGCAGACAGGGAAGCCCAGAAACAATGCCAGCAAGATGGCAACGG
AAGCTTCCAAAGCCTTTGCAGGCGCCGGAGCAACTGCAGCATAAGAATTGCATTAGGGCGGCAAACGAGCGCTGGTGAATTTCGCTTTGACTTAGTTCGGATCTGGAAAACA
TCTGCCGACACATTGCTGTCCTGCAATCTGCACTGAAAAAAAAAACAAAATATATTTATTCAATTATTTCTATACTTAAAGTAAAAGTCATCAAGTTTAAAGCTAATTGTAT
AATTTTTTTCTTTCGATTTTTTCGATTGAGCAATAAAATATGGTTCATATATGTTAATACTTACATTTTTTTTAAGCTAAGTAACTTGAAGCTAGCTACACAAATATTATAA
CATACCAGACAGGAAATGGAAAAGCTATTTCCGTGACTTTCAAAGGCGTTGCTTATTTCGTTGCTCCATTTATGTGAGTGCTTCTTCCGGTGGCAGTTAAACGGTATTTCTT
CGATTTTCGAAAACGAATGGCTGATTTGAGGACTGCATTTATCTGAGTGCTGCTTCCGCCTCCTGCTGCCGTCCTTTTGTGCCAACCCCTGCAGATGTTGCAACACTGATG
ACAGTTTGTTTGTGCGCTTTGGGAGCCATTACAAACACAAACACAAACACAAACGAGCACGGGCACCAATACAAGCAGAAAGGGCGACGCACACACACGCAAACACACA
CCTGGAGCAATCCTTGGCAAAGTGGGCAATGTAGCAAGAAGGAGGACCAACAAATGGCTGCTTGTATATCAAGTGTGAAAATATTGCAGTGGCAGTGACAGGAGCAGTTG
TTGCTGTAGTTGCACGGGCACACGCCCGCCAACTGGAGGCAAGAAAGGACGAAATCGGGATTTGCCTGCTGTCAAGGGCTTTGCAGAGGGTCCTGCGACAGAAGCTGAAATC
TCCAGCGAACAGCAGGCATTAGATCCCAAGGATTAAGCTCTTACAATTCAAAGGCACAATGGCGCAAGTAGCAACTGGATATGAGTAAGCCGTGCAGTACATTAATTGCATC
GGTTACGTAAGTAACATGTGGCATACAATGTGGCATTGAAATGGCCTATATATTCTATTCTCTGTTGATAAGTATGCAAATTCAACTTTCAATGAAAGCTGAACTAATATGT
TCATGACCAATAGGCGTATGAGTAATAATATTAGTAGACTAAATGTTTAAAAAACGCTAAAGGTGTAATATCAAAATTAATCTAACAAAATCATTCATGGCTTTGGTTGTTGACTT
TCTGGAGTGTAATAATAATACAAATTTAAATTTTCGTAAAAACAATTTGATCCGTACGTACACGCACAAATCTAACAAACTATTGAAATGGAATCAAATAGCTGAAATAATA
TTTATAAATGAATATATATTTTTAGGACTTAAGTTCACTGAAGGCTTAGCGGGAAATAAGTTTTTAAGGATGAAATATTAATGCTATTATGCTAAACTCTGTTGAGTTTCCA
GATGCATATATCCTTTGATTTTGAACTTTCAACGAATTTTCCACTTGATCAATCGACCTTTTGGAAACGAAACAAGACCCATGCAATTAAACGACATGCGTTGCCCATTT
TAAGCGCTTGCACTTGCAGTGAATTATGATTACGCGTGGAAAACATAATTAATGCATAATTAATTTCATTTTAAAATCAGCATTAAACGCCAGTTAATTAATAACAGTAAAC
GCAATTACTGCATAGCATAGCCATCAAAAGCCATAAAAAAGACAGTAAATTGAATTACAACGTCCCGTCAATGGTCGTGAATATTTAAGTAAACGCGAAAAGCTCGCAAATG
TTTGCAACTTAATAAATTATACTTGGGACGAATAATGATAAACAAGAGAACAGCCGCAAATATAAAAAGAAAAGCCAAGCGAAAAAAGGCGCGAGGCACGAGAAGCTGGAAA
ATTAATTGAGCGCAAATTGGTGAAGCTG
(SEQ ID NO: 94)

Exon: 1001..1445
Exon: 1885..2064
Exon: 2784..3172

FIGURE SHEET 44

Start ATG: 1001

Transcript No. : CT24036
ATGGAAGAGGATGTGTATGCCTCGCTAGGTGCCTACAACGACAGCGGTGGCGACGATTGGAGCAGCTCGGAGCACCTGGTCCTGTGGGAGGAGGATGAGACGCAGCGAACGA
CTGCTAATGCCACCAGTCGGCATAATCAACTGCATGTGGCCAGGTGGAATGCCACCGGCAATGCGACCATCAGCGCGACCTTCGAGGACGTACCCTTCGATGCGAACAACTA
CTGGGCCCCTATTGGCCCTCGTCCTCGTCCTGGGAACAGCGGCCGGGAACATCCTTGTCTGCCTGGCCATCGCCTGGGAGCGCCGGCTGCAGAATGTGACCAACTACTTCCTT
ATGTCGCTGGCCATCACCGATCTCATGGTCGCCGTGCTGGTCATGCCGCTGGGCATCCTTACGCTGGTGAAAGGTGAGTCCTTTGTCCCATTCAAAGTCCGGAACAGAGTGG
AAGAGTATAATAATCAAAGCCAGCGACAGAAACGTGGCAAAGACATTCAGGCCAGGACCTCCTGCGATGTCGCCAACACGATGAGGCACGAGTTGCATTTAATGAAGCTGCTGGT
GGGAATGGCGTTGGCGGTGTGCAGATTGCATTATGTCTCAGATATTTCGATCAAAGCTGGCAAACATGTTGCAACACTGATGACAGTTTTGTTTGTGCGCTTTGGGAGCCAT
TACAAACACAAACACAAACACAAACACGAGCACGGGCACCAATACAAGCAGAAAGGGCGACGCACACACACGCAAACACACACCTGGAGCAATCCTTGGCAAAGTGGGCAAT
GTAGCAAGAAGGAGGACCAACAAATGGCTGCTTGTTATATCAAGTGTGAAAAATATTGCAGTGGCAGTGACAGGAGCAGTTGTTGCTGTAGTTGCACGGGCACACGCCCGCC
AACTGGAGGCAAGAAAGGACGAAATCGGGATTTGCCTGCTGTCAAGGGCTTTGCAGAGGGTCCTGCGACAGAAGCTGAAATCTCCAGCGAACAGCAGGCATTAGATCCCAAG
GATTAA
(SEQ ID NO: 95)

Start ATG: 1

MEEDVYASLGAYNDSGGDDWSSSEHLVLWEEDETQRTTANATSRHNQLHVARWNATGNATISATFEDVPFDANNYWALLALVLVLGTAAGNILVCLAIAWERRLQNVTNYFL
MSLAITDLMVAVLVMPLGILTLVKGESFVPFKVRNRVEEYNNQSQRQKRGKDIQARTSCDVANTRHELHLMKLLVGMALAVCRLHYVSDISIKAGKHVATLMTVLFVRFGSH
YKHKHKHKHEHGHQYKQKGRRTHTQTHTWSNPWQSGQCSKKEDQQMAACYIKCEKYCSGSDRSSCCCSCTGTRPPTGGKKGRNRDLPAVKGFAEGPATEAEISSEQQALDPK
D*
(SEQ ID NO: 96)

Name: 5-HT2 receptor-like 1
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384504
TATAAATGAATTCTGAAAAATGTATAAAATGAAATGGACTCATCATTAGGTCAATTTGTTTGGAATCAAAAATTTCCCAAAGAAATGGTTTTACATTTCAGAAAGTGACCCT
TAATTTTCGCCATCAATATTTATTAGAACATTGACCTTAAAGCAATTTGTATAGTCGTCACTTTAACAGATCAAAGTTATACTTAAAGTCGTGCAGTTGCAACTGAAACTGA
TTCATTCTACGCCTTATCGATCCATCTTCCCCCGAACTTATCCCAATTTCTGTTGGCTATCTCGTTAGGAAATTCCTTTTCCCAGCGGCCATACGGATTCATGTTCGACCAG
ATTCTGGATTCACAAATCCCGCGCCCAAATCTCAGGGCACACGCAACAACACAGTAAACACAAGTATCACTCACCGAATGTGTGGGAGATTCTCGGCCACACAAGCTACAGA
GAAACAAACCCAATTCAAACTAAAAATTTCTAAATGGAAAATAAATTAATTTTATTAGTTCTTTATAAGATACTAAGACTTATACTAGTTGGAAATCTTCTAGGCATGGTTT
GTAAATCATCCTTATATCTTTCGATATTATTCTAAGACTTTTTTCGTAGTGCACACAATTGTATTTTTATGGGAATAGGGCGAGTGGTGCGCTGAGTTATGACGTCCA
ACAGCTGTGCAAAACGATGGCCACAGCATCGGGAATAGCCGCTCATATGTGGGCCAGTTGGCCTGAAATATGTTGCATAAGCTCCCCCCTCTTGGCAATATCATTTGGCAGC
TCACGAATGAACTGTGGCTCCCGGGAAAATATGGCCAAAAAAATAAAAAAAAAAAAGGCGGGGAGTATTAAATAAAAATGGCTAGAGAACATTGCATTGTTTGCCGCCGACC
AAGCCAATCGTAAATCGTGTGTACACATAGGTAGAAAGTATTGCAGCCACTTAATACAGTCATAAGTCGGCCATGGAACATTTACAAGCTGACCAAGAAATACAATGAAGAA
TCGGTTTTTTTTTTCTTTTACAGGCTACTTTCCTTTGGGCTCGGAGCACTCCACCTGGATCTGCCTGGATGTACTCTTCTGCACGGCCAGCATCATGCACCTGTGCACC
ATCTCCGTGGACAGATATTTATCGCTACGATACCCAATGCGATTTGGCCGGAATAAAACACGTCGGCGGGTCACTCTCAAAATTGTTTTCGTTTGGCTTCTGAGCATCGCCA
TGAGCTTGCCCTTGAGCTTGATGTACTCCAAGGTGAGTAATAATGCTATTCTTTTGTTTATATTCTATATTCCAACAATGCGTCAAAATATAGTACCCTTTTGGCATTCTAT
TTCCCTTAATCTAATAGTGAAAACCCATTAAATTCCCTAGTTAACCTAGTACTCAAAATCTAAAGTGAAAATTACAAACACTGTGCCAAGTCAATAATTAAAATCCAAAGCG
AGACAAGTGCTGAAATATTTTGCGCATACATATGTCCTTTACTTACCCAAATTAATTCCGTGCTCGCCCTGCTATCTTTCCTTTGATTCCAGAATCACGCCTCGGTGCTGG
TGAATGGAACTTGCCAGATACCGGATCCGGTGTACAAGCTGGTCGGCTCCATTGTATGCTTCTACATTCCACTGGGCGTGATGCTGCTGACATATTGCCTGACCGTCCGACT
TTTGGCCCGGCAGCGCCAGAATCTGGGTGGTGGACAGCAGACGGCGGCGGCCACTCCCGATGGGCCAGTGGATGGCTCGGCCAGGCACCGGCCTTGGGTAAGGATGCTAGA
CACCACACTTCTGACCCCCACTCTCACCCAGAAGTGTCCACGAAGAGCTGCTGCTTCTGCTGCAGCTTAATATGATTTTCAGTTTGCCTAAAATTTGCATTTTGTTCTCCGG
ATTGCACTTTTTGCACTGAAAACTTTACACGACACTGACAAAAGTAGAGAGTAGGAAATGGGCGGATCAGGATCAGCAAGGGAAAGTGCTCAAAAGTGGGGGAGGGGTGAC
AACACTAGACAAACAATGCAGAGACATGTGCCGGATACTCCCCGAATCCGTGTCCCTGGGCTTTCTGGAGCCCAAAGTGCGACTAAGCCGCAGCAATGCACACAAAATCGAC
ATTGTCGTCGACATTGAACCGGATGGAATGGGGCGGGGGGGGGGGGGGGCCAACACCCCAGGACAATCACCCATTCCACCCACTTGCACACACAACCTTACAAATAGGATGA
AAATCCAGCCCATATGTGTAGATAGCTAATTTCCACGTTGCCATGAATCGAGGGCCAGCTACGTAAATGGCTTGTAATGCTCTAAGAGCTCTTCCATAGTGCTCGACTAGTT
TTAAAACCGAAGTTTTAAGCACCAACTTTTCAACGAAGCCTCGTTACAGCCCCGTTGCGTAGGGTAGTTTTTAAAAACTCAAGAGCTGCGTTAACTTTTAGTTTTATTAACC
ACTTTTTGAAATTTCCATAACACTTTTCAGCGCATCTACAAAAAAGAGGAGGAATCTTTAAACATGTAGCTAATAAATAAAAAGTGAACAGTCTGTTATTTTAGATTTAAAG
AGTCTAAATTGCTTCCTGCATCCCTAATTACCCCTCTCGTTACTAGCCCAGTTAACTGGAGCTTTTGGCTAAAAACAATCCAAGATCCTTCGCTTCCATTATCCCTTCACAA
TTCAATAGACCAGATTCAATTTATTTTAAGCATAACTAAGTGGCTCCTAATGCCATTGTCTGCCCGCAGAATTTATTCAGCGCTCCCATTTCTCATCCAATTGGATTGCCTT
GAGCCCCCAAAGGGGACAGAGAGTAATTTTCTGGGGGACAAGCTGTGGATCTCTGGATGTTGAAAGTCAATACAGTTGGGGAATATTTAATGGAATGCTTCTGGTGGTGGCGA
ATGGTGAATGCTGAATGGTAAATGCTGATGGTGATGGTGACTGCAGTCGAATCGCGTGCACTGCAGGGCATTTTTGCGAAAATCGTAGCGTGCATTTAGGGGCGATTCGCAG
GACGCGGTGTCCCCGATTCGTCTAAGTGGATTTGAAGCCTCAGCTGCAGGCATTAGGGTGTGTATGTATGTATGTGTGGGTGCGCATCTGTGAGCGGCCAAGTGCGACTGTG
TTAGTGCCGTGGATTTGGGCAGTTATTTTAAGCCAAATCTCTGCTGTAAAGCGTCCGCATTTCGGTCAGGCACGTAGTCGGATTTGCCGTATTGTACTTTTTACACGCAGAG
CTAGGAGAAGAATTTCTCTCAGTGCCTATGTTGAAGGGGCATTTAAGTGTGTCGTGCGAGTTTATTAGCGAATTTGTGACTTTTCGTAGCGCACTATTGGACTGAATGCAA
TTTAATGGAAACTGTATATCCGTTTAACCCCGTGTTCGTGCTCCACGAACGACGATGCACCTGGCGGCGCCTTTTGAAACCGGGTCCAGGTAACGCCTCCTCGGTGCTGCA
CGCACACTCGGCCAATTCAACGGATACGGATCTCAGCACTTTGGACAACCACGAGCTCTGGCTGCCCGATTCCAGGTGAGCTATCGAGTTTGCGAGCCAGTGTTGCAGTGCA
AGTCGGTGGCCTCGTCATCCACCACCGGCTCACCCCACCAAATTTCCCTATCGAAACCACCTGCAGCTGCAGGTACCCCAGCAGCCCAGCAGCGATATGCCGCCCACCCA
CCAGCAGTCCCACCACCACAACCACCAGCAGCATCCGGCCGGAGTTTACCACCAGCAGGCATCGCCCAAAGGTCGCCACGGAACCACAGTTCTGGGTCGTCCACCACCACG
CTGGGCATCGAGCGGGAGAGCACCAGGAATTCCCTGGCCAGCAGTCGCATGGGCGGCGACAGAGCGATGGGTGAGTTCATAAAGTAGTAATATAAATAAGTGAGTCCAAATA
ATGGGGTCTAAAAATATACTATCTAAAAGTCTGGAAGCCAACCAAAATTATGGTTACAATTTTCTCAAGATGTAATATGATGCTCAAACATAATTAAATTGCTTCACCACTT
AACCAGAATCTCTGTTGTCACAAATAATATTAACACAGACAATTAAATTCTTTTAACTTTATCCCTTTGCCGGCCACAATTTTCACTAGAATTGTGTCAAATCCCTTGAAA
AGCATAGACAATTCGGGCAGGTACCTTGGAAAAACGTAAAGTTTTCGTGGCTCTTCACCTGACAAAAGGACAAACAGCTGCGATGGGCAAACCGTTTTGCCAGAGTGATCCT
TTCTAGTCGCTCGCAGGACCTTTTGTTGTCGCTGTCTCAGCCGGTTTTCGAGTGCCAGTACTGCGCTTGGCCAAGTGTGCTGACCACACCAAAAGCCAAGAAATGCTCACC
TCGAGTCCTTTTTGTGACTCGTTTACTTTCTCCTTTTCCATTTATTTAGTTTTCTTTTTTCGTTAGCTCATTTTTGTGGCATTGCCTTTTATTGTCCTTCCGCCTTCGACTT
GTTGTGAAATTTTTCGTAATAATTAATTTTTTTCGCTACGTTATCCTTTTTCTTTGTGTCGGTGCAAACTGTTTTATTTCTTTTTTTGGCCAAAAGGCAGAGGCACTGCC
TTTTTATTTGGCATTCGAGCCGCTCAAGTGATTTTGGCGTCGACTGAGGCCTTTGCCAAAATGTGTTTTTCATTAATTTCCTAAATTTAGTCTACTGGCTTATGCTGGGAT
AAGTGATGCGACGAGAAATTTAATTAAAAAATTGAGATAATAGAAGACGAATATATTTGAAATTACCGAGAATTTAATAAGAACTGGAAACATGGCTAAACTGGCATATTC
AAGTAAATAGGGCGCTTCATGTTTATGGGCATTCAGGTGGAACTAATATTAACTATTTAATTGCGTATGATATGAAATTCTATGGAAGAGCCTGGCAAATTCTAAAAATACT
TTTATTTTAGGCACTCAACCCAATTCGATATTGTACACGCATTTTATTTTGATTTAATTGGTTATCATATTTAGTCTGCAAAATCCATCCAATAAAAGCATGAATTTTTCAC
TGCAACTGCGAACATTGATATCTTGAATCCCCCGTTCGATTTTTAAGCTTGAATAAAAGGCAGCTCAACTTGCGAAATGACTGCACATTTTATCTCGCTCTCATATTTTTCCCAT

TTAACCAATCCCTTATGCATGTTTATATCATATATCATTGTGACTGTGCGCCTTTCAGCCAAATGCTTGGTATTGGGTATTGGGAGCACTATGTGCCACATTGTTTGACAGT
TGAACGAATTTGCACAATCAATAAAATGGATTTGGCTTTGGCTCCGGCTTCCTATTGTCCGCAATGGATGGGATGCCACTTGGCATAAAGGACGAAAAGAAACGGGACGAGG
AGCTCAACACTTCGCCACATAAGAGTATATATTATATGTATGTGTATGCGAAGGCGGTATCCTGCGATGTCCTGATGAGCTTGGCAGCTGTTTAATTCCTTTGTGAGGGGGA
AACAATAACAAAGTTGGCATCAGCTCGGCTTTGTTTCACTTGCATAATGAGTAGCTGGCCCCAAATACCACCTCCCCACTCCCCCATTGCTTAGCCCTGTTCCAACGCATCT
CAATTTATGCGCACGTCTCGTGCAAACAAATCAAAAACGCGAAGGATGCATAATGAGCTGACATCCTTATCCTGCGTCTTGGCAGCACCGAGCATCCCGATCCCTGTCCTCC
CTGCAGCCACCACCACTTGGCCTTCTGTCTGCTAACGCCTTCATTAGCAGCTAACCACGCCCCCAACGCCACCGCCCCACACCGTCTTGGCCAAATAAAGTTGGCGCGCATT
TGCATGCAGGGCAAAACGGGCGGCAGGACAGAAAACCGCAAAGGCAGCTCGCAAATTTATGCGCTTTATTAAAATGAATGCAAAATGAGGCGGTACAGAAAAAAAAATCGATG
TACATATGTTTATATATAACTTTAAATTAAAGCTACACATATGAGCTAAGTATTTCTGCAATTAATAATATAAAATTAAAAAAAAAAAAAAATCCCGCCAGTAAAGTACAGT
AAGCCGAACTAACATACCAAATATAATATAGTAAATAATAATGCAAGAATTTTTCAAGTGTACCACAAACAACGGAGCAAGAAAAAATGTTAGAAGGCGGTAAACCACAAAG
AGCAAACACAAAAAATGTTGCCTACTTCCCGGCAAAACAGGTGAAAGAAACGAGCTGACCACAAAGCGTGCTGGCTTTTGTTCAATTGCCGTTAGCGAGTGTTCACTGCATT
ACTAAATCAATAAATCGGTGGGGTATGACATAGACATATTTTATATATTTTCATTATTAAAACCACATGGTTCCTTTTGTTCTAGTCTGCTTTAATTTGATTCAGGAAAATC
GTTTAATAGACCACTTTTTTTAAAATGAAATGAAAATAATCATTTAAGGACTTTGACTGTAGTATGTCATTATATTTATTTAATCAGTAAAGTTCTTTTCCTTTCAGGACTCT
TTCACAGCTTTCCCAACGATTGCGAGCGTATAAAAAGCGACGAAGAGCTTCGTCAGCTGTTCCTGGACGTGAGAAACGTGCCGGGCATGAGGACGCAGACGAGGATGTGGAA
ACGCCCACGTCAACGCTGCGCCGCCACAAGCGCCATAACAGTCTGCCCAAGAACGCACTCTATCCGCGACACACCACTGTACAGGAGAGCCTCGATGACGACGACGACGAGG
AGGAGGAGAGCGCGCAACAGAAGGATCAGCAGACGAAGTCGAAGATCTGCCACTCGGACACTGAGCTAGATCCTCCGCAGAAGGCGAAGCAGTGCCACATAGCCGGGCAGAA
TCATCAGTCGGACTACCTGCAGCTGCCCTCGGTTTGCACTTGTCCGTATTTTGGGGACAGACCGCTCCAGAATTGTGTGAAATCGGCGGAGGTGAAGATTATTTCGTCCGCC
TTCCGAGTGACCACCACCACGACGGCGGTGAGCAGTTCGCCCAGCGAGATGGAGCTACTCATGTGCAGTAGTGGCAATAAAAAGTCATTGACCTCCAGTGTGAGTGCCGGCA
TAACAGGTGGACCGGCAGGAGCGGCTCCAGCCACAGTTGGCTCCACCCTCAGTCCACACTCTGCTCACAATCAGGGCAGCTCGCTGACAGTTCAGAGCGATGGTAGTGGGTA
GGCGGAGTGCGAACATCCCTGCTGTTGACGCCCACCAAAACAGCGACCACCTCCAACTCATCCACACCGTTGAGAAGATCGGCCACCTTGAGGAGTCACCAGAATATGAACT
ACCAGGGAGCGGGCGAATGTGGTGGCAAGACCAGGACGACAACATCCTCACCCTGCATGTTGCAGCGTCAGCAGACGGTGCGATCTCATCACTCGCGGAACTCCAGCGTGAT
CTCCAGAAACTCCTCGCGCCACGGCAGGATCATCAGGCTGGAGCAGAAGGCCACCAAGGTGCTGGGAGTGGTGTTCTTTACGTTCGTAATCCTCTGGTCGCCATTCTTCGTC
CTCAATCTCCTGCCCACGGTGTGCGCGGAGTGCGAGGAACGAATTAGCCACTGGGTCTTCGACGTGGTCACCTGGCTGGGCTACGCTAGCTCCATGGTGAACCCCATCTTCT
ACACCATCTTCAACAAGGTGTTCCGGCAGGCGTTCAAGAAGGTCCTGCTGTGCCGCTATTCGAGCACGAGTGCCTGGCGACCGAGCAGATAACAGACGCCCGTTAAACCGGG
CAAACTGAAGACGAATACCCACAAGTGCGCCAGTGTGGATTTTCAGGATTCCACTGCTCCGGTGCGGGGCGTTCTGAAAAGAAGTGTGGCAGTGGCAAGTGACATATAAATA
ACACGTGTGTCCTTGGGGCTTAAATTCTTATGTGCCTCTAATTAATTTCAAATTCAATTTGCATGCCATTGAAAACACATGTCCCAGGCGTAAGAAGTGGGGCCAAGTGAAT
TAGATATTGAAGTGGAGTCGGATCCCCGCAGGATTGCCAAGGGTCGGGGATTAAACTAGCCACAGACAACAGCATAACGAGCATGCTACTCACCCCTGGTGGTTCCTTCCAT
TTCCCTCAGCTCTCAGCAAACGGTGAAGATGCACTTAATTGCGGAATGTTTGCTTTCGAGCAACGTAATACCGGCAAACACATTTACTTTATAGCAACGCTCTTCAGTTATC
GACAAAGTTCTGGCTCACCGAAAGTTCATGTCAATCTGTTGATATTTGATAGCATTTTCCGCGAAATTCCTTTTAGATTCACTACGTACTCGAAAATAAACTTGAAAATTCA
CGTAAATTTAAAGATTGTATATATAAAGTTCAACTTTTGAAATTCTTAAAAATAAAGCGCCAATGTCGCTTCGCAAACTTCGATCGATAAACGCTATTTGGTTTGGCATTTG
GCAATTATGCATTAAATTTATGGCAAATTCACTGCCCGCCAATGCACAAAGAATTTCATCGGTATCCATTAAAGAAACCGACACGTACACAAATCCACGGCAATTTGTGACT
TTTGTTGTTTGTTTGTGTGTGGTTGGACCGGCAGATTGCTATTTTTATTTGAAAAGTTCATTCATTTTGTTTTATTTCTGTGGCCA
(SEQ ID NO: 97)

Exon: 1001..1264
Exon: 1550..1778
Exon: 7511..8268
Start ATG: 1001

Transcript No. : CT24060
ATGAAGAATCGGTTTTTTTTTTCTTTTACAGGCTACTTTCCTTTGGGCTCGGAGCACTGCCTCACCTGGATCTGCCTGGATGTACTCTTCTGCACGGCCAGCATCATGCACC
TGTGCACCATCTCCGTGGACAGATATTTATCGCTACGATACCCAATGCGATTTGGCCGGAATAAAAACACGTCGGCGGGTCACTCTCAAAATTGTTTTCGTTTGGCTTCTGAG
CATCGCCATGAGCCTTGCCCTTGAGCTTGGTGATGTACTCCAAGAATCACGCCTCGGTGCTGGTGAATGGAACTTGCCAGATACCGGATCCGGTGTACAAGCTGGTACGGCTCCATT
GTATGCTTCTACATTCCACTGGGCGTGATGCTGCTGACATATGCCTGACCGTCCGACTTTTGGCCCGGCAGCGCCAGAATCTGGGTGGTGGACAGCAGACGGCGGCGGCCA
CTCCCGGATGGGCCAGTGGATGGCTCGGCCAGGCACCGGCCTTGGGTGGACCGGCAGGAGCGGCTCCAGCCACAGTTGGCTCCACCCTCAGTCCACACTCTGCTCACAATCA
GGGCAGCTCGCTGACAGTTCAGAGCGATGGTAGTGGGTACTTGGCTGCTCCGGGAACTCCTTGTCCTGGCCGACGAAAGTTGAGCATCTCAAAGACCGCCTCGGTGGTCACG
GAAGATCGGCCACCTTGAGGAGTCACCAGAATATGAACTACCAGGGAGCGGGCGAATGTGGTGGCAAGACCAGGACGACAACATCCTCACCCTGCATGTTGCAGCGTCAGCA
GACGGTGCGATCTCATCACTCGCGGAACTCCAGCGTGATCTCCAGAAACTCCTCGCGCCACGGCAGGATCATCAGGCTGGAGCAGAAGGCCACCAAGGTGCTGGGAGTGGTG
TTCTTTACGTTCGTAATCCTCTGGTCGCCATTCTTCGTCCTCAATCTCCTGCCCACGGTGTGCGCGGAGTGCGAGGAACGAATTAGCCACTGGGTCTTCGACGTGGTCACCT
GGCTGGGCTACGCTAGCTCCATGGTGAACCCCATCTTCTACACCATCTTCAACAAGGTGTTCCGGCAGGCGTTCAAGAAGGTCCTGCTGTGCCGCTATTCGAGCACGAGTGC
CTGGCGACCGAGCAGATAA
(SEQ ID NO: 98)

Start ATG: 1

MKNRFFFSFTGYFPLGSEHCLTWICLDVLFCTASIMHLCTISVDRYLSLRYPMRFGRNKTRRRVTLKIVFVWLLSIAMSLPLSLMYSKNHASVLVNGTCQIPDPVYKLVGSI
VCFYIPLGVMLLTYCLTVRLLARQRQNLGGGQQTAAATPGWASGWLGQAPALGGPAGAAPATVGSTLSPHSAHNQGSSLTVQSDGSGYLAAPGTPCPGRRKLSISKTASVVT
WDSSRHRRRGSSFGGVRTSLLLTPTKTATTSNSSTPLRRSATLRSHQNMNYQGAGECGGKTRTTTSSPCMLQRQQTVRSHHSRNSSVISRNSSRHGRIIRLEQKATKVLGVV
FFTFVILWSPFFVLNLLPTVCAECEERISHWVFDVVTWLGYASSMVNPIFYTIFNKVFRQAFKKVLLCRYSSTSAWRPSR*
(SEQ ID NO: 99)

Name: 5-HT2 receptor-like 2
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384673
GACCTTTAAGCAGACTAAGGGGGTGAGGCAATCCTTTTTTCCCAACTCGTGTCAATTAACTCATTAAACTTCCCACCGTTTTGTGGAGCGTCGGACCCAATTAGCTTTCAAT
TATACCGTCTATGGGCTGGTTTTTCATAATCAAGCAAAATTTCAATTAATTAAAATGTAACCGAGCTAAAATGGAGGTGTGAGAAAGAGCCTTTATTACGAAGGACTCTATT
ACACATTAAAGTTTTATGGAAAGAATGAATATTCTCAGTGAGCAAGACCAGATAAGCTGCCAACATATTTTCTCTATCCTGTCAGCTTCATAAAATGTTGGTTTTGATGATG
GAAACTTTTGCCCATGAAACTTTTTGTTCGCAGATTATCGTGAAAGAGTTTTGAGCTCCGTTTCGCTGTATTGTTGGCTTGCCAAACTGTTGCATACTTTTAGGAAGTTGCA
AGGAGCGGAACATGTGTTTGCCATGTCAACTTTTTGCCATATTTGTAGCCATAACAGCTACACATCTCCGAGGAAGGTATTTTAGGAATTTTTTTTTGAGTACATCAAAGCCG
ATAAAGAAAATCCCCCAGACAATGGAAGCTTACCGAAAGAAAACCGCAATGATAATTCCCCAGAGAAAAACGCCGATCGAGTACACTGAAGTAAATAGACCATTTATTTAGA

FIGURE SHEET 46

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TGCTAGAATTTCTTGTTTATACAGAGAATTAATCCATTTGCACATTGAGTTACATTCAACAGCTACAGTTGGAGTTCATAGCATGGAGTTGGTTGGATTGTTAATGGGGCTC
TCAGCTGCTCACATATACGACATTTAACAGTTTAAAACGATTGACCTAACTTATGTTGCTTGTTTGCTCCGCTTGGTACTTGGTTTCGTCCTTTCATCGCACTCCAGCCTTT
AATAATTAGTACTAGCTAACTAATCGCACTCGCAGATCTGCGACACGGAAGTGGAAAGTTCAATGAAAGTTCAGTCTCTTAAGATGCACTTGCTAGGGATTTGTCTACACCG
AGTTCTCCTCGAGTCCTTGCTGGAATTCGAGAATGATTATTGGATGGTCTGTATGAGTGAGAAGAGCTGAATTCTGGTTCTCACCCTCATCAGGGGACTAATGGCCCGGGGC
ATTACGCTCAGAGTGCTGCCGGAACTCATGGCATTTGCCGCCAAAGTGGGCATCGTGTGCAGGGCATTGTTGGAGCCCCGGTGGAGTGAAAGTGGGGCATGCTGACCCACCA
GCGTGGTGGTGGTGGCCGAACTTACGCACGATTCCCGCTTGCCACGCCCATAGTAGCTGGTCAAAGGTCTGCAACGGAGTGGATGTCAAGATATCCCGTCACTTCTTAGCCA
CGATTGCCACATAACTTACCGCATACTCTCGGCTCGGGGGGAACCACCGCCTTTCGAGAAGCTTTTCGTGGTATAACTGCCAAGTTTACGAAGAAATGCGCAGAAAAAGTTA
GTGTACAATAGTGAAAATATTTTTAATAGCTGCCATTCCTAGTAGCAATCTAGCATTGCCACACTTTATGATAGGTTTAACATTAAAGGCATTTGAGGAGAAATATGTACAA
CTTAGTTGTTTCCTATATAAGTTTGCAGTTTTCTCTTCTCGAGTAGTGTATTTATTCTTAAGTGTACTTACAAGCAGACTTAAAAGTTTGGACTACTTACCGTCGGTTCTGG
TTAAGCTGAATGGTGCGCGTGTCCCGCCACGTGGAAATGTGGTGTCTCAGTGCATTTCGCACCTCCGAGTTGAGGAAACAGTAGAACAGCGACACCGAGAATCCCTGTGGCA
CACACACAAACAGATCTTTAGAAAAAAAGTGGCTAAGAGGATTGACAAACGAAACCCACCTGAGTGCTGAGTAATACCGCTCGCAGGACGGCAAACATGTGTCCCATTAGGC
CAGATTCCGAGGGACCAGCCAGCACCACCAGGTAGGTGATGCCAAAAAGTGGGATTAGCACCAGCAGTGCCTTAGCAGCTTTCCTATACTGACGAGTCTCCACTGTATTGGC
CGAGCGCAGCTTTGTGATTAGAACCTAAAAAGAGAAGCAACCCGATAATCTGGCTCAGTATTTTCGGCAATTTACAGTCGGGAAAAATGTCGGATGATAAATTGTAAATTCATA
CAATAGCTTTAAAGTGTTTCAAGAAACTAATTGGGTGATTCATAAATGTGAGTTTTTGCATCCATGTTAACTTGTTCAATCTTCTCTGATGTTCTTTTTTTCGCATATCAAT
ATTTTTTTCTGTGTAAATTCCATACGCACCCACATGATACGCAGCAGAAATGTGAGATTGATTATTAGCACCGCACAGACAGGTCCCTGGTATATCCAATCCACATGGGTCTC
CTGCATCCAGGGGCAGTTGATTTCGTACTGTCGGATGGGAAACAAAAGGAAGACTACTCTCCAGGGGTCTCTTCAAATCCCAAAATAGACATACCTTTTCGGGGGTGCTGTA
GGTGACCGTCAGACTCTTGGCCACAGCCCAGGTGACAACAAACAAGGCCGGGCCACCTGCCAGCAGGAGAAAGACTTAATTGGCTGGCACACAATCGGGCATTCACACTT
ACCCCAGCCTATGGAGGCGTAGATATTAAAGCGTAAATTGTCCCCGGAGAAAGTCTTAACCACCAGCATGTACAGGTACAAACCCTCGACCAGCATCCAAAAGAAGTTGGTC
AGGGTGAAGAAGTGGAACAGGGTGATCAGAGCAATGCAGCTGCCCACTCCACTTCGGATGGAGATCTGTAGATTAAGTGGTAGCCATTAGTCTTAAGCTGTCAGCGTCTGTT
TATAGTTTCCTTTCACTTTGGACTAGCACCCCTTTCAGGCACGAGTATGATTTAATAAGCCAGCAATTGCAATTATCTGGCAGTCTCATAATGCTCACCTGGACGGATAACA
AGAGTATCCAGAACAAAGCCGACATGATGTACGTGAAGAACAAGTTGGCGTGGATGGTGTTGCGCAGGCAACGCAGCTCCCTGGTGAACAAAGACAAATACAAAGGACGGGG
GGTAAGTCGGGGGTTAGGCAAAAATAAATGCCATACCCAGGGTATCGGGGTCACCAGGGAGGGGGCTGGGGTGGGTACACTCACTTGAAGTAGGCGAAAACAATCAGCGCCA
GCGAGAGCGGATACCAGGCTGAGGGTGTATCCAATGTAGTAGTAATAATGGTGGGCAGCTCCACGATGACCTCGAACTCCGGCACGGATTCTGGGGCGGGCAGGTGGGCGCAGGC
ATCGTAGTTGGTGTACTTCTCCCAAGTTCCATTGGCGTGGCAGAACCTCGTTGCATTCTCTGGTCAAATACAAAAACGCACGCAGCGAAAAATGCAAACAGTTTTTAAAATAG
ACTAGTCCTATACACTTGGATCTATATTGGGAATATGCCTTCTCTGTTTGGACATCGACTTAAAAAATTCCAATTTAAATTCATAACTTAGTGCAAAGCTAAACAGTTTTTTT
CAAACGCTTAGTTTAAATATAAGTCTAATGTTAAAGTATAAGGTCAAAGGGGTACTCACTGCTGCTATCGTAATGAATTCCCTGCAACTCGTCCATGCACTGGAGCACCGCC
AGGGTACCGCGAGCTGTCCTCGGCCAGCACAGGATCGAGTCGAACTGGGTGAGGCAGTGGCCACTATCGTTGCCATAGGTGGATGCCTCGATGTGCTCCTGCACCAGGCACT
GCAACTCCACGCTCTCACCGATGCCATCTAGGTTGTGCAGATCCAGGAGCGCATCACTCCCGCTGGCGTTCACCGAATCGATGTGGTTGTGGTCACTCATTCTACAACATCC
TGGCACTTGGCATCTCTGGTACTGAAATAAGTCAGTTTAAAGTTGAGGCAAAGATTGTAAAATACTTGAAGCAGTGGGAAAATTTAAAATATTTTAGAATCATTATAGAGTT
TTAATACATTTCATTTAAGAACCGTCGGACAATAACGTTTTAGAAAAATGGTAAGCTTTAATCGGAAATAAAAATATTATAGACTGATACGAAAATATTGCTGTCATTTCCTG
ACCATTTCCCTACGAATTGACAACGTTCATAATAACTCCCCAGCTGAATTCGTTCAATCAGAAAGTTATAATTTCCTCAATTGTTAGGGGATTCCCCGGCCGGTTGGCTGAAAC
TAAGCTGTCGGGCAAAGTTCAATTGCCAACCCTTCTGCTCGCTCCACCCGCAGCCAGTGGCATTTCGCCTGTGTGCGTTAATTGCATTGGCCATGTTTCACCGACAACGGGCC
CCCAGTGCCATAAAAATTCATTAGTTTTGCCATCAAAGGCCGACAGAAGCGTCAGCAAATCAGAGAAGCGGCAGGCAACCTTTTATTCTGATATGTGCCCATAAAAAGCACG
TCAAAGGACCCAAGTCTGGGGTGATGGTGATAGAAATTAGAAAAGCTAACTTCCGGCCAAAGATTGTGGCCTTTGTGGCCTGGTTCTGCCTGGTTCTGCCTCAGAGACGAAA
TCTCGCATTTATGTTCTGATAATAAATGGCATAAATGATGCATCGTTACATTAATGCACGACATAAAACGGGGCGGCAAGTAAGACACACACAAACAATACATATTAAAA
ATGTAGATGGGCCTGTTTGTACAGTGAGCTAGAAAAGTAAAAGTGCGCTCTTTAAAATTTAAGCGGAAGTGGCTTTCACTTTCTACTTAACAGTGAAATAAATTAGGCAAAC
AAGCCAGCTTGAATTCCAAGGAGAAGCCATAAGCCAAGGCAGGAATTTAAATCCACTCGGAGTGAAAATGGTTATCTCTTAAGTGATGCCCAACCCGAACCAATTACTTTCT
GTGGAATTTCCGATTTTCTCGGACGGCACATTCCCCAGGCGATTTTCTAATTGGCACAGGAATTTCTAACCACAAGCCATGAAATATTAAACCCGAAGGGAAATTGAAAATT
CTGCCCCAAGGCTTGGGTGCTCCACTTCTGGCTGCCACTGTATGCTCGGCTTCGTATTTTTCTTTCCATTGTTTCTGCTGTTTGTTTTTCTCGTAAATTAACGCAATGCATG
TACATAAAACAAAGGCTGGCTGATTATTACTGCACGGCACATGCCTGCACGTCCTTTCCGGAGTTTGCCAAGGTCCTGGGTCCTGGTTCATTAGCCGCTCGCTTACTTATAA
CACATACGCCCCGTTGCCTTCCAGCTTCGCACGCTCACGACAACGCAGATGAGTTAAGACAGCAATATACGCGCCGCAATTTTAAGTTGAAAAGCATATTATTTGC
AAAAAAGGGAAAGAACGGCGAAGGACCGCCTCTAATTACCTCATAAATAACGTCGCACGAAATTAGCTGGCCTAAATTATGGCCATAACTGCTAATTGCATATTTGATTTCA
ATTAGTTCAGCTGACAGGGGCCCAAAAACCCAAGAAGGACACATTTGAAATCAGCGTGCGAATGCAAATACGTTCTGACAGCTCGCTTGGACAAATCTCATTTATGGCCAGC
CAATTTGACGAATGTCCGCCCGCCGGGGAAACAGGCAAAACAAATTCAGCTTGGCCGAATCATCGCCGGCATAAAAAGGACATTACCAGAAATACATACATATACGGAGGCA
TAAGAAATGGTTGGTCCTGGACGAAGACCAACGCACAAATCGCACATCGCTCCTTTCTGCTCCTCTGCCTCTTTGCAGCATGCTATTATAGAAGATTGTATGTAATCTCGTAC
GATTGCACACAATGGATTTGCCAAAGGCGACACAAAAAAAAAAAAAAAAAAAAAAAATAGGGGATTGCGTGGGGGGAGTTTGCTTGTGTGGGTCCTTTACTTTTTTTCTCCCCCA
TGTGAGAGGTTCTGCAATTTCCTGCTGCTATAATGCTTATAAATGTTCACCCGCAATCGCCGGGGATTTCTTTAGGGAATTGAAAACATAATAACAGTGCGAATAGTGGCAA
GCATTCGCATTTTCCACTTATCCAACTAAATATGCAGACTAAAAATTAAATTCCAGTTTTTTCAAGCCCTCGAAGGGGATTTTTATTTTACGCCCTTATATGTGTACCTATG
AAGCATTTAAAATTTATAAGCGTGCCACACAAGACCAAACAGCACATTACGTATACGCAGCATGGACAAAGCCAGCTTGGAAAGCCAGCACGCAGGCATAAGCGTATAGAA
AGTTTGTAATTAAATTGCTCATTTAAGCGTGGAAACAATGAATTCGATCGGGAATACAGGGATGGGGGAGTGTTCTGAGGAAATATGTAATATTCAGCGTGTAATCCGAAGA
AAAATATATTACTAATTTTATTCATCCGCCTTGGGCGCTTAAATTTTATTGTTCGGACTTTTGTGGACTCTCCTCGGAGGCCGATAAGGAAAAGCCAGTCTAGACAAGCCAAC
ATCATAATTTGCAGGCACGCACTGCCATTTCCATTTCCGCCCAAGCTTGAGCCTGATCTGCTGGCCACTTCCATGCTTAAGTCAGCACATATCCTTTAGCAGGAAGATGGA
ATGGGATGGGATGGGGCTGACACTTCAGCGATTGCCAACAAGTGTTGCGTTTTATTGTCTGGCCTTTAACAGCTCTCCTTTGCCATCCGCCCATTGTGTGTGCGGCACGTGC
AGGCGCCTGCATTTGGAGCTACGTGAGGGATCTCCACTCCTGTGGATAGTCCGAGCATAAAACCATAAAAATCCGCCGCAAAAAAAGAAACGAACCTGGCCACCAAATCTGT
TATTTATTGGCCCAATAAAAATTTGGTTTAATGCATTACAAGTTGCCGAAATGCCACGGAGATTGCCGGAGATTTACTTGGCTTGCAAAGGGAAGTCCTTAAGGCCATGGCA
ACAAGTCCTTCCTGGTTAGCAGTTAGTTTATTAGAGTGGTCAAGTGCATGGAGTGGGGGGCATTTCGGATTTCGGGCTGAAATTTTCCCAATCGATACTGCAAACACGCAAA
ACAATGCCTCTGCTGCCAACTAATATCCATACTCTCGGCTCATTCAGCCACAGAGTTTTCGTTTTAGTAACCGCTGGCATTGTTTTCGACAGGTGAGCGTGTGTATGCACTG
GCATTTTAATTAACCACAATTTGTTTCTGCATTCCAAACGCCCTGAAAACGCTTACCTTCTACTCCTAGCCAAGTTTCTATCTGCAGAATGAGATTCCTTTCGCCACTCACA
CTCACAATTTGCGTTGGAATTCTTGGGATTACTTGCGTTTAGCACTCGGACTACGGACCGCAAAAGCGCCAGGAGGCGGGTCCTTTGTCCTTTCGACCACCTACTTGACCCG
TCCTAAATGCGTTTAACGCCTTCCAAGCTGCGAAATGATTATGTTAAAGCGGTTTTTGCTGGAGCGGTTATTTTTGCTAGTTGCCTTGGTTATTGACACACGCCCATTTACG
TGGGCAAACTTTATTGAGTTCACATTTATATGCGGGATTATTTGTTATAGACGACCCTTGACCTATTCGAAGCACTCAAAGCCAACGACTAGAAAAGTTATTCGACATTAA
TGCGCGGCACTTATTTGTTATTTCTTTTGCGTTTGCTAATTAAAATTTTCATTTTTCTCTTCGCACATTATTTAAAAAATTAGTTTCCACTTTAACGGCTCTGAGGAGGACAA
TAGGTTTTCGCAAGTTTTGAAATTCCGAAACGAACCGCACTCGTACACATCCCGCTGATAACTGCGGGGATACCCGAAGGATGTGTCTTAACAAGGCTCGCCTTCTTACCAA
AAGGCGCCAATTCTGGGTTCCACAAAGTGAAAAGCTCGCAAAGCTGCATTCCACAAGCTGTTGAAAAAGCTTTCCGCCGGGCAACAGGTGGAACATCCTGACGGGAGGTTGG
GTAAAAGGACCCCAAACAGAAACCGATTCGATTGCACTTCTAATGCCTGAAAATCTGCCTATTTGATTTATGCAAATATGTGCCGGAGTCTCATGTTTGCCCAGCAATTCGC
TGGCTGTTTGTTTAGGGCATGCGGCAAAAGGGGATACCCCGGACTCAACAGGATTCGGCAGGATTCGCCAGGATATTGTTTGTGAAACTCCTTGCAGGCCGTCTTTGAAGTCG
CAACCTGATTTAATTGTGATTTTCGGAGCCCGTTCAAAACACCTCTCACGTGGGCCTAATCAAATTAAACTGAAGTGGCAGCGCCTCGGGTCTGACAGTTATTGAAATATCA
TTTTATCACAATGATAAACATTTAGACGGATGTCCTGGCTGCTTGGAATGCGTGCGACACATGAGGGTTGCCTGTGTGGATTTTTGGGCGCGCAAGGATATGGGCGGGGGTGGT
GGGGGCGGATCTCCAACCAAACTGTTTGATTTTTTAAACAAATGCTAATGTCAACTGCCACTCAGAGGCATTTAAATTCCAATTTAAAAATGCTTTCTCTCGATGCCAAAAG
CAAAGACATGTTCGTTGTCCTGTTTCCTGAGTCCATCCACTCGTTCTTTTTCTCTCAGATTCTCCGATTCTCTGACCCGTTTCTCCAGTTTTCTGCTCGCATTAAAGCGTTCGT
CCTGTCTCATGCATATTTAATGTCACACG
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(SEQ ID NO: 100)

FIGURE SHEET 47

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Exon: 7877..7337
Exon: 3829..3532
Exon: 3307..3109
Exon: 2992..2899
Exon: 2753..2579
Exon: 2520..2447
Exon: 2379..2269
Exon: 2040..1852
Exon: 1784..1669
Exon: 1420..1364
Exon: 1300..1093
Exon: 1027..1001
Start ATG: 3796 (Reverse strand: CAT)
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Transcript No. : CT24513
CGGTTCGTTTCGGAATTTCAAAACTTGCGAAAACCTATTGTCCTCCTCAGAGCCGTTAAAGTGGAAACTAATTTTTAAATAATGTGCGAAGAGAAAAATGAAAATTTTAATT
AGCAAACGCAAAAGAAATAACAAATAAGTGCCGCGCATTAATGTCGAATAACTTTTCTAGTCGTTGGCTTTGAGTGCTTCGAATAAGTTCAAGGGTCGCTATAACAAATAAT
CCCGCATATAAATGTGAACTCAATAAAGTTTTGCCCACGTAAATGGGCGTGTGTCAATAACCAAGGCAACTAGCAAAAATAACCGCTCCAGCAAAAACCGCTTTAACATAAT
CATTTCGCAGCTTGGAAGGCGTTAAACGCATTTAGGACGGGTCAAGTAGGTGGTCGAAAGGACAAAGGACCCGCCTCCTGGCGCTTTTGCGGTCCGTAGTCCGAGTGCTAAA
CGCAAGTAATCCCAAGAATTCCAACGCAAATTGTGAGTGTGAGTGGCGAAAGGAATCTCATTCTGCAGATAGAAACTTGGCTAGGAGTAGAAGTACCAGAGATGCCAAGTGC
CAGGATGTTGTAGAATGAGTGACCACAACCACATCGATTCGGTGAACGCCAGCGGGAGTGATCCGCTCCTGGATCTGCACAACCTAGATGGCATCGGTGAGAGCGTGGAGTT
GCAGTGCCTGGTGCAGGAGCACATCGAGGCATCCACCTATGGCAACGATAGTGGCCACTGCCTCACCCAGTTCGACTCGATCCTGTGCTGGCCGAGGACAGCTCGCGGTACC
CTGGCGGTGCTCCAGTGCATGGACGAGTTGCAGGGAATTCATTACGATAGCAGCAAGAATGCAACGAGGTTCTGCCACGCCAATGGAACTTGGGAGAAGTACACCAACTACG
ATGCCTGCGCCCACCTGCCCGCCCCAGAATCCGTGCCGGAGTTCGAGGTCATCGTGGAGCTGCCCCACCATTATCTACTACATTGGATACACCCTCAGCCTGGTATCGCTCTC
GCTGGCGCTGATTGTTTTCGCCTACTTCAAGGAGCTGCGTTGCCTGCGCAACACCATCCACGCCAACTTGTTCTTCACGTACATCATGTCGGCTTTGTTCTGGATACTCTTG
TTATCCGTCCAGATCTCCATCCGAAGTGGAGTGGGCAGCTGCATTGCTCTGATCACCCTGTTCCACTTCTTCACCCTGACCAACTTCTTTTGGATGCTGGTCGAGGGTTTGT
ACCTGTACATGCTGGTGGTTAAGACTTTCTCCGGGGCAATTTACGCTTTAATATCTACGCCTCCATAGGCTGGGGTGGCCCGGCCTTGTTTGTTGTCACCTGGGCTGTGGC
CAAGAGTCTGACGGTCACCTACAGCACCCCCGAAAAGTACGAAATCAACTGCCCCTGGATGCAGGAGACCCATGTGGATTGGATATACCAGGGACCTGTCTGTGCGGTGCTA
ATAATCAATCTCACATTTCTGCTGCGTATCATGTGGGTTCTAATCACAAAGCTGCGCTCGGCCAATACAGTGGAGACTCGTCAGTATAGGAAAGCTGCTAAGGCACTGCTGG
TGCTAATCCCACTTTTTGGCATCACCTACCTGGTGGTGCTGGCTGGTCCCTCGGAATCTGGCCTAATGGGACACATGTTTGCCGTCCTGCGAGCGGTATTACTCAGCACTCA
GGGATTCTCGGTGTCGCTGTTCTACTGTTTCCTCAACTCGGAGGTGCGAAATGCACTGAGACACCACATTTCCACGTGGCGGGACACGCGCACCATTCAGCTTAACCAGAAC
CGACGTTATACCACGAAAAGCTTCTCGAAAGGCGGTGGTTCCCCCCGAGCCGAGAGTATGCGACCTTTGACCAGCTACTATGGGCGTGGCAAGCGGGAATCGTGCGTAAGTT
CGGCCACCACCACCACGCTGGTGGGTCAGCATGCCCCACTTTCACTCCACCGGGGCTCCAACAATGCCCTGCACACGATGCCCACTTTGGCGGCAAATGCCATGAGTTCCGG
CAGCACTCTGAGCGTAATGCCCCGGGCCATTAGTCCCCTGATGAGGCAAGGACTCGAGGAGAACTCGGTGTAG
(SEQ ID NO: 101)
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Start ATG: 575 (Reverse strand: CAT)

MSDHNHIDSVNASGSDPLLDLHNLDGIGESVELQCLVQEHIEASTYGNDSGHCLTQFDSILCWPRTARGTLAVLQCMDELQGIHYDSSKNATRFCHANGTWEKYTNYDACAH
LPAPESVPEFEVIVELPTIIYYIGYTLSLVSLSLALIVFAYFKELRCLRNTIHANLFFTYIMSALFWILLLSVQISIRSGVGSCIALITLFHFFTLTNFFWMLVEGLYLYML
FGITYLVVLAGPSESGLMGHMFAVLRAVLLSTQGFSVSLFYCFLNSEVRNALRHHISTWRDTRTIQLNQNRRYTTKSFSKGGGSPRAESMRPLTSYYGRGKRESCVSSATTT
TLVGQHAPLSLHRGSNNALHTMPTLAANAMSSGSTLSVMPRAISPLMRQGLEENSV*
(SEQ ID NO: 102)
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Name: Diuretic hormone receptor-like
Classification: G_protein_linked_receptor
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Celera Sequence No. : 142000013385198
CATCGATTAACCACTATCCCATTTATTGCCTGCCCGTCTACACAAATCGGCACGTGAACGAGGACTGGTATCGACTTTATAGGACCTACGACACCGAGGGATTTGTTTTCGG
GCAGTTTTACGAGCGTCTCCAGCGGTACGAGTTGGACTGAATTAATGCCCTTTTTCAGAAAGAATAAGATTTAGACAAAATCTGTGATATCGATACTGTGGTAGCGTTGCAG
AGATCCCAATCGCGTGTGTGGCGAAGGACGCAGACAGATAACACATTCCTCCGTGCTGAAAATCAATTATAATTAGTCGTGGGAAACAACTAAAAGAATATAAAAATGGCCC
GTTGGTTTATAAAAAATATAATACTTTAATCTGATCTCTTTATAATGTAAACTATCATGCAATACTTAGGGACGAACGGGATGTGGTCTACATGTATGTCGTACGTATATTT
TTGTGTGGTGGTTGTTCATTCATAGTGTCCAGTGGGTATAGGACTTGTTGATGTCAGTCTACAATAAACGATAAACAGAAAAAGGAAAACCCCAATCAGAAACATAAGAAAATAAG
TAAGAATAAAAAGGATATCTAAAGCCAACCAACCATGCAGAATAAACATAACATTAAGAACTGATGTAGGGAAATGCACGGTTTTAAGTAGATCACTTTAGTTGGCACGAGT
GTGTTAGTATATTTAGAGAACGGGTGCAATTTAACTTTGGAATTATTTGGATGGGTGGATGTCAAAGAAGTAGAAAGCATATACATGAGCATTGCGTATACGCACCGTAGAC
CTACAATATCAGCCATAGGCCATAGCCACATCAACTAGGTAGTGCAAATAGTGAAAAGCCAATATGTCGACAGCCAGGGTTATATAAATATAATCCAACAACAATAATGTGCTAGAATG
CCAAATGAGTGCAGTCGCCCCTCAATGATTGGTTAGCCCACCTGCGATTCTTGATGGAACTGTTCCGATGGATATTCCTGCTCTCCCGCCACCGGGTGAATCCATGCCTCAG
CGTCTGGCGCACCTCTGAGTTAAGGAAACAGTAGAACAGAGCCACAAAGAAGCCCTAAAGAATGGATTTTCGAAGATCAATGTTTATGGAAAGACTGTCACCTAATCTATAT
ACCTGCGTGCTTATGAGAAAGGCTCTTATGGCCTCGAAGAGATTACGACTGATACCCTGTTCCGGGCCTGTTAGCACCAACAGATAGGTGATGCCAAAGAGAGGTATCAGCA
CCAGCAGCGCCTTCGAGGCCTTGTAATACTGCCGCGTTTCCAGGGTATGAGCAGAACGTAATTTAGTGATGAGTACCTGTACGATATGATATAATAGCATGAAGCTAACTCA
CTTAAGCCAGAAGTTAACCGGGGGACTCACCCACATGATGCGTATGAGGAATACTAGATTAACCAGCAAAGCCAGTGATGCAGGTACCTTGAATATCCAGTCAATGTGAGAT
TCACGCATCCATGCACAATCAATTTCCAGCTTTTGAAAAATCAGAAGAGGTTAGCAAGCATATCTAGGTAGGTGGCAATTGGTATCATACCCCATTGAAGTGCTCGTTCTCG
GCACCACCAGCGTGTACAGATAGAGGCCTATAAAAAGCAATGATAAAACCGAGGAAATTCAATTGATACCGCCTTTGAACCCACCCTCCACAAACATCCAGAAAAAGTTGG
TTAGGTAAAAGTACTGAAACATGATTACCAACGTTATGCAGCCAGCCTGACTAGACTCTGTGGTTATCTAAGTGAATAATTAATTAGTGGAGTGGGATATATATATTCCAGC
TTATCTTACCACTTGCAGGAACAGTGTGAGTATCCAGAGGAGTGCGGATGTGATGTAGGTGAGGAACAAATTGGCATGAATGGTGTTTCGCAGGCAACGAAGATCTCTGAAG
AGTTTTAAGCATGAAAATGATGCAACTCATGTGTGGCATTACAACTCACTTAAAGCTGAGGAATATGATGAGAGCCACCACCAAGGTGGCGAAGCTCAGGAAATAACCGCCG
GCATATATGATGGCCGGCAGTTCGACGTTGGGTGAGAGTCGGGCACCACCGGATGATGGCCACCGGTTCTGGTGACAGCGGTCATAGTCCGAATAGTGATCCCACGTTCCGT
TTGGAAAGCAAAAGCGGGTGGCATTGTCTGCAAATATATTGATTTTATTTAAGATCTAAACCCAATCTGGAATACCCACCTGTGGTGTCGTAGTGCACGCCCTTGAATTCCT
CGAAACAGGGTAGTACAGCCAGACTGCCGGCGTTTGTGCGTGGCCAGCACAGGACCGAATCGAACGAGCTGGGACATTGTAAAATCGTAAGAAATAACAATTGAGAATATA
CAATGATTGGCAAGGTAAACTTCGTTGAGCATTTACTGCAGTATAATTCGTGTTTCCCCTCTGTAAACGCAACTGACCTAGCCCAAAACCCATTAAATCAGAGTACATAAGA
ACACACACATACGCAGCGTGAGCCAAATATCGATGTAGTCCCAAAAAAAAAATAAAGAAAGAATCACCCAGCTACCGCTTTATTTATATATTTGCAATGGCGTGCTAAACAAT
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FIGURE SHEET 48

TTCGTGCATACGGATACACAAGTTATATGTACATATATGTATATTAACGTTAAGTATACGACGACCCGGCGATTGTTTACCCAGTTCAGTTCGTAGCGCCAAATTAATCGCG
ACGCGCTATGGTAGCGGTGTTAGAAACAGAGCTTCATTGATATTTTTTTTATTGACCTTATCAGGTGACGCCGAGAGCGCGGAGCGGAGACTCGTCGAAGAATTCACCAAAT
TGGCAATTCTTTTATGGCCGGTCTTCCCATTACTGATAAGCCCGAGAACCTTTTTGCGACAGCTAATGCGATCGGACTTAGCCACGCGACAAGTGAGCTGTCAACGAGTAAG
CCAAACACTGGAGACTGGAAACTCCGGCAATATTTGTTTCTTTGCTCTTCTGATTTTCACTCATTAGCCTCGTCATTTGGACACAGTCATAGTACGAATACATTTTATGACA
TTTTCGAGGAACAACGCCCTTGATCGTGCATTCGGTATAAACAAAAATGGCTAAATGCAGCCTCAAGTGGATTTCCTTGGGTCTAGTTTTGTTTACAGGCGAGAGGAATACA
TAAATAAATATGTGCTGCATTTTCCGGAAATAAAATGCCAAAATAATTTAATCCGAAAGCGATCGACAGTTTACTTGCCTGGTTTTTCATCGTATCGTACTTAAAGTGAAAG
AGATTGACGGGCGGATGGATTGAAGCCAATTATTTCGGAACAGAAGATGGATCAATTAGCGGGTGCGATTAATTGGGAAATTCCTCAATCGGCAAAAGAGATGAATTCATTG
GCCAAACAAAGGGTAATTAGGGAATATTTATTGGC
(SEQ ID NO: 103)

Exon: 2731..2708
Exon: 2549..2432
Exon: 2379..2178
Exon: 2122..2026
Exon: 1971..1878
Exon: 1819..1659
Exon: 1597..1487
Exon: 1420..1235
Exon: 1174..1001
Start ATG: 2731 (Reverse strand: CAT)

Transcript No. : CT24959
ATGAAGGCATCATTATTATACCGAATTTTACAATGTCCCAGCTCGTTCGATTCGGTCCTGTGCTGGCCACGCACAAACGCCGGCAGTCTGGCTGTACTACCCTGTTTCGAGG
AATTCAAGGGCGTGCACTACGACACCACAGACAATGCCACCCGCTTTTGCTTTCAAACGGAACGTGGGATCACTATTCGGACTATGACCGCTGTCACCAGAACTCGGGCTC
CATACCGGTGGTGCCCGACTTCTCACCCAACGTCGAACTGCCGGCCATCATATATGCCGGCGGTTATTTCCTGAGCTTCGCCACCTTGGTGGTGGCTCTCATCATATTCCTC
AGCTTTAAAGATCTTCGTTGCCTGCGAAACACCATTCATGCCAATTTGTTCCTCACCTACATCACATCCGCACTCCTCTGGATACTCACACTGTTCCTGCAAGTGATAACCA
CAGAGTCTAGTCAGGCTGGCTGCATAACGTTGGTAATCATGTTTCAGTACTTTTACCTAACCAACTTTTTCTGGATGTTTGTGGAGGGCCTCTATCTGTACACGCTGGTGGT
GCAAACATTCTCCAGTGATAACATTAGCTTTATTATCTACGCCCTCATCGGCTGGGGCTGTCCAGCCGTATGCATTTTGGTGTGGTCCATTGCCAAGGCATTTGCTCCGCAT
CTCGAGAACGAGCACTTCAATGGGCTGGAAATTGATTGTGCATGGATGCGTGAATCTCACATTGACTGGATATTCAAGGTACCTGCATCACTGGCTTTGCTGGTTAATCTAG
TATTCCTCATACGCATCATGTGGGTACTCATCACTAAATTACGTTCTGCTCATACCCTGGAAACGCGGCAGTATTACAAGGCCTCGAAGGCGCTGCTGGTGCTGATACCTCT
CTTTGGCATCACCTATCTGTTGGTGCTAACAGGCCCGGAACAGGGTATCAGTCGTAATCTCTTCGAGGCCATAAGAGCCTTTCTCATAAGCACGCAGGGCTTCTTTGTGGCT
CTGTTCTACTGTTTCCTTAACTCAGAGGTGCGCCAGACGCTGAGGCATGGATTCACCCGGTGGCGGGAGAGCAGGAATATCCATCGGAACAGTTCCATCAAGAATCGCAGGT
GGGCTAACCAATCATTGAGGGGCGACTGCACTCATTTGGCATTCTAG
(SEQ ID NO: 104)

Start ATG: 1 (Reverse strand: CAT)

MKASLLYRILQCPSSFDSVLCWPRTNAGSLAVLPCFEEFKGVHYDTTDNATRFCFPNGTWDHYSDYDRCHQNSGSIPVVPDFSPNVELPAIIYAGGYFLSFATLVVALIIFL
SFKDLRCLRNTIHANLFLTYITSALLWILTLFLQVITTESSQAGCITLVIMFQYFYLTNFFWMFVEGLYLYTLVVQTFSSDNISFIIYALIGWGCPAVCILVWSIAKAFAPH
LENEHFNGLEIDCAWMRESHIDWIFKVPASLALLVNLVFLIRIMWVLITKLRSAHTLETRQYYKASKALLVLIPLFGITYLLVLTGPEQGISRNLFEAIRAFLISTQGFFVA
LFYCFLNSEVRQTLRHGFTRWRESRNIHRNSSIKNRRWANQSLRGDCTHLAF*
(SEQ ID NO: 105)

Name: Diuretic hormone receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013385192
TTTCCGCTGCCATCTGCAGCTGTAGCTGCCTAACAAATGCAATTAAAATCTTTGCGCAAGAAAATTGTTGCAGCAGGCACGCAGAGATACTCGTACTGTATGTGCTGCAATA
GTTTGGTGGCAGCAACGGGGCGGCAGATAACATATTGCCCACGTCCGGCTGAAATTGTACGGACAAGGCGAACTCAAAAAAAAAAAAAAAAAAAAAGGAATCCCTCAAAAGGA
GAACCAAGAAAAATGGGATTTATCTCTGGCCAAGCTCCAGCCATACAAATCTAATTTAGACCACACGACGGCTTCAGATATTTTATATTCCCCACTCAGTTGCGGTCCATCC
TGATCTCCTCCAGCTTGCTTGATGAGCCCAGCCGTTGGCCAAATGAAATTATTTATGGGCAGTCCTAGGTCAGTGAGAATTTGGTTTTTTAAGGGTTTGAACTTTGCGGCTC
AACAATGCCTGTGATTTTTTTTTTTTTTTATTATTTTTTTGCATTGCATCCATTAGAGAAAGCACTCCTTTGGCATTCTACTCAGCTACTTGCCACATAAATATCTACGGAGG
GTAGCTAACTAGTCCTTATCTCAACTTCCCCATTTATCCTCGCCGCAAGTGCACTTTTCCTGCTGCTAATTAAGTTGCAAGGCAGCTTTCTCAGCAGGCGTTGCACGAAGTA
GATAAAAGGAAAAGCCCCCGATTTGCAGACACTATGCTGGGAAAGATATATATATATATATATATATTTGCCAGCATTGCTAATCGGCTTAGGGCAGCCACCATGCGACCACAA
CAACAACAACAACAGCAGCAGCAGTGTGCTCCATGCAATATTTAATCACATTAGTTGATGGGGTAACGGCCATGTACGCAACAATTTACAACTTGCATTAATTATACGTCTA
GTTGGACAATGGCGCCTCTAACTATCCCACTCTAAATGTATCTCTATCTCTATCCTTATTTGCAGGGGACACCCGTTGATAATAAATTATTAATGCATCTGCTGGGAAGGCG
GCACTGCACGGCTGTCCTTGGCAGCAAATCCAGTTGCAACATCGGTGAGTGACGGGCGGCAATCACAAAGGACTTGCAACAGTTGCCGTTGCTTCTGCTATTGCTGTTGCTG
GGCCAAGGGGCTTTTCCACCAGACATGGCGACAACAATACCATAAGCCAACAGTTGGGGGCGTGGTCGGGGGCGGAGGCGATGGTGGCAACATCATAGCCATTAGCTGCTGG
CGCAAGGGAACCGTTCAAAAATCGATTATCGCCCATTTCGGGGGAGCTTCTATTTTGATTTGCCGTACAATTTTCTCGGGCGATTAAACGACGAAGCAGAACGAAAACAAA
AAACAGATTTGTCAACAGCAAGGTCAACAATTGATGGCTGAAATCAATTTAATTGACCATATCCTACGGGCCCTCCAAGTGGCCATCTGCTGCACCTATAAAAAAGTGAATC
TAATTTAAGCCGAGTCACCATTCTTCGAAGTTCTTACATGTAAGCGATAATAAATAGTTAAGTCAATTGGCCAATAAACCTATTAATATTGTGCATTTACCACGATTAGACT
TTGATTAAAGTGACAATGCTGATTTCTGTAGAGGAAATCTAGTTCTAGTCTTCCCACAAAGCTATTTAGTTACTCTTGAATAAATATGTTACTTTTCTTTTGCCAAAACCAA
CAGAATTTTAAATTTAATAATTTGGATTTTTTGCAATAAACTGTACTGATTAATGGGCCACACAAAAATGTCTAGTTTATTATGGAGCTCTTGGTTTCATAAATTAAGAACA
TAATCCAATCGGCATATAAATCATTGATAGCAATTTATTTTCCGTGATGAAACTGTGCTCCGTGTGAACTGCGAATTACTCATTCTACGGTTGCAAAAAAAGCCACCAACGG
TCAACATTTAGACCAGGACTTTTAGTTTTAATTAGAGCCAGCCTGGCCAACAGCAGTGTTAATGACCACAAAGTGGCTGGCCACAGGATCAGCATCCCAGAATGCGATGCCG
CATTTGCTTTAATTAAAGGTAGTAGCTGGAGTTTGAAAGATGACTGTATGGCAATTAGATGTGTAGCCAGAACACTTGGCCATTTACTTTTGTGTCAAAGTCGTGCCAAATT
GCCAGCGGAGGCGACACTTGACGCTGTCACGCCCCAGACAGACGCAGACCGGCCCAAAAGCACCCACTCAGCCGTCTCCAGGCGCCACTCAAGCGGCAAAGGAACGCCAAA
CACTAGGACACAGAACGCCAGAAGACTCGAAAAAAAAGTATAAAATTCAAACGCGTATACAATTCAATGTGTCACATCGAAGAAGAACCCTTTCTCTGGCGGCAACGTGACG
TATACGCAATATTAATGGCAAAGCAAAAGGGCCTCAAGGCCTAACGAAAAACCGCAGCATAACACGCACAAAACAGGCAATTAACATAAATAATAAAGAACGCACAAAGGC
GTTCGGCTCTCCGTTGCCAAAGAGAAAAAGCCAACGAAAGGAATAAAAAAACGCCAAAAAGCCCGAAAAAAAAACCGAAGACCCAAAAAATGTGTAAAATTGATTTCGGAAAT
ATTTAATTTACCAAATGCATGCTCGCTTTTTGCGGCCGTGTACGCCCCGAACAAATAAAACAAATAGGCACACATCGTCTGGCATTTCATGTTAAAGGCTTCTCATGCTGAT
GGACAGGATACAGAAAATATATATACGAAGTGAGGTGTGTGTCTACGTGCCACAAAAACAGCGAAATTGAAACGCTTTCCGAATGCCGGCGACACTTTTTGGCGGCACAACC
CTCGTCTTGTCGACCAACTCCTGGGGAATTTACAACTCCATTCATCAAACTCACAAAAACTTTGCCTGGTGTACGGTCTTGGGTTCGTCGTCGCAGGATTTCACCTGGCTAA

FIGURE SHEET 49

50/89

AAATCCAGACTCCCAGCCATCCCTGAGTCTAATTTATGGCCTTTGATAATCCATGTTGATGAATGGCGGCAACGACAACAACGTCGACGACATGAATGAAGTCCTGGAATTG
TTTTGCACCAGGATGGCATCGGGGCTCCAGGTGGGACGTACTGGCTCAAAGTTATTGGCCCAGAAATCAGGCATAGTTAGCTGCCGAAATGAAACCCAAATACCGAGAAAAC
TAGCCAAAACAAACAGTAGTACACCGGAAATGCATATCATTGTAAAAACTACATCAGTTTACCTAAAAGGCTTGGCTTTTAAGCTTTCACATTTATAAAATATTGAAAATGC
TATAAGTTCAGAATCGAGAGTTTTATGCCAAGTTGGGCACAGTTTTTTTTTTCCCCAGCTACCTAAAATAATAGAGACATTTTCCTCCCACTACAACTGATTGCATTGCCGG
TGCAGAAAGTTTTTTCAGTTGGTTCGGAAAAATTTGGTTCGCAAACAAATTAATATGAACTGGCAAGCATTTTTCGGGCAAAAAGCTCTCATCTATGTAGATTGGAATGGAA
ATTCCGGCTAGAATTGCATAAGACCACCTGCAGTGTGGGCTAACATGACTAAAAAGTTGTCCACAAATTTGGCTTAGATTCTCCAATAAAACTGTCGTTCGGCCAGGAATCC
GGAGAGCTTGGAGTATATTAAACATTTTTTCCCCACCAGTCAGCCGCAGGACTTGCATCGGTCTCGCCTCGCATTTTCCTATATAAATTTTATGCTAAGTCTAATTTGTTGG
CTGCAACTTGCACAAAGGCAAAAAATAAACAAGGGCGAAATGCCGAAAGCCAAAACCCAACCGAAACCGTTGAGGGCTGCCTCGCTTTTTTCCTGTGCCGAATTCCCTAAAA
CTTTGCACATAAATTTGAGTCCTGCGCCTGGGCTTTTCCTCTTCCACCTTTTTTTTTTAGCCTCAAAGCGCTCGACGAAAACTAAACAAAAGCTGGTAAAATGTTTATCCCAG
TTTATTGCCTACTTTTGCTGCGAGAAAGCGGACTAGACATGGAAGTAACAAATTGGTTAAGGCTAACTAGAGCATAATAACGAAACATCAGAAACATAATTTGGGAAATGC
CTGCCACTCACCGACAACATTTCGATTTGTGTCTTTATTACACTTCTCTGCCGTGATGGGTTATAACTTTTGGATCCTTGCAGAGAGTTGGGAAATTGCTTAAAAATAAAAT
TTGTTTAATTTAATTTGAGGTGGTTTTTTCAAACAATTTTAATGGATTAATAAGTTTAGGAAGTTAAGTATATACATCTATCTATTATACCATCTTCAAATATTGTTGAATTG
AAGAGATAACTCGGAGCTAATCCCATATTTTTCATTTTTTTCAGCTACAAGAACATGCATGGCTATGTTTCGCTGGTGGTCTGCATCCTGGGCACCATCGCGAATACCTTGA
ATATCATTGTGTGCTAACCCGACGGGAGATGCGCTCCCCCACGAATGCCATACTCACGGGTCTGGCCGTGGCCGACCTGGCAGTTATGCTGGAGTATATACCCTACACCATACA
CGACTACATCCTGACGGACAGTTTGCCGCGGGAGGAGAAGCTCAGCTACAGCTGGGCCTGCTTCATCAAGTTCCATTCGATTTTCGCCCAGGTTCTGCACACCATTTCCATT
TGGCTGACGGTGACCCTGGCTGTTTGGCGTTATATAGCGGTGGGTTATCCGCAAAAGAATCGCGTATGGTGCGGTATGAGAACCACCATAATAACGATAACCACCGCTTATG
TGGTGTGTGTTCTGGTGGTGTCGCCGTCGCTCTATTTGATCACGGCTATAACCGAATATGTCGATCAGTTGGATATGAATGGCAAAGTGATAAACTCCATTCCCATGACCCA
GTACGTAATCGATTATCGTAATGAGTTACTGAGTGCCAGGACGGCTGCCCTGAATGCCACGCCCACCAGTGCACCACTGAACGAAACTGTGTGGTTAAATGCGAGCACCTTG
CTGACATCGACAACCACCGCTGCACCACCCACGCCATCGCCAGTGGTGCGAAATGTTACTGTCTATAGGCTATACCACAGCGATTTGGCGTTGCACAATGCCTCGCTGCAAA
ATGCCACATTTCTCATATACAGTGTAGTGATTAAGCTGATACCATGCATAGCACTCACCATTCTGTCGGTTCGATTGATCCTGGCCTTACTGGAGGCCAAGCGGCGGCGGAA
GAAGCTCACCAGCAAGCCCGCCACTCCGGGTGCCAGTAATGGAACCAAATCACCGGCCAATGGTAAAGCAGCGGATAGGCCCCGGAAAAATAGCAAAACTCTGGAAAAGGAA
AAGCAGACGGATCGCACCACGACGATCGTGCTGGCGGTGCTACTCCTCTTTCTCATCACTGAATTTCCACAAGGGATTATGGGTCTGCTGAATGCTGTGCTCGGAGATGTCT
TCTATCTGCAGTGCTACCTAAGACTGAGTAAGTAAATATGTACTATGCATAACGCCACAGTAAATTCCACAGATTCCCATTTCACTTTAAGATGTAATAACCCAATGCCTTT
TGCCTTTTGCCACCAGGTGACCTGATGGATATCTTGGCCCTGATCAACTCCAGCATCAACTTCATTTTGTACTGCTCCATGAGCAAGCAATTCCGCACCACGTTCACGCTGC
TCTTTCGTCCAAAATTCCTGGACAAGTGGCTGCCGGTGGCGCAGGACGAAATGGCAGCTGCTCGAGCTGAACGCTCTGCGGTGGCACCGGTCCTGGAAAAGGGACGACAGCA
AAACGCGGCAGAAGGCGCTCCTCCGGCGAAGGAGGAGGCGTGGGAGGAGGTGGTGCGCCGTTGGCCGGCAACGATGCGGTGGAACCAGCGTTCCAGGCCATCGTGGTGGTGG
TGGACAAGGTGAGCGGTGCCACGGAGAATCAGCTGTACACCGCCGAGCAAGCTCGTATTGTGACGTAGTAACCCTGATAGTAGTACATATTATATGCCTAGTTATCCTTGTA
AAAAGTAAACTAGTTGTGTAAGAATCGCAGATAACCACAAGTTATGTGCATACTTTGGTGGGAAATCGTAAAACCCGTACAGTCATAATAATAAAATGCTGGTTCATCACTC
ATACGCACCGTTTGACTTCACTCTATTCCACATTCACAGTCAAGTAGGAGCTGTAAAAATGCTGTGCATAAACGAGCTCGTATACGCTACAGCTGGCGTCACAATAATAGTT
ACCATTGGGTTGGCTTCACAACATAGATCAAAGTCAAAAAATATATAGTTTTGTAAAATGTTTCATAAATCTATCTTCATATTTAACTAACACAATTCAGAAACTTTCGCTT
GCATGGAAAATGTTTTATTTTCCCCACTTGACCCAATTGTGCGCAACTGTTCAGCTTTTCGGCATGAATCAAATCAAATATAGTAAACTTTTGCATCTTTTCCACTTTGATC
CCATGCGTTTTCATGTTGATTTCATTCGCATAAAGTATGCAGCACACGTACTCACTCAAAACTACGAATTTTCGGCAACGATTTGAGCAGAATATTTGCCATTTGTTGTACA
GATTATATATACACACACACACTTATGTCCGTATCTTTAATAATGGCAATTAAGTCCTAGAAATTTTGACCTGATATTGATGCAGGCATTGGAAAAATAAGTGGCAGTTG
CAGTGCGGTGCGTTGATAAATGAAATACTTTGCGAATTCTATTATTGGAAATCGCAATTTGGGCTGTGAATGAAATTATAGTTTTCTTGAACGCAATTGAGAATTCAGTTCC
GTTTCGTGGGTTACTGAATTTATGGGAAATAATTTAAGGCAGTCACTGCAGCTGACCGAATAATCCAATGAAACATTGCATAAACAGTTTGCAGTTTTTCCACACTTGCGAA
AATTGTAATTGCAAATCGCTTAAGCCCCCACGACGAATGACAAATGGCCAGCGAACGCATA
(SEQ ID NO: 106)

Exon: 1001..1202
Exon: 4861..5963
Exon: 6065..6282
Exon: 6331..6564
Start ATG: 1135

Transcript No. : CT25824

GGAAGGCGGCACTGCACGGCTGTCCTTGGCAGCAAATCCAGTTGCAACATCGGTCAGTGACGGGCGGCAATCACAAAGGACTTGCAACAGTTGCCGTTGCTTCTGCTATTGC
TGTTGCTGTTGCTGTTGCAACAATGGCCAGTGGCAACAATGAAACTGAGCCGCTCTACTGCGGCAGCGGCATGGATAATTTTCATCAAGCTACAAGAACATGCATGGCTAT
GTTTCGCTGGTGGTCTGCATCCTGGGCACCATCGCGAATACCTTGAATATCATTGTGCTAACCCGACGGGAGATGCGCTCCCCCACGAATGCCATACTCACGGGTCTGGCCG
TGGCCGACCTGGCAGTTATGCTGGAGTATATACCCTACACCATACACGACTACATCCTGACGGACAGTTTGCCGCGGGAGGAGAAGCTCAGCTACAGCTGGGCCTGCTTCAT
CAAGTTCCATTCGATTTTCGCCCAGGTTCTGCACACCATTTCCATTTGGCTGACGGTGACCCTGGCTGTTTGGCGTTATATAGCGGTGGGTTATCCGCAAAAGAATCGCGTA
TGGTGCGGTATGAGAACCACCATAATAACGATAACCACCGCTTATGTGGTGTGTGTTCTGGTGGTGTCGCCGTCGCTCTATTTGATCACGGCTATAACCGAATATGTCGATC
AGTTGGATATGAATGGCAAAGTGATAAACTCCATTCCCATGACCCAGTACGTAATCGATTATCGTAATGAGTTACTGAGTGCCAGGACGGCTGCCCTGAATGCCACGCCCAC
CAGTGCACCACTGAACGAAACTGTGTGGTTAAATGCGAGCACCTTGCTGACATCCACAACCACCGCTGCACCACCCACGCCATCGCCAGTGGTGCGAAATGTTACTGTCTAT
AGGCTATACCACAGCGATTTGGCGTTGCACAATGCCTCGCTGCAAATGCCACATTTCTCATATACAGTGTAGTGATTAAGCTGATACCATGCATAGCACTCACCATTCTGT
CGGTTCGATTGATCCTGGCCTTACTGGAGGCCAAGCGGCGGCGGAAGAAGCTCACCAGCAAGCCCGCCACTCCGGGTGCCAGTAATGGAACCAAATCACCGGCCAATGGTAA
AGCAGCGGATAGGCCCCGGAAAAATAGCAAAACTCTGGAAAAGGAAAAGCAGACGGATCGCACCACGAGAATGCTGCTGGCGGTGCTACTCCTCTTTCTCATCACTGAATTT
CCACAAGGGATTATGGGTCTGCTGAATGCTGTGCTCGGAGATGTCTTCTATCTGCAGTGCTACCTAAGACTGAGTGACCTGATGGATATCTTGGCCCTGATCAACTCCAGCA
TCAACTTCATTTTGTACTGCTCCATGAGCAAGCAATTCCGCACCACGTTCACGCTGCTCTTTCGTCCAAAATTCCTGGACAAGTGGCTGCCGGTGGCGCAGGACGAAATGGC
AGCTGCTCGAGCTGAACGCTCTGCGGTGGCACCGGTCCTGGAAAAGGGACGACAGCAAAACGCGGCAGAAGGCGCTCCTCCGGCGAAGGAGGAGGCGTGGGAGGAGGTGGTG
CGCCGTTGGCCGGCAACGATGCGGTGGAACCAGCGTTCCAGGCCATCG
TGGTGGTGGTGGACAAGGTGAGCGGTGCCACGGAGAATCAGCTGTACACCGCCGAGCAAGCTCGTATTGTGACGTAG
(SEQ ID NO: 107)

Start ATG: 135

MASGNNETEPLYCGSGMDNFHTSYKNMHGYVSLVVCILGTIANTLNIIVLTRREMRSPTNAILTGLAVADLAVMLEYIPYTIHDYILTDSLPREEKLSYSWACFIKFHSIFA
QVLHTISIWLTVTLAVWRYIAVGYPQKNRVWCGMRTTIITITTAYVVCVLVVSPSLYLITAITEYVDQLDMNGKVINSIPMTQYVIDYRNELLSARTAALNATPTSAPLNET
VWLNASTLLTSTTTAAPPTPSPVVRNVTVYRLYHSDLALHNASLQNATFLIYSVVIKLIPCIALTILSVRLILALLEAKRRRKKLTSKPATPGASNGTKSPANGKAADRPRK
NSKTLEKEKQTDRTTRMLLAVLLLFLITEFPQGIMGLLNAVLGDVFYLQCYLRLSDLMDILALINSSINFILYCSMSKQFRTTFTLLFRPKFLDKWLPVAQDEMAAARAERS
AVAPVLEKGRQQPQVHRRSRGRRTLLSRLLSVLKRGRRRSSGEGGGVGGGGAPLAGNDAVEPAFQAIVVVVDKVSGATENQLYTAEQARIVT*
(SEQ ID NO: 108)

FIGURE SHEET 50

Name: G-protein coupled receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384565
TAACCTTCTTTTGACCTTCGTAAGTCTTCCACTGGCACTTGAAAAGCTTTGGGAAAACAGCTGTGAATTTGCCCAGCAGAGCTTCCGAAACGACGGCTTTTAGTACCTCCGC
CGTAACACCACCCACAGTGGGTCGGTTCTGGTCCATGGTGGGGATGGTGTGGTGGTTCCGATGATACGGGAATCGCTGGAGAAGCGTTACTGATGCAATGCACTGGATACCG
TTCCTGTTCAGATCATTGAGTACTCCAGGCGGCATTTCTATTGTGGTTACAATAGTAAGTAAGGAGTAGTAAAAGTTATTCTGAAATTATATAAACGGCTTGTTGGGGTTTT
AAAAATGTTGCCGGTTTTAGATTTAGCAGTGACTCCAACCATCTGATGGGGAACTTTGAGCAAGTGAGCTCCAATAGTTTTGGCGTCGCTTCCAAAAAGCTCTGGAAAAGCT
TTTATCAACAGGCTTGCCAAAATCCGCTATACTAGCATATGTAAAAGAAAAACTTGTATACCCTACCAATAGGCATACATCGCATCAGGACTTATTTAACCAACAAAAATAA
AACACAACATGAATGTACATTCTGGTTTAATCGCTTTATTTAACTTCAACTTTGAAATTCATGTCGCATGGCTTAACTTGGTTTTCACAGACGTTCAGGTATACATAAGCTG
ACATATACACAGTAAATACTCTAACAACATTAAACATATGTATGTACATAATTAACTAGTCCGTAGAAACGTATTATGACCATACACTCAAAATAAATGCGCATAGCTCCTA
ATCTCTATATTTCACTACCGAACTAATTGATTTAGTATCCGATATAGAATTTGACAACGTTTCCGAAAGAGAGCCTAAGAGAGCTGGAAAGTACTTAACGTAAAAGCTTTGAC
TTGCGAGTATTTCCTCAGGGGTCACCCCTTACCCCTTTCGGCATCCTTGTGATCCTCTTCCAGTGGACTTTCCTGCTGATCCCGCTTCTTTTCCGACCGCGAAGGTCAACTCT
CCGCGCTGGTCGCCAGAAGGGACGGCGAGGAGGTGGTCGACCCACTGGAACCGATTCCTCCTGAGCGTCGGCCCATGGGCGGTGGTGATGGAGTGGGGCGTGGAGGCCGTGGA
GGATGGTTGGCTGGCTGCGGATGCTGTGGAAGTACAGAGGACTCCTGATCCCTGCAGAGATTACTGCTGGGCTCGTCGTCGGAGACCCCTCGTCCCTTAGCGATGGAGCTACAGT
TGCAGGATCGGCTCTTCTTCAGCGAACTCCGAGTGAATGCCGTGCCCTTTCGATACTTAGGCTTGTGCCCATTTGAGCCGGGACTCGCCTCACTATCGATCACAAAGATACC
GGATTGCTCCTGGGGAGCAGGACTCGCCGTGGATCCTGGCAGGCAGTGAGCGCTATTGGAGTTGCCAGCAAGCAGTTTGGCCCTCAGAAGAGCCGGAAGTGGGCCATTTGTG
GGAGATGTTTGAGTGGAGAGCGGTCTCTCCCTGGACTGTTCATCTATGGGAAGATCCTGATTGTTGCCCATTGGCCTGGAGTCCGTGTCATCCGATCGCAATTTCTCCCTCA
TTCGTCCTCATCCTGGCTGAAACTGTAGTTGTGGTTGTCATAGGAGGCGGACGGAACTGAGGGCTTCGCAGGAGCAGGAGGAGCTGGTGGGACTGTGGAACTGCTATTTCGT
TCACTGCTGCGCTGGGAACCCGGAGCGGGGGAAGGGAACTCGTAGCTGGTTTCACCCAGCTCGGCGCCACTGGAGGCCTCCACTATGTTCCACATTTCTCGCTCGAGATCTG
TGGTCACCGAAGCCACGGCGGCCACCGTTTGGTTGATGTTGTTGAAACAGGGCGACACCACTCCGCACTTGGGCAGGAGCTGGGAGTTCTTCAGGGCCTCCTGCTGCTGCCT
CAACCAAATGGGTGAATCTGCAGGGAATGTTACGAGAGTTATAGGGATTTTGCCCACAGTTCCAAGGAGACAACGCGCACTCACACTCACCCACATAGAGGCGCGGCTGCGTG
GAGCGCATATTGGAGTCCATGGACTGCAGGCGATGCTGACTGGCCACCGAGAAGCGGTGATTGCCTCCGCCTGCTGATCAATGTCCACGCCCATCATCTTCAGGAGTAAGT
TCTTCAGCGCGGCCCTGAAGTCCTTGAGGTGATAGGCATACAGGACCGGATTTACCGCCGAGTTCAGATGGGACAGAATGATGCAGAAGAGCGTCAGCTTGGGATGCACATA
GCAGTCGGGACAGAAGGCCTTGATGCAGTTGATCGTATAGAGCGGTATCCAGCAGATCATAAAGAACAGCACGATAATGGACAGATTCTGGGTGGCCTTGACGTCCCGCTTC
CTTGCCGGCGCCCAAGACCCGCAGCATGGTTCCCGTGTGTCCACCTCTTCCGGGTGTCGTCACCTGCACCACGGCCGCCGAGGAGCGACGACTGAGATCGGAGGCGGGGTTCA
TCGTAACAATCTGACGGACCTTTAAAGTTCAATTGAAAACGGATAGTTAATATTCCAAACTCTATGGAATATATAAAAAACTTTACTGGCGAAAATCTATCTACCACTCACC
TGTTTGATGATGACCCGGTAGATGTGCGTGTAGAAGGCCAGCATCAGCAGAGCCGGAGTGATAATGGTGGCAAAATAGAGGAAGACGAGGTAGTTGTAGTCCATCACCTCCA
CGAAGAGACACTCCTGGTTGTGATTGACATCGGCGTGCCAGCCGAAAAGCGGCAGGAAGCCCACTATCGTCCCGGCCACCCAGCACATGGAGATGATGACTGCAACGGAAGA
GGAACATTGGTAATCAGAGTGCCCTGAACTGAAGCCCTTGAAGTGGAGCTCCCCCAGACGTCATTTGAGCAGATTGCAGGAATCCCTGCCGTCTTCGCCACCAAGCACCATA
AAAACTTTTATCGAATTGCGGGAAACTAAACAAAACTGGCAGGCAGGGTGAGTGCACTTCCCAAATGACGCAAATAATTACCAATTTTCCGGACGTAGCATATTGGAAAGTA
ATCTTGCCTTGAGCGGCCATTTATAAAGCACTATATAGTAGGTGATATATAGTAGTCTTAGAAAATTATATATTTATGAGATATTTTTTAGCTAGAGGCCAATTATTCTGATTCC
AAACAGTTGCTATAAACATCTAATATGAAAATTCTTAGAATCAATTTGAATCTAGTTAGGCTAGTAAGACTATTATGTTACGGATTTTAAGGATGTTTATTACTGTGTACTG
CATCCAGAGTCATTAGTATCACGGCAACAAAGGCACAATACTAAACAATGGACAACTTAAAGTCGAAATAGTTTGACAAGTAGGTGAAACCAGAAAACTG
GTCCTTTAAAGTGGGTTTTAGCATACCATTTTGTACCTACTGATTTTATACAATACATTGTATATACCCCCATATATACTTACATATCGCCGTGCGGGTGCGGACATTCCTT
GAGTAGGCCATCGGATATAGGATGGCCCAGTATCGATCCACGGACACGGCCACCAGACAGAAGATGGAGATGGTACACAGCACCACGAGCAGGGAGACTGTGAAGAGGCAGG
CATGAAGGTTTCTGGGTAGTCCCATGGAGGCCAGGATGGCGAAGGGAATACCCAATGCGCCCACTAGCAAATCGGCCATGGCCAGGGATACTATGTAGTAGTTGGTGCGGCG
TCGCAACTTTCTTTCCCGGCGGAAGACGATGATCACCAGCACGTTGCCGATGATGCTGACGATGGCCACCAGGACCTCGAAGACGGTGTAGGGTATGTTCAGCTCGGAACTG
GGGCTGTCCGAGTCCTTGGCATCCTTGCTCGTGGTGGCCGTGCAGCGGTAGCAGAGGTCCCTCGAAGGAGAAATCGGTGATCGAGAAGTAGCGAAACGCGGACATGGTGG
GCGGTGTTGCGGGTATTTTACGGGTTCCACGGGGTTCCCTGCCCCGATCGAGTATTTAAGGCTAGTGCCGAGCTAATGAAAGGGCGGAACAGGTGTGGGCTTCAATTACAGT
GCCCGCTGGCCTGTGAACTCCCTAATTGACTTGAGGTGGCCGTGGCAGTAGCAGCGATAGTAATAGCACATGCTGCGCATTGCGTATACGCCATGCCCGCCGCGCTGCGGTT
AAAAAAAGGGAAAACTTAATCATCGTTCGGCACGTTTGTTACACACATGCAGCAACTTAATTGTAGCAATTTTTTAGTGTAATAAATTGATAAATATTTGCAAAAAAATAC
ATGTCCATATTGATAACGTGTGCGGCGAGCAAAACAACAAAGGCCGTATCACAACTATGCAATACCCTAGATAATCGGCCAGTACTTGAGTATATTATTTGAAAGGGGCCAT
CAGTTGCAGGTCTTCCTTAAAGCCAGCAGCTCAAGGATCACAGTGAAATATGTTGGAACTTCGATGGCTTTTACGATGATGGTGTTTCTGGTTTGGCTTATGGGGTATATAT
ACCCGCAACTCTGCGAGTACACACTGCCACACTATCTGATTCGCGTGCGGCAAATACAAAGCTCGAAAAGCAAACAACTCCCGACTAGCAACAAAATCAATTGCCAGACAAT
CGAACCGGGCGCTGCAGAACAATAAAAAGTGTATAAAAAGGACGGAACAGCGAGAACAACGCAGAAACAGACGTCCCATAAATAAAAGAGCATCCTACACAGAGAAAAAAG
AATTAGGCAGGGGTTTACGAAAATAATTCATATTCAATTCAAAAGTATTCGCTTTTTTTGTAATTATTAAGATAGATGATGTATTGCTCCTAAAAAACTC
(SEQ ID NO: 109)

Exon: 4251..3780
Exon: 3011..2800
Exon: 2707..2212
Exon: 2145..1001
Start ATG: 4251 (Reverse strand: CAT)

Transcript No. : CT27563
ATGTCCGCGTTTCGCTACTTCTCGATCACCGATTTCTCCTTCGAGGGACCTCTGCTACCGCTGCACGCGGCCACCACGAGCAAGGATGCCAAGGACTCGGACAGCCCCAGTT
CCGAGCTGAACATACCCTACACCGTCTTCGAGGTCCTGGTGGCCATCGTCAGCATCATCGGCAACGTGCTGGTGATCATCGTCTTCCGCCGGGAAAGAAAGTTGCGACGCCG
CACCAACTACTACATAGTATCCCTGGCCATGGCCGATTTGCTAGTGGGCGCATTGGGTATTCCCTTCGCCATCCTGGCCTCCATGGGACTACCCAGAAACCTTCATGCCTGC
CTCTTCACAGTCTCCCTGCTCGTGGTGCTGTGTACCATCTCCATCTTCTGTCTGGTGGCCGTGTCCGTGGATCGATACTGGGCCATCCTATATCCGATGGCCTACTCAAGGA
ATGTCCGCACCCGCACGGCGATATTCATCATCTCCATGTGCTGGGTGGCCGGGACGATAGTGGGCTTCCTGCCGCTTTTCGGCTGGCACGCCGATGTCAATCACAACCAGGA
GTGTCTCTTCGTGGAGGTGATGGGACTACAACTACCTCGTCTTCCTCTATTTTGCCACCATTATCACTCCGGCTCTGCTGATGCTGGCCTTCTACACGGCACATCTACCGGGTC
ATCATCAAACAGGTCCGTCAGATTGTTACGATGAACCCCGCCTCCGATCTCAGTCGTCGCTCCTCGGCCGGCCGTGGTGCAGGTGACGACACCCGGAAGAGGTGGACACACGG
GAACCATGCTGCGGGTCTTGGGCGCCGCAAGGAAGCGGGGACGTCAAGGCCACCCAGAATCTGTCCATTATCGTCGTGTTCTTTATGATCTGCTGGATACCGCTCTATACGAT
CACCTCAAGGACTTCAGGGCCGCGCTGAAGAACTTACTCCTGAAGATGATGGGCGTGGACATTGATCAGCAGGCGGAGGCAATCCACCGCTTCTCGGTGGCCAGTCAGCATC
GCCTGCAGTCCATGGACTCCAATATGCGCTCCACGCAGCCGCCTCCTATGTGGGTGAGTATTCACCCATTTGGTTGAGGCAGCAGCAGGAGGCCCTGAAGAACTCCCAGCT
CCTGCCCAAGTGCGGAGTGGTGTCGCCCTGTTTCAACAACATCAACCAAACGGTGGCCGCCGTGGCCTTCGGTGACCACAGATCTCGAGCGAGAAATGTGGAACATAGTGGAG
GCCTCCAGTGGCGCCGAGCTGGGTGAAACCAGCTACGAGTTCCCTTCCCCCGCTCCGGGTTCCCAGCGCAGCAGTGAACGAAATAGCAGTTCCACAGTCCCACCAGCTCCTC
CTGCTCCTGCGAAGCCCTCAGTTCCGTCCGCCTCCTATGACAACCACAACTACAGTTTCAGCCAGGATGAGGACGAAGATGATGATGATCTGGAGTTTGAGGACGTATTCGT
GCCGGCCAGCTCTGTTCCAAATCCCGTTCAGCCTGGCATAGATCCCGTGGAACTGCGTCGCTCCCTGGCTTTGGTCATGAGGGGAGAAATTGCGATCGGATGACACGGACTCC

AGGCCAATGGGCAACAATCAGGATCTTCCCATAGATGAACAGTCCAGGGAGAGACCGCTCTCCACTCAAACATCTCCCACAAATGGCCCACTTCCGGCTCTTCTGAGGGCCA
AACTGCTTGCTGGCAACTCCAATAGCGCTCACTGCCTGCCAGGATCCACGGCGAGTCCTGCTCCCCAGGAGCAATCCGGTATCTTTGTGATCGATAGTGAGGCGAGTCCCGG
CTCAAATGGGCACAAGCCTAAGTATCGAAAGGGCACGGCATTCACTCGGAGTTCGCTGAAGAAGAGCCGATCCTGCAACTGTAGCTCCATCGCTAAGGGACGAGGGGTCCAC
GACGAGCCCAGCAGTAATCTCTGCAGGGATCAGGAGTCCTCTGTACTTCCACAGCATCCGCAGCCAGCCAACCATCCCACAGAGAACTTTTTTAGTCCGCTGAGATCGGTGG
GCAGTTTCATGCAGCATTCCAACTTGTTTCACTTCCTCCAGCCTCACGCCGCCCGTCCCACCTCATCGACGGCGTCGTCCACGGCCTCCACGCCCACTCCATCACCACCGCC
CATGGGCCAGGCTCAGGAGGAATCGGTTCCAGTGGGTCTGACCACCTCCTCGCCGTCCCTTCTGGCGACCAGCGCGGAGAGTTGA
(SEQ ID NO: 110)

Start ATG: 1 (Reverse strand: CAT)

MSAFRYFSITDFSFEGPLLPLHAATTSKDAKDSDSPSSELNIPYTVFEVLVAIVSIIGNVLVIIVFRRERKLRRRTNYYIVSLAMADLLVGALGIPFAILASMGLPRNLHAC
LFTVSLLVVLCTISIFCLVAVSVDRYWAILYPMAYSRNVRTRTAIFIISMCWVAGTIVGFLPLFGWHADVNHNQECLFVEVMDYNYLVFLYFATIITPALLMLAFYTHIYRV
IIKQVRQIVTMNPASDLSRRSSAAVVQVTTPGRGGHTGTMLRVLGAARKRDVKATQNLSIIVLFFMICWIPLYTINCIKAFCPDCYVHPKLTLFCIILSHLNSAVNPVLYAY
HLKDFRAALKNLLLKMMGVDIDQQAEAIHRFSVASQHRLQSMDSNMRSTQPRLYVGEYSPIWLRQQQEALKNSQLLPKCGVVSPCFNNINQTVAAVASVTTDLEREMWNIVE
ASSGAELGETSYEFPSPAPGSQRSSERNSSSTVPPAPPAPAKPSVPSASYDNHNYSFSQDEDEDDDDLEFEDVFVPASSVPNPVQPGIDPVELRRSLALVMREKLRSDDTDS
RPMGNNQDLPIDEQSRERPLSTQTSPTNGPLPALLRAKLLAGNSNSAHCLPGSTASPAPQEQSGIFVIDSEASPGSNGHKPKYRKGTAFTRSSLKKSRSCNCSSIAKGRGVH
DEPSSNLCRDQESSVLPQHPQPANHPTENFFSPLRSVGSFMQHSNLFHFLQPHAARPTSSTASSTASTPTPSPPPMGQAQEESVPVGLTTSSPSLLATSAES*
(SEQ ID NO: 111)

Name: Adenosine receptor like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384520
GAGCCAATTCTTTTTTGGCTTTACGTGACGTTGGCAGAACAAATCGTTTTTGTTTTAGCCATCTGACTTGTTTGCTCCTTTATGGCCCGCTGCGCTTTGGACTTTGACGCAT
TTGCGTCGCTTTAATGCGATTGCTCATTACGGCCAATCCTTACTAGTACTTGCACTTTCTGTGAATTCGTCTGGGGTTTCCATTTGGCTGATTGCATTTTCATAA
CAATTTGGAGGATTACTAATGCGCCACGTTGTCCCTGCATTTGCATGACCTTGAACCAGTAGCCACCTCATTAGAATTTCATTTGTAGTCAACAAGGCGCAGACGACAGGGC
CACAATCGATAAAAACCCAAATGTATTTTATGGCCAAATTACATTTTTACTAGAATGAATCCATAGAAAGATGCGGAAAATAAGCGGGCGCGGAATATGCTAAGCTTTATTT
TCGAAATCTTATTTTAAATGCGATTCAATACAATATACAGAATCTACTATGTTTAAGATCGCAACATTTTTTTTTACACTTTCTTAACTAAACACTTTAAAAGCACATCTGT
GTTACACTTTGGTATGCATGTGAAACATTTGGTTAACTAAAACATATATCTACGCAATTTAAAAGGCGATCTATTAAATTTCAAGGGGCAAGCTTTTCGTTTTTAAATTTAA
TTCCTATATTTAAATGGTGGGCGTTCACTAGTGATTGATTTATGCTTACCATTATCGATAATATTATTAAGTTATATCCGCCTCAGGCTTGTTTAAGAGTAAATCCCCCGAG
CTCTGACCAAAGTTTAATTTTAAGAGCGCCAGTATGCTGAATAGTATGAGTCAAAAGATTGAATATTCTTAGACTGAATAATTCTGAATACTTGAAAGACTAGTTTAGGAGT
TTTTCCAGCCGTTGTCCGCAGCTGAATGAATGAAAAACTTAATGCTTAAGGGAGAGTGTGCGCTCGAACTGTGATTAACTTTTAATTGCCAAATGCAAATGAATGCAAAAGCA
GTTTAAACAAAACGCTTTGGTAGCAGCAGCAATAGCAATAGACGACAAATAACTGGCTTAAACAGAATTCAAATAAATTAGCATCAGGAAGCCGCACGAGAGAGTGAGTTCG
AGAGAGCCAGTTAATATCGAACCTATCCATTGATTATAGGGGGCACTTGCCTGCATTATCGACGGTTTCGGCTGCTCCGCCGACTCAATGGAGAAGCGCTGCGTTTGACTGG
AATTGGTTAGTGCCCTCCTCAGGCGGCGGCGATTCGATGTTGTTTCGGCGAATTCAGCGAACCCTTCGATACCTTCTTGCCAAACAGAACGGCCTAAAGGAGTGGGAAATCGGT
AAGGTAATTAGTTAAATAGAAAAATTCAGACATTCGAATTATTAATAAATATATTAATAAATATATATAAATATTTATAATACAGATAAATTTGAAATATAGTATTGCGCAT
ACTATAACCCCCACTTCCGTTTTACTCACCTTGAATGCCTCTCGGAACTTGTGGCTCATAATGTTATATAACAGCGGGTTGATGCAGGTGGACAAGTAGTAGAGGACACCGG
AGACATAGGTCATCACCGTGTAGACAAACTCGTGCTGATCCCGCAGTTTGGCCCCCCGTGCAGGGGCGTAGATGGCAATCAGTCGCTGGGCGTGGAAGGGGGCCCAGCAGAG
GAAGAAGCACACCACCACGGCCACTAAAGGGGAGGGGGGGCGGTAAAAGTCAGTGACGTGGGGATGAAAATGGAATGGCAATGGAAATGGGGAAGACACAGCGAGAGTCAC
AGATAAAGAGTCAACGATTATATTTTTTGGTAATCGCAATTGTCATCATAAATGGAGAGTGCCAAAATGACAAACGCAGTAAATTGGCTGCAGACGGGTTGATTAGCCCAGC
TTAGGGCATATGGTCAAACAGTTGGCATACACTGAGCAAAAGTTGAAGTAAAGCTTCTAAAATGGTTCTTCATTGCATATAAAGAAAGATTTAGATATCATATTTCAGAATT
TTTAATTTGCAAGACTTTTGTGAGAAGACTAAACCTTATTAAAAACGGAGTCTTCTACTTTTGTTTTTGTCAAAATTTCTTACTAATTTAATCATCTGAATACTATTAAGTC
ATGTTTACTTAATGGTTAGCGGTTTAGAGATCTGTCATTTAATTTGTGATACCCCGTACTATTGCTGGTATTTTTCGCCAGTGTATATCGTGCTATAATTACCTAGCATCC
TGAGTACTCGCCGGGTGCCATAGTGATTGAGCCGACCTCTCACCGAGCTAAGTTGAGCCCCCGAGCCGCCCATCAAGCCCGCTGTCCCTGCTCCACTTCCTCCGCCGTTGAA
ACTCATAGCGGTACCGGATCCACCATAGCGATATAGGATCGTATCACTGGGCACACTCTTCAGCTGCTGCCGTCTGGCAACGCAGGCAGGACCCTCCACCAAAGTGGATCGA
TACAGGTGCACACCGATAAGTAGGTACAACACTAGGATAATAGACATCGGAGCCAGGAAGAATATGAACGTGGACAGCTGGAATGAGTGCTTCACTATGACCCGCACTATGC
TTTACTCATGGCCTGGCCCAGAAACGGATGGCAAATGGCAATATACCGCTCCACCGTGAAGGCCGTAATCGTTAGCACCGTGGCATTCGCCGATGTCTCCGCCAACAGACCA
CGTCCGATGCAGATGTACTCCCCAAACACGTACGGGTACTTGGACCAGATGTAGGACACCTCCTGCGGAACGCCCGACAACAGGAGCAGGGAAATCCGAGATGGCCAGCGAAA
AGAGGTAGTAATTCGTGGCCGTGTGCATTGAACGGTTCTTCTTAATCACAATGCAGGTACTTATGTTGCCCACTACACCGGTTATGAAAATGAGGGAGTAGACCACCGTTAC
CCACTAACAGCGCTAAATTCCACTGCCGTTTAACTGCTGCGGCTCCGGCTGCGACTCGATGTCCCCTCAACTATGCTAATTATAATAATTTATTGGAGGCGACCGGGCGGAG
GAGGGACAGGTCTGGACTCGCGCTTCGCAATGCTAGATACTCGATTCTAAGATTCAGATACTCGACTGGCACGCAAACGCACCAAATTACCGACGAGGTCGAGATCCGTATA
CCGTATTCAGTATTCAGTATTCCGTATTCCCGGCTGTTTTTCTAGGGGGCCCGACTTCTCTTCAATAAGTTATCGAGTTAATTTGATTTCGATTCGAATTCTGATTCCCGAG
AGCAGCCTGCAACCGCACTCCAGCGCGCTCCAAACTTATCTGATAAGCCGCGGCGACATTTCATTCAGATTTGTATCTGTATCTGAAAGCCAGCGACGAAGCGTCGCTGTTT
TTCCCTCACATGACACGCGGAAGGTGAGCGACATGGTTGTAATGACCGAGCGGTCCAGCGAACGTGCCGGCTCAATTAAATCTTGAAAAGCGGCGATATCTTGATGGGACTAGC
CGATGTTAGAGACTAAGCACAATGGCTCCGAATACAACGCAATTTTTGGGTAATTAAAAAGGCTAATTAACAAAAACTTGTAATAATGTTTGCTTTGGCCCATTTATAAAAC
ACTTAGTTGGGAATTTTGACTTTGTGATGCACATAATCCTAAATAAACCACGATAATGTAAACAACACATCTTGGAATTAAAAGCCAAAATAAGATGCAATAATATTAGATG
ATGCAATAATACCAAATGACCGAAGGCCACCGTGCGTATGAGTAATGTCCAGCCAGCTTACTTGTTAGCTTATAAGTAAGAATATTGTTCTTTGTTTATCTTACTAAAGTAT
ATTGAAATGTAAACAAATAATAATAATTACAATTCAAATCTAATTTAGATTAATTAAA
(SEQ ID NO: 112)

Exon: 3314..2456
Exon: 1927..1710
Exon: 1547..1367
Exon: 1029..1001
Start ATG: 3314 (Reverse strand: CAT)

Transcript No. : CT27924
ATGTCCGCTGGCAATATGAGCCATGATCTTGGACCGCCACGCGATCCGCTGGCCATCGTGATACCCGTAACGGTGGTCTACTCCCTCATTTTCATAACCGGTGTAGTGGGCA
ACATAAGTACCTGCATTGTGATTAAGAAGAACCGTTCAATGCACACGGCCACGAATTACTACCTCTTTTCGCTGGCCATCTCGGATTTCCTGCTCCTGTTGTCGGGCGTTCC
GCAGGAGGTGTCCTACATCTGGTCCAAGTACCCGTACGTGTTTGGGGAGTACATCTGCATCGGACGTGGTCTGTTGGCGGAGACATCGGCGAATGCCACGGTGCTAACGATT
ACGGCCTTCACGGTGGAGCGGTATATTGCCATTTGCCATCCGTTTCTGGGGCCAGGCCATGAGTAAACTCAGTCGCGCCATTCGCATCATCGTCCTGGTTTGGGATTATGGCCA

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TAGTTACGGCCATTCCGCAGGCTGCCCAATTTGGAATCGAGCACTATTCGGGAGTGGAGCAATGCGGCATAGTGCGGGTCATAGTGAAGCACTCATTCCAGCTGTCCACGTT
CATATTCTTCCTGGCTCCGATGTCTATTATCCTAGTGTTGTACCTACTTATCGGTGTGCACCTGTATCGATCCACTTTGGTGGAGGGTCCTGCCTCGGTTGCCAGACGGCAG
CAGCTGAAGAGTGTGCCCAGTGATACGATCCTATATCGCTATGGTGGATCCGGTACCGCTATGAGTTTCAACGGCGGAGGAAGTGGAGCAGGGACAGCGGGCTTGATGGGCG
GCTCGGGGGCTCAACTTAGCTCGGTGAGAGGTCGGCTCAATCACTATGGCACCCGGCGAGTACTCAGGATGCTAGTGGCCGTGGTGGTGTGCTTCTTCCTCTGCTGGGCCCC
CTTCCACGCCCAGCGACTGATTGCCATCTACGCCCCTGCACGGGGGCCAAACTGCGGGATCAGCACGAGTTTGTCTACACGGTGATGACCTATGTCTCCGGTGTCCTCTAC
TACTTGTCCACCTGCATCAACCCGCTGTTATATAACATTATGAGCCACAAGTTCCGAGAGGCATTCAAGGCCGTTCTGTTTGGCAAGAAGGTATCGAAGGGGTTCGCTGAATT
CGCGAAACAACATCGAATCGCGCCGCCTGAGGAGGGCACTAACCAATTCCAGTCAAACGCAGCGCTTCTCCATTGAGTCGGCGGAGCAGCCGAAACCGTCGATAATGCAGGC
AAGTGCCCCCTATAATCAATGGATAGCTGCGGACAACGGCTGGAAAAAACTCCTAA
(SEQ ID NO: 113)

Start ATG: 1 (Reverse strand: CAT)

MSAGNMSHDLGPPRDPLAIVIPVTVVYSLIFITGVVGNISTCIVIKKNRSMHTATNYYLFSLAISDFLLLLSGVPQEVSYIWSKYPYVFGEYICIGRGLLAETSANATVLTI
TAFTVERYIAICHPFLGQAMSKLSRAIRIIVLVWIMAIVTAIPQAAQFGIEHYSGVEQCGIVRVIVKHSFQLSTFIFFLAPMSIILVLYLLIGVHLYRSTLVEGPASVARRQ
QLKSVPSDTILYRYGGSGTAMSFNGGGSGAGTAGLMGGSGAQLSSVRGRLNHYGTRRVLRMLVAVVVCFFLCWAPFHAQRLIAIYAPARGAKLRDQHEFVYTVMTYVSGVLY
YLSTCINPLLYNIMSHKFREAFKAVLFGKKVSKGSLNSRNNIESRRLRRALTNSSQTQRFSIESAEQPKPSIMQASAPYNQWIAADNGWKNS*
(SEQ ID NO: 114)

Name: Growth hormone secretagogue /neurotensin receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384297
TTAAGCCACAAATGATTGAAAGGAAATGTTGTGGGGTAAAAGTAAAATTCTCAGATCGATGAGTACAATGTACTATGTACTTCCCTCGGCAGCTCCTGCTGTGTTCCTTCA
GCCGTTTGTGTCTGTTTGTCCCTAAAGTAATTAAAAGTAAGTAAAGCAAAGTCACCCCCTCGTCGGTGGGCGTGGCTGTCCAGTGATTTGCCACCCGCAACGATTTTTTTTT
CCAGTACTTTCCTTTTTTTCTTTTTTTGCTGTTTATGCAAATGGCCGCTGACCAAAAGAATTAATGCGTCCCGAAAGTGAGTTGAATTGGAATGAGCCGCAATTCTCGGAGT
CCAAAAACTGCGGGCAGCCTGTCAGCCGTCTGTTTTCACTTCTTTTGCGGGCGGGACGAAACATCAACGAATGTCAATGAATTTACAGGGGAATGCTATAAAAAGCCCGACC
AAACAAAAAATGTAAAGCCCGTAATTCCCCATTGTCTCAGTGCGTTGCTAATTTGGCCATATCTTTAAATAGCCAGCCGAACGGAAAGGAATCATTTGTAATTTAAAGTCCA
ATTATTGTGCCATTTGAGGGGAAAACTGTGGCATGCCAGGGAATGGAATGCCTCGTAAGCCACATCGCTGCACTTCATTAAATTGACGAGACAAAAGATCTCTACACATACA
ATAATGGAAAATATTTGTTCCACAATAAAAGGGGTTGAGGAGGCACTTTGTGTTAATGCCCAACAGCTGCAAATCTCGGTCTGCGGCGGCCTTAAAAATAGAGAAATGAAGA
TGGACGGTCCGATGATGATCCGCTTGGCTGAAATTATTCTGTAAATTCTACCTATTTATATCGTAAATATAGATTTTGATGCTGATGCCGATGCTGCGCGAGTAAAACCAAA
TTCGGCCCACGCGGCGTATGCGCGTTTTTCGCACTTAACTCATTAAAACGTTTGCCGCTGGCCCATTGAAATTTAATGGGAAACACGCGCTGTTTTTTTTTTTTTTAGAAAT
TCGCCTCAATAGATTAAGCTCGTAAATTATTTAATTGCATTCTTGATTTTTGATTTGAAATCAAAACATTCCCTCATTTAAAAACTCATTAGGAATAGCAATGGAAACGTGG
GACACAAAAGTTTCCATCAAACGAAATGCAAACGAAAACAATGCTCTGAAAATATTTCATCGATATATTGACCGAGCACTCAGATGTCGTCACTTGAAGGACCCTTCTCGTC
CAGCCCCCGAGTGCACCAACCCCACTCACCTTGTAGAAGGCCTTCCGGAAATTCTCGGAGAGGAAGGCGTAGAGCAGCGGATTGATCACGAGCTGCTGTAGGCCAGAGTCT
GGGCGGTGACCTGGATGACTAGCTTGGTGAGGGTGTTCGTCTCGATGACATCCAGTGACTTGAGCAGCAGGATGAGCTGTTCAATCAAACGAAAGAATATGTTTGATTATTT
AAAATATATGTGGGTTTCATATGTATTATTGCGTCTCACCTGGACAGGCAGCCAGAGCGAGGCGAAGGCGATGACCACCACGACGCGAGTCGGGTGACCCGCTTGCGACCG
CGCTGCGACTCCTTGGACATGCGGACGCCGGTTCCCTGGCGCCAGAGCCGCATGATCATGCGCATGTAGAGACCGCTGATGATCATCAGGGGCAGCAGGTAGGAGCTGATGA
AGAAGGTGACCTGGTAGGTGCGCGGACCAAGGAAGTCGTTCGTCGTGAAGGTGCACATGCCGTAGGTGATGTTCTTCTTTGCATCGTAATCCACCTGCGGATATCGATGAGA
ATGTGGTTGTGGGAACTATGAAGAAACGTGTGCGGTGTGGGAATCGAATATTGCGCATACGTCATGTTGGCGGTGACAGTTGCATGGCAGCCAAGCAACGTCAAACGGCCAA
CAGCCAGACATCGTAAATAAAACTAAACTGTCATACGAATAGTTCGGACGTCGACAACTAACTCACTTTGTTTCTCTGTCGCTGACATTTGGCTGACAAATTGT
TCAGCCGGAGTTTTGGATTTGGATAAAAGCGCAATGGGTATGGGCAATCGGGCTTTCGAGGCTTGTTGTTTGGGGGATGGAGAATCTATTGGTCTGTTGGCTAGACGAGACT
GGTTTGCTGACGCTTAGGAGGGTCGTAAACTGCCCGGTGAATCGTAAAAATATTCGCAGCCTTTTGTTTACATTTTTGTTTACAATCTCCGCCCCTTCACCGCGCTTTCAAT
CGATGAATGCGTGTGGAAAATTGCATTTAAAAAAATCTTCCCATTAATGCCGGCATGAATTGCTTACAAAAATGTTTGTTTATGGCCCGCCCTTGTTTTCGTTACACTGAGCG
AGCGATGTTGGCCCACAAATTGAGTTCGAACTCTGAATCTGCGCAGCGTCAAGTGGCCAAGGCCACAGAAGTAGACAAATCATGGCCAGACCCTCCGCTGATTTATGGGTTC
ATTTCGCTGGCATGTTCTCCGCAAAACCCAACGACTTCATAGACTTGACAAGCCATTAATGCCCTTTCCTCGTTCGCGAGAAATCAGCCAACAGCTGTCAATCAATGCCATG
ACCTGGAGATCGCATATCTAGTTACGCCAGTCGGACATATGTGCATTTATGATTATTATTTGATATCGATTTCTAATAAAAAGATAATGGCACACGCTCTCACAGGCTCATTT
GATATGCATATACCAAGCATGTAGCTGGGCAATGTAATATGGAAATAATTAATAGCAAACTGTTAATTAACATGTTGATCAAACATGACTTAATTATGCCTTTTTATCGCCT
ACATAAACAAACAATAATGCCACCCATTGGAGCACTCTCCCCAATGCGAACAAAAACCGAACGAGACAAAAATAACAATATAACGAAGCGTGAAATGCCATTTAATAAAATA
TTAGGTTACAATAACAACACCGGGAGCAACAGTGGGCCATTGCCATCTCACAGATAAAAAAAGTTCATCATCCGTGTGAAGATGAGATTCGTTTAATTAACCGCGACTGTCG
CTTTTGGCCAAGGAAAAGGGGAAACACAACGGCACAAACAAAAAGTTGGTCATGTGTGATGTGGGAATCGCTTTATTGGCACTGGGAAATCAGTGGAAAAAGCCCGCGGGCC
ATTTATGAGTATCAACAGAAATTGGAACCAATGTCCGACCATAATTACGTGTAGTTGATACTCGCAATGAAAAAAATATGATAGATATTCAGTATTAAATAGCACTCAACAAT
TGTTTGAACTGTACCGGAAAATTGAATATTAGTTAATAATCCCAGTGTTTTCTTGCGAATAAAACTTAAGGTTAAAGTCTGCAAATACAAATACATTGTATATCCTCAAAA
TCGCCGGTAAATTCCCCTTTTCATTTTTGATATCACCCGCTGATCTCGAGCAAAACAATTCCGATCTTCGTCGATTATTCCGCAATTAAATTGTTTCTCGCACTTTTCGCAT
CGATCATAAAAGCCTAATGTCCAAGATGAGCATTTCAAGGTCGCCACCCGCGAAGACATTTATCATACGCAGTGTGCGCCCAAAGTTCGCAAGTGCAAAGTTTCCATAATGG
CCGCTTGTTACGACTTACGACTGCCCATGATTTACGCGCTTTTGGATCAACAGTTGAATTTGAAATTTTGCAAGCCACACGGAGAGGAGGTGGGCAGATATGGGCAGATACC
GCCCAGTTGGCAAGTGTTTCTCGCTGGCTATCTGGTCTATAATTAAAAATTTATGAATTCAAAATAGCAAATTAGTAACAAAAACAAATCGGGCGCCGCGCATCGCGAAATT
TTCAATATAAACACAAAACAGAAAATAAGATAAAATGGGGATACTTTAATAGGGGCATATAGTAAAAACAAATGAGTTGTATCAGGATCAGTCGATTGGACGATCGCTGGTT
TGTGCGGGGTCTTCGCTTTCTGGATTACGATCTGGCAGAAGGCAGACCATCTATCTAGGTATCTATAGCTACATTAGAACCAGGCAGTCGGCACCATTGACGTGCAGCGAGA
GGAATCTAACGAGGTGACGATGATGGAAAGCAATAAATTTGCCTGGCCCGTGTTCTTCACAGCAAATTCAGGCACAGCAGGCCCACTTATAGCATTCTACCCACTCCTCCCA
CTCTTCCACTCCCACTTACCACCACGTCGTGGGTGAAGGCCACTGGCACCGAAACGACCAGCACCGACTCCACAGAGTCACGATGGCAATCAGGGTAATGTTCTCCGTCCT
CATCATCCGCGAGCGAATGGGATGAACCACCGCCAGGAACCGATCGATGGACATCAGCACCAGCGTGTAAATGGAGGCGAAGGCGGTCACCACAATCAGGTACTGGACACTG
CGGCACCAGAACCTTCCATATGGCCAGTAGTACACCATGTAATCGGTGGCCGTGAAGGGAATGCAGAGGATTACGAACATCAGATCAGCGGCAGCCAGATTGACAATCATCA
GGTTGGTGGTGGAGCGCATGTTGTTGTTGAAGACCACCACCAGGATGACCAGCAGGTTGCCGAAGAATCCCGTGATGGCGATGACGCCGAAGAAGAATCCCACTATCCACGG
CAAAGTGCCCATTGATGGCCAGCCACTCTTCGTCGGTGAAGGATGAGGTGATATTCTCCTCATTTCTGGTTGCATTTAGGCTAATATTAGCCAGCATTGTGGTGTTCTCCATG
TTTTCTCAGCTTTAGTGCACAACTTTCCGGTTCACTTTGTACTGGGTCTATTGGCGATTTCGCTTGATTGTCACGGGACATTTTCAATTTTGGGCTCTTTTTCGCTCACAGTTC
ATCGAACGCAAATAACAAATTTCCAATTAGGAGAGTTTCACAAAGCAGCCGCCACAAAAATTCAATTATCATGCGGAATACTACGACCGTTGAGCTTCGGAGACCTCAAAAA
CGTTTCGCATACGCCGTGTGGTATCGAACTCGACCGGAATTGTTCGCAACGTGGCGGGGGCAAAAGCAATTTGGTCCTTCCACGATAACGGTAATTGTAGGTGGGTAGCACA
GGTAAGACAACAATAAAGGACAGCACACAAGGATCACGGTGAGGCGAAAGGCAAGAGAGTGAGTTTAAAGGTGAGGGCACGTGCAAACGACACCGACACGGCAAACTGGTGC
CGAGTCACACCCTGACGACAAGGACACCGGGGTGTCCTTAGGTTCGAGGACCACGTTGCTGCACCTACACCATAAATTCAATATGATGTCTTCCTTTCCGCTGCGTTTCTGTT
TACATTTCTCGTTTGCTTTTTTATTGACAAACGAACGGCATAAATTTTGGGGCTATAAGGCTATGGCCAAAAAACCACGTTCCTATTGTTGCTACCGACTGCTGCGCCGCGG
TACGCTATATATTTTCGATTTTATACTGCTGCTTTTGGCCAATTCGATAGTCCACACTGCTCGCGTCCGTATCCAGCGCCCAACTGATTGCTGGCTGAGCTTGTTGAGGAAT
ACTTCGATGCCTCGGCGGCGGCAAAACGCCGGCAGCGACGCCAGCCATCCCAGCAAGAATAATGGCAACAATAGCAACAACCAGCGCAGCTGGCATCTGTGCGTGTGATGGT
TTTGGGTGGCCGCCGGAGCCACCTCTTCCTCCTCATCCTCCTCATCCGATCCCAATCCCCATCAGCTGGGCTGGAATGTTTGCTCTTGTTGCTCCCACCGCTA

FIGURE SHEET 53

(SEQ ID NO: 115)

Exon: 4927..4388
Exon: 1886..1608
Exon: 1532..1374
Exon: 1012..1001
Start ATG: 4927 (Reverse strand: CAT)

Transcript No. : CT28187
ATGGAGAACACCACAATGCTGGCTAATATTAGCCTAAATGCAACCAGAAATGAGGAGAATATCACCTCATTCTTCACCGACGAAGAGTGGCTGGCCATCAATGGCACTTTGC
CGTGGATAGTGGGATTCTTCTTCGGCGTCATCGCCATCACGGGATTCTTCGGCAACCTGCTGGTCATCCTGGTGGTGGTCTTCAACAACAACATGCGCTCCACCACCAACCT
GATGATTGTCAATCTGGCTGCCGCTGATCTGATGTTCGTAATCCTCTGCATTCCCTTCACGGCCACCGATTACATGGTGTACTACTGGCCATATGGAAGGTTCTGGTGCCGC
AGTGTCCAGTACCTGATTGTGGTGACCGCCTTCGCCTCCATTTACACGCTGGTGCTGATGTCCATCGATCGGTTCCTGGCGGTGGTTCATCCCATTCGCTCGCGGATGATGA
GGACGGAGAACATTACCCTGATTGCCATCGTGACTCTGTGGATCGTGGTGCTGGTCGTTCGGTGCCAGTGGCCTTCACCCACGACGTGGTGGTGGATTACGATGCAAAGAA
GAACATCACCTACGGCATGTGCACCTTCACGACGAACGACTTCCTTGGTCCGCGCACCTACCAGGTCACCTTCTTCATCAGCTCCTACCTGCTGCCCCTGATGATCATCAGC
GGTCTCTACATGCGCATGATCATGCGGCTCTGGCGCCAGGGAACCGGCGTCCGCATGTCCAAGGAGTCGCAGCGCGGTCGCAAGCGGGTCACCCGACTCGTCGTCGTGGTGG
TCATCGCCTTCGCCTCGCTCTGGCTGCCTGTCCAGCTCATCCTGCTGCTCAAGTCACTGGATGTCATCGAGACGAACACCCTCACCAAGCTAGTCATCCAGGTCACCGCCCA
GACTCTGGCCTACAGCAGCTCGTGTATCAATCCGCTGCTCTACGCCTTCCTCTCCGAGAATTTCCGGAAGGCCTTCTACAAGGCGAATTTCTAA
(SEQ ID NO: 116)

Start ATG: 1 (Reverse strand: CAT)

MENTTMLANISLNATRNEENITSFFTDEEWLAINGTLPWIVGFFFGVIAITGFFGNLLVILVVVFNNNMRSTTNLMIVNLAAADLMFVILCIPFTATDYMVYYWPYGRFWCR
SVQYLIVVTAFASIYTLVLMSIDRFLAVVHPIRSRMMRTENITLIAIVTLWIVVLVVSVPVAFTHDVVVDYDAKKNITYGMCTFTTNDFLGPRTYQVTFFISSYLLPLMIIS
GLYMRMIMRLWRQGTGVRMSKESQRGRKRVTRLVVVVVIAFASLWLPVQLILLLKSLDVIETNTLTKLVIQVTAQTLAYSSSCINPLLYAFLSENFRKAFYKANF*
(SEQ ID NO: 117)

Name: Allatostatin receptor type
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000012806866
ATCTTTTAAGTAAAAAGCGCTCAAGTCAAAACTTTTACTTTCATTTAAAAGTAAATTTTCTTGATGTTTCAAATTTATAGCAAAATGCCATAATTTCAGTTCGTTTGAAACA
AACGAAATGAAGCGGAAATTGCGAACCGAATTTATTCGTACAATTTATGGGCCACACATGAACAATAATAATTCATTCGGCTGCATGTAATTAAGAATAATAAAAATACTGG
TATATTTTGTTTGTTTGCTTAATGACTCGAAATGTTTATTCGTTTTCGTTTGGTAATTAAATACAATAATAATTACATTAATAAGCCTTTCTGTTTTTTAATGACAAATATT
GTACATTACATTTGCTTACATCCAGCTGTGTGCTTGTGTAGGATTTAATACATAATCGGATTGTTGTTAAAATACTATTTAAATAATTTAATTTAATGCTACTTAATTGATT
TCAGGTGCTAATTTAATTTGATTCATTTTTTGTTCAGCTAATAATACATTTGATTTGGTGAGTTTTGGTTTGAGTTTGATAAGGTCATTAACGAATCGATTATTTACAACGT
TTGGACTTCGTGCTTTAAGGATCGCAATTTGAAGATACCATTATTATAATACTGTACACGGCTCACGACCAGCATTCACACTCATTCAATATATATCCTTCTGCGAAACAAT
TATCAGCAATGGGACTTGTAATCACAATTCATTAAGACGAAATCACAGAGGCAAATGGTCATGTTCCAATGACACATTTAGTTGCGGGATATCTAAACACTGTAAAGGGGTT
TTACTAAAGCCTTACATACAATTACAATAAAATTTAAACATATTAGTGTAGTAGCTATACCCTAATAATAGTCATTCACTAAAACATTAACACACATACGTTAAATGAATGA
GCTATGACAGCCAATTTACTGGAATACACATCATATGTGAATGCCGACTGGCTGCGGAATGTGTCATTGGAACACGGCTATAACTTAGATCGCTCTAGTTTAAATTAAAGTG
GTTGCCACAAGGACTTGCCCGCATCCTTGTCCTTCGCCTGCGAGCCGGGCAGGTGGACTCGCGACACCTCGCTGAGTATGCAGGTGCCATCGCATTCGGTTTGGCTGCCAAA
TTCCTGTTCGCAAATGCAGCTGGAGCTCTCCCTGCTTAGCAGGGCCAACTGGACTCCGGCCCCGGATGCCAACTCCTCGCTGGGGGGCGTGGTTGATGGCAGCTCCATGAGT
GCCACGTCGTCCTCGCATTCGATTACGTTCGGATGCAGAGGTTTGAAGTTGTTTCGCCGCCACGGCGGCATTGCAACGCCAACACCTGGTGCCGAAACACCCGGAGTGGCCG
CAAAGGTAACCACGCTTTGATGCTGATGATGTTGGCCATTGACATTGTTGTTCTGCCCACTACTTCCGTTGTAAATGCCGCTGTTAGCACCGGATCCATGCACCCGCGGCAT
ATGCAAGCCCGGCTTCCCATTGTTGACACCACCACGCGCCGGACCAAAGAGATTACTCCGGATTCGCATCGAGGAGTTGGCGTAGGTTGACCTTATGGAGCTGGCGCGGGTG
TGCATCGAAAAGGTCCTTTCGTGGGCGTCCATGCTCGTCTTGAACTTGCAGAAACAGGCCGCAAATCGCTTGTTGAATTCCCGCTTAAATTTTCCTGTGCAGAGAAAAATA
GACGACGGTTTAGGTTAATCCATCCCAATAACATATCACTAAAGTAAGCGAAAGTACTTTTATTCACTTAAATACAAATTAAAGTGCATTGCATAAATCATAAACCTCTTAG
GCATCTTTCTGGCTAATGAAAGTGCTCTAGGCAAACCTCCATCTTCGCTGACAAATCCCATTTGTCTTCGCTGACAGTAAAATAGAATATCTGTTGACAAAGTTTTTCACGC
ACAGCTCAGCAGGGGAAAAAGTTTACGAGTTTTATTCGGAGATCTGGCTCTCAATCTATCTTTTACAGACAATTTGAGTGTCAAAGCAAACAGCCGACGGGTTTTTTCCCGCTT
TTATCGGTTTGCCACTTTGGCATTCTGAGGATTTTTGTGGATTTCGCTTCAGTTTTGCGGTTTCACAATTTCTGCGGCCCAGACGGTAGGTGTTTGCTTATTGGCTACAGTG
GAGCGCTGCTTTAATTAACTTTGACAAAGTATTTTTTTGTGTCAGCTATTTTAGGTGCGAGGCGAAAGAAATTGGAAATTGTTTCAAAGTAAGGCAGAAGTTATTTTTGAT
TAAAAAAAAGTGACGCGTATGCTTATAAATCAGCGAGAAGGAAAATGGGAAAACATCAACAAAGCAATCGATTCGCTTACAATGAAATTAAGTTAGACATATTTCATTCTT
TTTTAAGCTTCTTTGATTTTTGAGACCATGAAAACTTCCGTAAAAGTTTCATTTGCTTTGCGTCTATGTTTGTGTTTCATTTGATGAGATAATAGAAAAAAGCTAATTTTGGA
AGCACGTGCAAAGGCTTTTTTTCTTTTAGGTCTAAAAGTACGAAAATAATATAGAAAAAATTACTTTTTTTTACTTTAACTTCATTATTAAAAGCAAGACGTTAAGTATGTAG
GTCCCTCATCAATCCCCACATTTCCCCGGCAAATTTACCACACATTTATAGACTTTATGTCTTTTTAGTGCGTGTCAAAGAACGTGTCCCTGAGCACGACAAACAATCCAAA
GGATGTCAATCAAATCCCAGCCAGACAAATGCAAATTTAACACTCCGTAAACAAATCATCATCATCATTGGAGCCCACACTTACATTGTAGATGCCATAAATAAAGGGATTG
TAGCAGCTATTGCTCATGGCCAGCCAATCGCAGCAAAACCAGACGATGCTAATGAAGTGGTAGTCGTTGATTTCCGGTATCGTGACATACAGAATATTATAGAGCTGCAGTG
GCAGCCAGCAGAGTCCAAAGATAATGACCACGATAATCAGCATTTTGATGACCTGCAAGCGTCGCAGAAAAAGGAAATTAAACCCAGTCCCGATTTGCATACCACATCAACG
CTGATGACACAGAATGGAACCAGATACTGCACAAAAACCAGGGTGTAGCGAAAGGATTGCAATTGATCATCGGATAGGTTCTTGTTCATGCAGAATGGCCGCGTCACATTGT
AGGTCTCATTGTTCTCTGTTCAAAGGATGAAATTCAGTTAAGGTCGCTGGCACTTAATCCATGCAAGTTGACGTATTGACTTACCGCGAAATCTTTCGGTCAACTCCTCCAC
ACGAAAGGCAATGGCAAAGGGCACCGCAAATAGCAGGGCCAGCATCCAAATTCCACCAATTATGAACTTCGATACGAACTTGGTGGGACGTGCCCTGCATGCGTAAGCCGAT
TTTTAATGATTATGATTGACGAATCGAATCGTTTCGAATGTGGGAGCCCACTCTCCCCCCCAGCGACTCACCTAAGTGGATTAATGATGGCCCTATGCCGATCGATTGCAAT
GGCGGTCAGCGTGAATACCGAGACATTTACACTCAGGGCCTGGACGAAGGATTGCGAAGCTGCACATGAACCACGGCAGGTTCCAACTCTGCAGCAGGGCAGCCTGGAACTAC
ACGGAATGAAAATATTGCAATTATTAGTTTAAAGTATTGCAGATTATCAGAAACAACTTGACTATACAACTATGCCTAACCTTTAGCCTGAGCATGATGTTTACAAATCACA
AATAATCCCTTTAAAATGTTCACTATATATATATTCATTTTAATTAAAGTGTAAGGAAATAGGATAGCTACAAGTGAGTCGTCCGCCTGAGGTTTGATATGATTTAATCAAC
CTCGAAAGCCCAGCGGTGTTGTTTTGGACACTGGATTTGCCAGGAGTGAGTGAAAAAGTGTGTGTGATTACTGCGGATATTTGAAGACCGCGCTTTCTCCGTTCTCCACA
CAAAGTCGGCCGCAAATTGCAATTTCTCGCCGGCTTATTGATGACACTTACTGGCGGCTGTGACAGGACCAAAAATCTATTTGATTGCGGCATTAATATAAATTAAGTGCCC
AAAATGTGGCTGGCTTTGGGTCAAGTTCAAGGTTCAACGAAGTGTACAGATTGAGCTTTATTAGTATGAATTCTGAGGTAAAAATCAATTTACTATTTTTATTTGAAACATA
GAAAGATGTAAACAATTTGTACTACCAATTAATAATTATTTCGACTATTCAGTTCGATGGTTACATTCAATATTTTACGTCTAAAACAAGCTAAAATGCAATTGCGGCATTC
TGCGAAACGAGCTGAATACAAAGTAACGATTCAATTACTTTATTCAAATGTCCATTGCTCATTGATTGACCATTTTCCGACTAAACAGTATTTTCAAAGCAAACTGCGTTCG
CGTTTTGCATTCGACGACACCAGGGAATCAATTGAAGATAATGGCAATTCAATTACTCGGTATCACATACAAATTCCAAAGAAAGCCCAGAAAAACTGTTCACATAGCTTTTA

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GCACTCTATTTTGGGTACTTTATAGAATACAAATCCCATTAACACATAAACCGAAAATCACATTTAAATTTGATGTAGGTAATATTCCATTACCACAACTTTTTTCGACAAG
ATGCGCGTAGGCCATGGCAATTTTCTAATGCCAAACATGAGCGCTCGTTGCCCGGAAATTAAATTGATGCCGGATTATGCTGAAATTGGTGTCCCTGCGCACTGTGGGTTTC
AAAAACTGGGCTGGCTACCTTTCTATGGTGAAAATAAGCGAAAACTAATGCTAATGTTGTTGGCTTGTGTGATTTATGCGTTAAAGTCGATATCCATTTACTAGCGCAACAG
TGCGTATGGGCAATTTTGCATGTATGCATTTCATATCCGCGAAAAAAAAAATCTCGGTAATTACCCGCATTATAATTAAGCTTAACTGTTGCAACTCACCTGAAATGGTATG
CAGAAGAGGCCAATAATCACATCGGCAAAAGCCAAATTAGCGATATACATATTTGTCACGGTCCGCATTTGCCTGGTCGTGGCCACCACCCGATGACCAAAGTGTTGCCAA
TGACGGCCACGATACTGATTCCCCCATAGAAAATGGACAACAGGGCCACAATCTCAGCGGGAGCCGCGTATAGACGCTCTGTGAATGAATTGAAAAATAGTTGTGCATTAGA
TTTATATCACTCGGAAAAAGTGCTTGCAACATTATTATAAAACTAAATGAGATATAACAATCTGTTTTACACAAAAATTTAAGAATGTATCCAATACATAATGCGCTCCTAC
TAAGTTACTGAAATTTTAGTTATTTATTACAAGACCATGCTTTTATGAGTGAATAAATTTTGTGTGTGGTGCTTAGCTTCTTCCAATCCATTAGTTTCAGTGTTGAACTTGT
GAAAAATCGCGCTTGCTGACAGAAGCAGATTAATTCAAGTGTCAGTTGTCAGTCAACTGATGGCAGGACAGACGACATTCACGTTCCTGCTGACTTGTAAACGTCAAGGAAA
TTGAACCGTATTTTATAGCCAAAGAGGGAATTTTATAAATGCCACTTTGGACAGTATATACCTGTATATATATATACCTATATCCAATTTAATATAAAATATTGATAGTTAA
ACCCAACTTTGATATGAATTTCATTAGCATATCCGAACATCACCTGTTTCCTCATATCAAAGTCAATGAGATGGTTGAGCCCAAGTTTGGTCTTTAAATTCGGCACCCCCCA
CACTCATGAATGATTCAAGATCAAAGAACTAACGGCGAACTGTCAGAAGAAAAAAACACTTGTCAATGTTTTTGATTGATGATACGTCAAGTCAATTTAATCCAGTTGGATG
AGTCGCGTCCCCAGTTGCTTGAAGGGATTAGAGAGTATACTTACCAAATTCTGCTTCCTCCTCGGCTCCGGGCAGGAATTCCAGGCGGGACTCCTGCTCGATTAAGTCCATT
GCCATAACACTTTTTCGTTTTTTAGTTTTAGTTGTGTATCCTAATGAGGATATGATATCCTTCAAACCTTGTATTTTAGTTCGAATGCTGCTGCTCTATGTAGTGCAATACA
TCTTCAGGGGCTTCTGAGCTTCATTGCAATCTAAACTGGAAAGATATAAAATTACAGCATTTGTTCATTTGTTTTCTGAAAATTCGCAAAAAAGTTATCTGCCACAAGTCCAG
TGGTCAGGGAACAACAAAAGTGCAGACAACAAGAGAAACAAATGATCTGAAAAAAAATCATTGAAAAGCTATACAAGCAATATCAGTCTTGCCCTCAAGGAACTGACCAAAT
GGCACTGCACTAGAATTTCGCTTGTATTTCGTTTCTTATGAAAACAGTTCATGTTTTCATGTTTTTATTGAAGAGTCATGCCAACGCTCAAATGTTGCCTTAGCCTTATTGA
GGTGGCTCCTAAAAAATAAACAAGAAAGTCAGCAAGTTCATTGAATGTTTGAGAATAGAAGCCTCACTCAGGTTAATTGGCCATTTATCGAACTGTTAACATTGTTGGGACT
TGTTAATTTATCTTCTTCAGTGTAAACACTGTCAAGACTTGTTAATTTATTGGGTAACTAAATGTTTATTCTATAGGCAGACGGAATTGTTATAGATTGACTTAGGGATGCT
TGTAGGAAATAGGCTGGGAAATTGGCGAATGTCGTGAAAAAAAGATGTATTTAGTTTTGAATGACTGTACTATTTCCCCCAGAAAGAAACAGGTTCACAGGCTTTAAGTTTA
TATGGAAATGCAAAAATTTGTTTCGAGCATTAAATTACTCATTTTATTATGCTGGTCACAAGCTAAAAGAACTAAAAGGAGCCACCCTAACGCATGACCCCAA
(SEQ ID NO: 118)

Exon: 6383..6317
Exon: 5566..5364
Exon: 3916..3768
Exon: 3678..3557
Exon: 3487..3261
Exon: 3188..2997
Exon: 1663..1001
Start ATG: 6383 (Reverse strand: CAT)

Transcript No. : CT29768
ATGGACTTAATCGAGCAGGAGTCCCGCCTGGAATTCCTGCCCGGAGCCGAGGAGGAAGCAGAATTTGAGCGTCTATACGCGGCTCCCGCTGAGATTGTGGCCCTGTTGTCCA
TTTTCTATGGGGGAATCAGTATCGTGGCCGTCATTGGCAACACTTTGGTCATCTGGGTGGTGGCCACGACCAGGCAAATGCGGACCGTGACAAATATGTATATCGCTAATTT
GGCTTTTGCCGATGTGATTATTGGCCTCTTCTGCATACCATTTCAGTTCCAGGCTGCCCTGCTGCAGAGTTGGAACCTGCCGTGGTTCATGTGCAGCTTCTGCCCCTTCGTC
CAGGCCCTGAGTGTAAATGTCTCGGTATTCACGCTGACCGCCATTGCAATCGATCGGCATAGGGCCATCATTAATCCACTTAGGGCACGTCCCACCAAGTTCGTATCGAAGT
TCATAATTGGTGGAATTTGGATGCTGGCCCTGCTATTTGCGGTGCCCTTTGCCATTGCCTTTCGTGTGGAGGAGTTGACCGAAAGATTTCGCGAGAACAATGAGACCTACAA
TGTGACGCGGCCATTCTGCATGAACAAGAACCTATCCGATGATCAATTGCAATCCTTTCGCTACACCCTGGTTTTTGTGCAGTATCTGGTTCCATTCTGTGTCATCAGCTTT
GTCTACATCCAGATGGCCGGTACGATTGTGGGGCACACGTGCTCCTGGTAACGCACAGGATTCACGGGACATAACGCTGTTGAAAAACAAGAAGAAGGTCATCAAAATGCTGA
TTATCGTGGTCATTATCTTTGGACTCTGCTGGCTGCCACTGCAGCTCTATAATATTCTGTATGTCACGATACCGGAAATCAACGACTACCACTTCATTAGCATCGTCTGGTT
TTGCTGCGATTGGCTGGCCATGAGCAATAGCTGCTACAATCCCTTTATTTATGGCATCTACAATGAAAAATTTAAGCGGGAATTCAACAAGCGATTTGCGGCCTGTTTCTGC
AAGTTCAAGACGAGCATGGACGCCCACGAAAGGACCTTTTCGATGCACACCCGCGCCAGCTCCATAAGGTCAACCTACGCCAACTCCTCGATGCGAATCCGGAGTAATCTCT
TTGGTCCGGCGCGTGGTGGTGTCAACAATGGGAAGCCGGGCTTGCATATGCCGCGGGTGCATGGATCCGGTGCTAACAGCGGCATTTACAACGGAAGTAGTGGGCAGAACAA
CAATGTCAATGGCCAACATCATCAGCATCAAAGCGTGGTTACCTTTGCGGCCACTCCGGGTGTTTCGGCACCAGGTGTTGGCGTTGCAATGCCGCCGTGGCGGCGAAACAAC
TTCAAACCTCTGCATCCGAACGTAATCGAATGCGAGGACGACGCTGGCACTCATGGAGCTGCCATCAACCACGCCCCCCAGCGAGGAGTTGGCATCCGGGGCCGGAGTCCAGT
TGGCCCTGCTAAGCAGGGAGAGCTCCAGCTGCATTTGCGAACAGGAATTTGGCAGCCAAACCGAATGCGATGGCACCTGCATACTCAGCGAGGTGTCGCGAGTCCACCTGCC
CGGCTCGCAGGCGAAGGACAAGGATGCGGGCAAGTCCTTGTGGCAACCACTTTAA
(SEQ ID NO: 119)

Start ATG: 1 (Reverse strand: CAT)

MDLIEQESRLEFLPGAEEEAEFERLYAAPAEIVALLSIFYGGISIVAVIGNTLVIWVVATTRQMRTVTNMYIANLAFADVIIGLFCIPFQFQAALLQSWNLPWFMCSFCPFV
QALSVNVSVFTLTAIAIDRHRAIINPLRARPTKFVSKFIIGGIWMLALLFAVPFAIAFRVEELTERFRENNETYNVTRPFCMNKNLSDDQLQSFRYTLVFVQYLVPFCVISF
VYIQMAVRLWGTRAPGNAQDSRDITLLKNKKKVIKMLIIVVIIFGLCWLPLQLYNILYVTIPEINDYHFISIVWFCCDWLAMSNSCYNPFIYGIYNEKFKREFNKRFAACFC
KFKTSMDAHERTFSMHTRASSIRSTYANSSMRIRSNLFGPARGGVNNGKPGLHMPRVHGSGANSGIYNGSSGQNNNVNGQHHQHQSVVTFAATPGVSAPGVGVAMPPWRRNN
FKPLHPNVIECEDDVALMELPSTTPPSEELASGAGVQLALLSRESSSCICEQEFGSQTECDGTCILSEVSRVHLPGSQAKDKDAGKSLWQPL*
(SEQ ID NO: 120)

Name: Tachykinin receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384568
AGTGGAAATTTCGAAATTGAAATGGACCCTTTCCGCCGAAAAATCGATTGATTTTCAATTTCCCCTCTGCGCTTTCTTGTTTTGCTAAGTTTGAAAGTTATTTGCTTTAACT
CATGCTGAAAGAAAAATATCAGTTGACTAGCCGCTTTTTAACCTTTTATTCGAATTTTATCCTTAGTTGTTGCACAAAAGAGTCTATGTGCTTAGTTGATGATATCAGTCGAT
ATCTCTTTAATTGGCCAATAACTGCTGAATATGTGGCAGCACAATATAGTTACGAAAGTAATCGGCTTAAGAGCCCACACTGCGATGTGCATTTTAGTGCATTAAAAGGACT
TGCAATGCACTACTGTCTAATCCAGATTACGACGACAGCCAATGGCTTTAAGCGCAAGTATTTTAAAACTGAATTGTGAGCCGTGATTCCAGCTGGAGTTAAATAGGAAAAC
TGTTGGGCTTAAAGCAGCTGTAGTGGCAAATACCAATCGAGCATGGCTTCAAATCACGTTCATTTCGTTCCACATGACATGACATCATGGCAATGGTATCAAAGTGCACACT
TGTAGACACAGAAGCCTCGGGTTTGCTTAAATTTTTATGGCCTCAACACTTACCAGGTGCACAGCTTTTCTTGCCAGCTACTGGATGTTCAGTAGCAGGGAAATCGACAGCT
GGAAGCTCGAGTATCAAGAAATGAATGAAAATGGGTTACCACTCTCTTTGTTGCAGACAAATTTCTCCTTTTAATTGAAGGCAAAAAGGGATATATATTTTA
AATAGTTGGCTTCTGACAGAGACTTACATGCGAAAATAAAAAATTTAGTATTAATTAAATCGACTCGCTGGGAAGTATTGTCTTATTTTATATTAGAATTTTTAAATTTTAA
TTTAGGGACCTATACATAATGGCAATCAATTAGCATAAAATATAACGTTATTAATACATTGGTCCTGGACCTTTGTTCGTCGGGGAATACGTATTTTAGTATATCTACTGAT
GTGATCTGCTGTTGTAGTTGGTGGATGAGGTGGTCATCGACTGGAGCTCAGTGGTGCGCTTTTGGACATCCAGCTCCATCTTGGTGGGGCAAATCAGACCCCACCCACAGCCG
ACGGTTCGTGGAGTCCAAGAGGACAAAGTAAATGAACATCACAAATCCCTGCATAGTGGCCGTGATGCAGAAGAGGTATGAAAAAGCCACACCTGCCTGCATGAAGGCGAAT

FIGURE SHEET 55

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ATTCCAAAGATCCAGGTAAGACCCAGCAAAAAGAAGAGCATTATGGAGAGTCGGATCTGCTTAACCACCATTTTCTTTTCGTTTTTATGGATGCTCTGGCTCAAAGAGTGCG
AGATGCTGTAGAAAACATACACGAATATCACCAAGTTGCACACAGTAATCAAGGTCACAGGGAGCACCACCCCAAAAATGAGACCATAGCCCGATGGATAGCAGATGCCAGT
GTCCGTGGAAAGTTGGGCAGCCGAGGGGACGTACGAATCGGGATCTATAAGGGCCACCAGCAGGGTGGGGACCAAGGGCAGTAGCCAGGCCACAATGGCGGCCTTCAGGATA
TAGCGAGGTGGTCTCTCGATTCCGATAACTGTGACGTAACGCTGGAACTGCAGGAAGGCCGATGATTAGCATCCAACTGAAGAGAACCAGAATGGAGTACTGCATGGCAGCGC
CCAGAGCCACACAGCGAACTGTGTTTCCATTCACAACAAGCGCTTCGGATACATCATCTGTATTGAGAAACACGAAGAGCATCATCTGGAGACACATAGCCAGGCAAAGGTG
CAGTAAGACCTTCGTGGAGGCCTGACTGCGCCAGCTTTTGAAGAGTGCGGCAGTGAGGAATATTCCCAGTATACCCAAAAGGGAAAGACTGCAGCCCACTATCGAGATAATG
TCCAGCACTTTCTCATTAATCGGAGTAATTAGAATCTCCTCGCCAAGGTCGTTGGCTCGATAGCTTCCACCCACCAGGAATGCAAACTGTGTGAGGTGGTTAGTGTGGCACT
CGATGATGGCATCCTTCAAGAGGTCCGAACTGCTTTCAGTGCTTACTCCCTCAGTTGACCAGGTTTCATAGTTCCAATATCCGCATCCACTCCCAATGCTAAAGGCCTTTGA
ATCCGGATTGCGAAGATTTTTCATTACGCAGAAGAAAGGGCAGTGGCAGAGAGAGATAATTGCCTATTTAATGGAAGGGTATTCAAATTAGTTCGAGTATTCGAAAACAAATT
TTCATGCGTTTCTTACTTCTCAGTCCTGGTATTGAAATGGAGATTACTTTGCTGCGCGGCTTACGAGTGCGTTGCAATGAGGTTTCCACGAACAGAGCATCGTGGGCATAGA
CTTTAAAGATGAGATAGGTTGCTCCCCTGCTTTTCACTTGCCGCCAGAGATTCTCCGGCAAAAATGCAGCTGTCTCCAGATTAGATTCCTCCTTGACCTTAGCCAAGTCTTC
GGAGAATCGAATGAAGCGGTACCAGAAGCCACTGGCGGAAGTCTTTCGTTGATCCCCTGGCGCAGAGAATATAGCTAATCCAGTTATGCGATCGCATTCGGGGTTGGCGAAG
AACACGCTGATATTGCCGGTAATCAGAGCTTGGACACCGATATCTGAGAAGTTGTACGTTTCCACTCCAGTAGTGGCCGTTTCTGCTTCATCACTGGTCGGCTTGGCCACCA
CCTTGCCGCATCTGTCCTTGGGAACCAGTTGCTCCGGAAGAGCATCCATGTAGCTTTCGAACTGGCTGAGCAGGGAATTGGTAGCGTTGAGCTGAGCTGATAATCTAAGAAC
CTTACTGTCGCAGGACATTATCTCCTTGCAGACACTGACCAAGTCCACACTGACCGTGGCATCCTTGTCCTGCTGCATCAGGGCGCCGAACATTGTCCGGTCATGTGAACA
CATGCAGGCTATTCAAGTCACCGCTGATCGTGTGCTCCCTGAATCGCCTCAAACACACCACCGGGATCCCAGTGTTCGGTGGACTCCCAGTTGGCTCGGTTGTCCTTCACTCT
GCACTCCCTGGTGACCGGCATTCCGTTTCGCAGAAGGCAAACATCGTGCAGGGTGGCACGTTCGCCGATTCTAGCCCGTTTCCACTTGTTCTGGTGAGGTGTTTGATCGTGG
TTACGCGTTATGTAGTCGTGCTGAAACTCCTCCGGCTCGCAGAACATGGACGTACAGTAAACCAGATGTGTTTGCATAAGTTCGTCCGATGAATTACGTTCCTCTCCATCAC
AGTACTGAAACGTTCCGTTTCTCAAGCACATTTGATTTTCCTTTGGGCAGGCGGAATAAATCGGCGAAACCAAGGCCAAGACCACAAAGAGCCCAGCACACCAGTTGAAATT
CATGGCGATGAATCAGGTGCCACAGCTGTTTGCAGCTCTCCGAAAATGTTTACAAATTCTTTGGCAGATAGTACTTTTCACGTCCGACGTTCTTGAAATATCGCGGCACACT
GAGCTGTCTGTCGATCGATTAGATTTCTGTAGACCCCTTCTTCATGGTGTTTGCTATCAGTTGCCACCACGAGCGCTAATCGACCCCCGTTTTTTGTATATCTACACACTAC
TCACAAAAAGACCTCAAGTCTGCGGCATTTGATACAATTTACATTGTGATTAACACGACCACGGCAATTGAAGGCGAATCCGACGGAACCCTTTGAGGCAGGGAAGTAACAC
CAAACTTGTGACGTCGTCTTTATTTGTGCAAATAGCGATTTCACGCCCTTTTTACCGGTCTTGGTACTTAAAATGCTCTGGCTGATTCATTTTTTACGCGCTTGAATTGCCAG
ATAAGAAGTTCTTACCAGGAAACACGGCTGTACATGGGCTATTTATACATCAAATAATGTTAAAAAAAATTTAAAAACTTTAAAAACTAGTTTTATTTGCAT
CCGTTCAAGAAAGAGATTTTTTTTAGATTTGTTTGATCAATTCATTGCTATGGCTTCTAATAAATGTGAAATGTGAAACACCTTCACATAAAAAAGTATTTACGCAATTCAC
TCAAGCAAAACAGATCCTTTGTCCTTGAAAAAAGTTATGAAATGCAAAGCACTTCACCTTGGTTGCATAAAGTGCGATTTTCATTTTGACAGGCTACGCGTTTTCAAAGACT
CAGCCTTCGATTATAATCCACCTGTACTCACTTCATTGTAAGCCAGTTTTTGGGCCAAAAAGTAATTTTTACAGCCGACTTCGCAGCACGTAGACTGCGTGTGCTAGCGGAA
ATTGTTAGCTTGTTGACACGTTT
(SEQ ID NO: 121)
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Exon: 3391..2257
Exon: 2190..1001
Start ATG: 3391 (Reverse strand: CAT)

Transcript No. : CT31591
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ATGTGCTTGAGAAACGGAACGTTTCAGTACTGTGATGGAGAGGAACGTAATTCATCGGACGAACTTATGCAAACACATCTGGTTTACTGTACGTCCATGTTCTGCGAGCCGG
AGGAGTTTCAGCACGACTACATAACGCGTAACCACGATCAAACACCTCACCAGAACAAGTGGAAACGGGCTAGAATCGGCGAACGTGCCACCCTGCACGATGTTTGCCTTCT
GCGAAACGGAATGCCGGTCACCAGGGAGTGCAGAGTGAAGGACAACCGAGCCAACTGGGAGTCCACCGAACACTGGGATCCCGTGGTGTGTTTGAGGCGATTCAGGGAGCAC
ACGATCAGCGGTGACTTGAATAGCCTGCATGACGACGTTCTCGAGGGCAGGAGGCGCACCAATGACACCCAGGGGCGTCGTGAGATGACTGGCATAATGAGGAACATGTTCC
GACAGAGAGGTGGGAATCTTCTACCCGCCGATGTTCACATGACCGGACAAATGTTCGGCGCCTGATGCAGCAGGACAAGGATGCCACGGTCAGTGTGGACTTGGTCAGTGT
CTGCAAGGAGATAATGTCCTGCGACAGTAAGGTTCTTAGATTATCAGCTCAGCTCAACGCTACCAATTCCCTGCTCAGCCAGTTCGAAAGCTAACTGGATGCTCTTCCGGAG
CAACTGGTTCCCAAGGACAGATGCGGCAAGGTGGTGGGCCAAGCCGACCAGTGATGAAGCAGAAACGGCCACTACTGGAGTGGAAACGTACAACTTCTCAGATATCGGTGTCC
AAGCTCTGATTACCGGCAATATCAGCGTGTTCTTCGCCAACCCCGAATGCGATCGCATAACTGGATTAGCTATATTCTCTGCGCCAGGGGATCAACGAAAGACTTCCGCCAG
TGGCTTCTGGTACCGCTTCATTCGATTCTCCGAAGACTTGGCTAAGGTCAAGGAGGAATCTAATCTGGAGACAGCTGCATTTTTGCCGGAGAATCTCTGGCGGCAAGTGAAA
AGCAGGGGAGCAACCTATCTCATCTTTAAAGTCTATGCCCACGATGCTCTGTTCGTGGAAACCTCATTGCAACGCACTCGTAAGCCGCGCAGCAAAGTAATCTCCATTTCAA
TACCAGGACTGAGAAGCAATTATCTCTCTCTGCCACTGCCCTTTCTTCTGCGTAATGAAAATCTTCGCAATCCGGATTCAAAGGCCTTTAGCATTGGGAGTGGATGCGGATA
TTGGAACTATGAAACCTGGTCAACTGAGGGAGTAAGCACTGAAAGCAGTTCGGACCTCTTGAAGGATGCCATCATCGAGTGCCACACTAACCACCTCACACAGTTTGCATTC
CTGGTGGGTGGAAGCTATCGAGCCAACGACCTTGGCGAGGAGATTCTAATTACTCCGATTAATGAGAAAGTGCTGGACATTATCTCGATAGTGGGCTGCAGTCTTTCCCTTT
TGGGTATACTGGGGAATATTCCTCACGATGTTCTTCAAAAGCTGGCGCAGTGATGCTCAGGCCTCCACGAAGGTCTTACTGCACCTTTGCCTGGCTATGTGTCTCCAGATGATGCT
CTTCGTGTTTCTCAATACAGATGATGTATCCGAAGCGCTTGTTGTGAATGGAAACACAGTTCGCTGTGTGGCTCTGGGCGCTGCCATGCAGTACTCCATTCTGGTTCTCTTC
AGTTGGATGCTAATCATCGGCCTTCCTGCAGTTCCAGCGTTACGTCACAGTTATCGGAATCGAGAGACCACCTCGCTATATCCTGAAGGCCGCCATTGTGGCCTGGCTACTGC
CCTTGGTCCCCACCCTGCTGGTGGCCCTTATAGATCCCGATTCGTACGTCCCCTCGGCTGCCCAACTTTCCACGGACACTGGCATCTGCTATCCATCGGGCTATGGTCTCAT
TTTTGGGGTGGTGCTCCCTGACCTTGATTACTGTGTGCAACTTGGTGATATTCGTGTATGTTTTCTACAGCATCTCGCACAGCCTTTGAGCCAGAGCATCCATAAAAACGAA
AAGAAAATGGTGGTTAAGCAGATCCGACTCTCCATAATGCTCTTCTTTTTGCTGGGTCTTACCTGGATCTTTGGAATATTCGCCTTCATGCAGGCAGGTGTGGCTTTTTCAT
ACCTCTTCTGCATCACGGCCACTATGCAGGGATTTGTGATGTTCATTTACTTTGTCCTCTTGGACTCCACGAACCGTCGGCTGTGGGTGGGTCTGATTTGCCCCACCAAGAT
GGAGCTGGATGTCCAAAAGCGCACCACTGAGCTCCAGTCGATGACCACCTCATCCACCAACTACAACAGCAGATCACATCAGTAG
(SEQ ID NO: 122)
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Start ATG: 1 (Reverse strand: CAT)

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MCLRNGTFQYCDGEERNSSDELMQTHLVYCTSMFCEPEEFQHDYITRNHDQTPHQNKWKRARIGERATLHDVCLLRNGMPVTRECRVKDNRANWESTEHWDPVVCLRRFREH
TISGDLNSLHDDVLEGRRRTNDTQGRREMTGIMRNMFRQRGGNLLPADVHMTGQMFGALMQQDKDATVSVDLVSVCKEIMSCDSKVLRLSAQLNATNSLLSQFESYMDALPE
QLVPKDRCGKVVAKPTSDEAETATTGVETYNFSDIGVQALITGNISVFFANPECDRITGLAIFSAPGDQRKTSASGFWYRFIRFSEDLAKVKEESNLETAAFLPENLWRQVK
SRGATYLIFKVYAHDALFVETSLQRTRKPRSKVISISIPGLRSNYLSLPLPFLLRNENLRNPDSKAFSIGSGCGYWNYETWSTEGVSTESSSDLLKDAIIECHTNHLTQFAF
LVGGSYRANDLGEEILITPINEKVLDIISIVGCSLSLLGILGIFLTAALFKSWRSQASTKVLLHLCLAMCLQMMLFVFLNTDDVSEALVVNGNTVRCVALGAAMQYSILVLF
SWMLIIAFLQFQRYVTVIGIERPPRYILKAAIVAWLLPLVPTLLVALIDPDSYVPSAAQLSTDTGICYPSGYGLIFGVVLPVTLITVCNLVIFVYVFYSISHSLSQSIHKNE
KKMVVKQIRLSIMLFFLLGLTWIFGIFAFMQAGVAFSYLFCITATMQGFVMFIYFVLLDSTNRRLWVGLICPTKMELDVQKRTTELQSMTTSSTNYNSRSHQ*
(SEQ ID NO: 123)
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Name: HE6 Receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384531

FIGURE SHEET 56

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GTGTTAATCCCCTTGGCTTATCGGTTTAATCTATTTATAAAATCAATTCAAACATAAAGCGGCGCATATCTCAGCGATGTTGGGTAGGTAACCAAAAGTAAATACACTCTAA
TTCCTATTGATCTTGTATAAATACGAGTGGATAGTTAGTTAGATATCACCATTTTGCACCGTGCATAAACATAAAGTGAGATACTCGTTTTCGAGAGATGCACTTCTGAGTA
CCCGTATTCAAATCGTACTCTCAGTAGCCAAGTACTCAGTACTCAAGCTGTTTGTCTTACGGGTGTGGACGTGCGAGCAGACACTTTAGGAGTGGGATAGCCGGAGCAGACC
GGCTGAAGTGTCATCCGATCGAAGGTCGCCTCAACAGCACAGCGATTTCGATTCCGATTCCAAATCCGATTCTTTGGCCATAGGAATTCCTCTGGGAGGTGGAGCATGTGGC
TGATTTATTTATTTCGAGCGATATAAACAGAGCAATACGAGAATGGGCGAATATAAGTTTGCTCGAACGGCTGGTCCGTTCCGAGCTGAAATTGAATTGTAAATGGCCATAT
TAATTGGGAATCATTTAAAATTTCCAATGATTTTTTCTGTGTTTTGGTGTCGGCAGTCTATGCATGTTCGGTGGCATAATTTATGGGCGCTAATTACTATCGCCCCATTTTG
TGTATTTCGCGTGCTGTCCAAGGCCAATTACGCTTACTTATTGCAATTTATGTGGCCACAGTCCGGCCGTAATTGGAAATTGTGTAAGGTCGCAGGCAATTTCATTATTTGT
ATGCACTTCTGGACGCTCCGGTTGCCGGGTCTAGCATTTTTCTAGCATTTTTTCTAATGACGCCAGCGCGTTTGGGGACGGACGTTACCTAGCCCAGTTTTCCCTTTGCAGCCA
TTTGATTAAGTGACCTACGTTTCGCCCACACAGAATCATCAATTTGTTCATGTCGCCGACGGTGCGAATAAGGTCCAACCTAAGTGAGTGAGCTATCCGCCGGCATGGCGGC
GTTGGAACATCCGGATGCCATGCTGCCATACTCCAAATTGTTGTCAACAGCCCTCACTGTGGCCAGTGGTAACTCGAACTCCTCCGATGGTACTTTGCTGCTCATCCAGACC
AGTGCGGCACCAGGTGGCGATGTGATGGCCACCGGAGCCGGAGCCGGAAAGTTGGGTGTGCCCTCGATGAACTCGTACCTGGTGAGCATGGCGTGGCCCAAGTCGCTGGCAG
CTTGGCCATCACCGACTGGCTGGTCGGTCGGCCACCTGCGTGATGCCTCCATCGGTGGTGCTCTACATAACAGGTGAGAATGGCAGCGGAGGCCTGTCCATCGCATCGATGGCCA
AAGATTTTATGGCTCTGTGGGGGCTTTACACTTCCGGGGAAGGTGGAATCGGGGCAAGTGTTTACTATTCGAAGCCCTCCGGTGGAAGTTCGGGTAGTAAACATTTGCCCAAA
TCGATGGGGGAGCACATTGGTCGATTTCGATTTAAAATAATCCCACAGCGGAAATTATAAAATTTCTCCGTTGGCAAAATATACATATTTTTGATTGCAAAATATCTTGTG
AGTGGTGTGCGAGTGTTTTATGGGTTTCGCTGGAAAACCTTTGATAATTTTTTCTGGAATCTATATTTTTAGCAGAATTTTGAATAAAGCATAACAACATTAGTGGTTAAAA
ATTTTGTATAATTTAGTAATTTTAAATAAATTATGTATCTTTAATAATTAACATCTCTTATTTAACGCATTTCATAAATGTATAAAAAGCAATCAAACATGTGATCTTTTCG
AAGCCAAATGAATATACAAAGTTTAATATTCCTTGTCATAACTTGAACAATACAAAGAAGAATTTATAGTGGTTTAAATTGAAGGATCTGCCAGTGTAATGCCTCCTTAATC
CCGGCCAGGTGCACAAACCGATTGAAGCACGGCGACAAATATTTGTTCTTTGCAGGCACTTGGCGCTTTGGCTGGATACTGTGCGACATTTGGATCTCGCTGGACATCCTGC
TCTGCAGCGGCTCCATCCTCAGCCTGTGCGCCATCAGTCTGGACAGGTGAGTTGGCCAACTAATTTCGTAATTTGCCGTTGATGTCATAGCAATGACCACAGTCCATAGCCC
GTTGTCCACGGTCCTCGGTCCTTAGATAAAGTCATGGCAAGGTGCAAAAACAGTGCAAATAATTTATTTGTTGACGTTTTTATTGCCGCATGACCGTTGTCCTGGCCATTCC
CAGTGCATATCCTTTGAGTGTGCGACGCCCACAATGGCAAGGATTGGGTTGGGCTTGGATTCCCATTCACCCATTCCCTATTTCCCCATTTCCTCCATTTAGCCATCCCCACCG
TTTGCTTTTGTTGGAAGTTTCAATTACATTTTAATGGCATTTCCAAGTTTTGTGTTGTGGCTCCCGAGTTGAGCTGATCCAGCTGAGCCATGGAGCCATGGACCTGAACCTC
AACCAGGACAAACACCGACGCCCACTGGCGTTGTGTGTGCCTTTTGGCCTGGCCAGAAAGCCGTCTGCGGCTTTGCGAACAATATGTCCGCTTGGCTTTTGTTTTTTCCAG
GACGTACTCCAAGAAGCGCCGATCCAAGCGACTGGCCCTCCTCATGATTCTCGTCGTGTGGATAACTGCCCTGTCAATCACATGTCCACCCTATTTGGGCTGGTAAGTTAGC
GCCAGCTGCACGGGAGAACAAAATCAACCTTAACCCATGATGGATCGCCTATTCATCTGTTAAGAAAACCATTCATGTTATAATCATTTAATTGAACGCATTAAATTGGGTTG
GGAGTACAGGCAACATGTGATAATGATCAGTATCCAAAGGAAGAAAAATAATATATTTAATATCATATAATATTATTAATAATATTATATTATAAATATGGCCAAGATAAAT
TTATTTGTAGTGCTCTATTAAGTTTATAGATATATATTTTTTTGAATTTTGTAATATTATTTTCACTCTTTCCCGTGTAATTCGAAATATTATATGTAATATTTTTATTGAG
CACCCATTTTTTTTTACCAAATTTGTCCTTCCGGAGGCGTGACAATACTTTGTGGCTTTTGTGGCTGAAAGTCCTGCTCGCTTTTTTTTTTCTTTTTTGAGCTAATGGCT
GTGCGGTGGCGCAGCATAGATAATGTGCTACAAAAGGGTCTCGAAATACACACGTTTATTTATATTATATTTGCGCCTTTGGCTGCGCCTAAAAAACATTACGTAATTGACG
ACGGGTTGTTGCTGTTGCTGCTGGTCGTGCAGCCATTACATTGAAGTTTTAATGAGTTGTTAATGACTTTGTTTGCCGCGGCGCATTTGCTTTGTTCTCACCTACGCACACA
CACTCAGCGCGAAAGCCGCACACTTGTGTGTTGCATACTTCCAGGCGCCCAAATTAACCAGCACTCACTCACACACACACTCGCACTCACTCACACACACACCACAAAGCCAGCAT
GTCCTTAATGCCATTGGCCATGGCTTAGTTTTGGCCCCCTTTGGCTGAAAGCGAAGAGCATTGCTTTAAAGGGCACATTAAAACGGTCTGAGGCCGAATTACAGCCACAGCTG
CAGGACATTGGAAAATTTGGAAAATTTGGCGCTGGGGGAAAATCGCCAATTATAAGCGCCAGCAGATGGCGCCACTTACATATTTTCATTCTTTAAGCGGACTAGTTTTATGA
AAAAAGTTTGCAAATGCAGCGGTTGCAACAACTGTTTGTTTTACTCACAATCTGTTATTTGTTATTGCCTAATGAATACTAAACTGATTGTGTTTGCTTGCTATTTAAATTT
AGATTTAAACTTTTGGCTAATTGATTTAAGCATTGTTTATTTAGTTCATTTTTTAAATTTAACTAATGCATAGCTAATGTATTAAATTGCCCTCAATTTCGGATTGAATAATTA
ATGTTAAACAAGAAGTTTAGTAGGAAAATCGGCTATTTCCATTCGGGTCTTGTAAATACCAACCTTAACAAAGTTGCATTTGTACAATTATACTGTCAGGTTATTTTGGTAT
CGGGTAGCAGTAATTACCGTGAGTTTTTGGATAACACATACTTGGGGTAACAAGCAGCTAGTTTAGTTGAATTACAACACCGGAAAATTCCATTGACAGTAGTGACAATGAG
GCAATAAACTTTTTGAAAGAGAAACATTATAGGAAACTGTGTATCCAGTGGGCGTGCCCCAAACTTTGGTTGGCATATTTGTAAAAATTGGCCATCCAAAAAATAAATCAAA
ACAACTGGCAATCATTTTATAATCGTGTGGGCGTGAGTCTTTTAGGCGATTGGGGGGCTTTAGAGTGGGCGTGGTAATGTTCTGAAATAAGCTTGTTCCCGAGATTTGGACT
CCGGGGGACAAATGGACATAACCGAATCAGAGATATATATACTTCATGCTTCGTCTGCTACATTCAGTGAACCTAGTATTCCTCTAAGAATAGTGGGTACAATAACCCA
GTATGAACTGGAAGAAGCTGAATCTTGCCACCTACAGTGGATGTATGTGACAATTTGCCCATTTTTTTTACTCAATTCCCCACAGCACACGGGTGTACCTTTAGTTGACACA
TTTGGTGTACGCCACCACATTACTCTGTTGTCTCGGAATCGTTTTCTTCCGCATATTGATTTAAAGTCAGCTCCGATTTGTACTGCCTGAATGACCAACACACTGCGATGTG
CATAAGTAAAAGGCTTACAGGTGGGACTACTCTGACTGGCTTAGGTTTAGGATTTGAATTCGAATTTCGCCCGGCTTAACTCAGCCAGTTGTCATTCCCCAAGTCCCAGTTC
CCCAGCCGCAATCACAACCGCAAGAGCCACCAAACCAGAGCAGGTACCAGGTACCTCCCACATCCACCATCTCCACATCCTTCCAACCCGCAAACCGCATTCAACTTCGAAC
TGGAATTCAATTTGCCATTCACATCCACATTCGCCAGGTACGAGGTCGGTCGGCACCAGGCGGAGTTCGTGGACTGCCGCTCAACCAAAACAAGGGCTACGTGGTCTTCTCG
GCGATGGGATCGTTCTTCATTCCCCTCACCGTGATGCTCTACGTTTACGTGAAGATTGGTTATGTCCTCACGTCACGGCGACAGCGCATTGTGCGCGATGCGGTAAGCTACA
TCTCCAGCTCCATCACTATATAAGCATATATGTATGTGTCCACCACTTTGGTGTCCCCTGAAATGTGTCCGGAAATTTATCATGTCACACCTAACACATCTAACCAGCTAAC
CAGGGGACTAAGTTGTCAGGCACTGGGGGAAAAAGATCCAGGAGTGCGCTCAACACTTCAAGTGCAGATCTTCATTAAGTTGGGATACCCACTCGGGTATCCCACTTGAGTACC
AGCCACTTATCGCACAGTACTGCAGGTGATATTTTAAGTGCTGAGCTTTGATAACAGAAGTCCAACTAATATATCTAATCACAAATTAAATTTGCTGTGAATTCTTGGATGT
AAACTGAATGAATTATCTTTTGTTTGTTAGCATGAAAAATGAACTTCAGTGTCAATAAATGAAATGAAAATGCAATAAGAACACTTTTTGAATATTTAAAAAGAGTGCATAG
TAGTTGATAAATATATTCTTTTAGTTTAGTACTAATTGAACGTTTGCTGCCAAGAGCAAGTGAAGTAAATTGTAGAAAGTAGGTGACGTGAAATGGAACGAAGTAATTACAG
CAATCCAAATCCCGAATCTCTATGCCCTGACATGCAATCTAAATTATTCCTCACGTTTTGTCAGTGCTCTGCTTACATATTCCTCTTCTATTATGTCCTTCTATTATGCCAACAGTACT
CGGAGCGCACGGCAGACTACGATGTGGATGGGGACAACTTCATCTCGGAGTCGGAGCACTATCATTGCACGCCAACCAAGTGGCTGCCGAACAGGAAGTCCCGCTGGAGGTT
CAACTCCCTGCACGACCCCACCACCCAGCGCCGCCACGAATGCAGCAGCGAAGGGACACCAGTCGTCCGTCAAGTGCTCCAAGTGCTCCAAGTGCTCCTCTGCCACTGGAACT
GCTGGAGCTGGAGCTGGAGCTGGTGTGGTAGACAAAACGCTGACGTTCAAACATCAGCCCACCTTTTACGAGCTGGTCGAGGTGTCGCGTCTCTCGTCGCTCATTCACTGCT
CGGCAATTAGCTGCAAGTATGGAGGACCCTGCATGCACTCCACGCCCTCGGGCATGCACTACGTTGGCACGGAGGGCTCCTTCTCGGACACCTGCCTGGGTGGCAATGTGAG
CAACAACACCACCACCACCACCAACACCGTCGCACTGGAAAACCAACGAGAAACTGGAGGCGGAGGCCAAGCAAAAGCAACAGCAGCAACGATCCTCCTTCGACCACCAT
CACCCGCATGCACACCATCATGGCTCCCATGGCCCAGCAGAGCCATCACAATCATCACCATCGCATGCCGATGCGAGTTTCGACCACGAAACGTGATAGCAAGACGCCAAGA
CCCTGACTATTGTGATGGGCGGCCTAATTGCTTGCTGGCTGCCCTTCTTCGTCTATTATCTGCTGATACCCTTCCTGCCGCGACCCGCCGTCCTCGAGGACCTCATGTTCGG
CTTCACCTGGATTGGCTGGGTCAACTGCGCCATCAACCCGTTCATCTACGCCTTCTACAATCCGGACTTTCGCACTGCCTTCTGGCGGCTCACCTGTCGCCCCATTTGCAAG
CAGAAGCGTCCGCCCAACCACCTGGCCATGTTCCCAGGTGCTAGTTTCCGGATGCAGATGCAGTTGCGGATGCGGATCCGGATCCGGAGACCGGAACCGGATTTCCGAATCACTGAGCACTT
GAGTGTGTGTCATAGTGCCGCCATCTCCAGTCGCACAATCGACGCTCACTTGGGTGGTGGGGGAAATATCTCAGGCATATCCTTAACTTTTCGCCGTGCTGGTTCACCAACT
TCTATGTAATTAGCATAAAAAATAAGTGGAGAAACTACCAACTCGCATTTCGATCTTTTTGAAGTACAAGTTATGCCAATGCAAGGACATCAAATTGACTCTAGACTACAGT
ACAGATAGTAAATAAAAAAGAATTTAAGGAGTATTAACTACAATAGATAAGCTGTTTGAGAAATGCACTATCTCTTATATTTAAATCAATTGAAGATAATGAAAATCAAATAT
TAGCTTAACAAAACTGCTGAATTTAATTCAAGTTTATTTCATGAAAACAAATATATAAAGATTTATCACACATGTCCCTCCAAAAATTGTAACTAATATTT
TGGCAAACGAAGCCAATGGAGGGACCTTTTGGCCAACTCGTCGCCACTAGCTCACCAACTAAGTATTCATTTGCCAGGCACTATAAGCTGTTTGCCGCCACTCTATCTGCATC
GTTTATGCCAAACGCAGCTAGTAAAACTAAGACTACTTATGGTCAATATTGATTGGAGCAAAGATTGCCTTGTTAAACCCAAAAAATCGACTGCCTTTTGAAGCTTCAAAAGC
CGCATTTCGAGCAGCATCTTAAAGGTCACTTTTACGGTCGCAATTTTTTTTTTTTTAAGACTCACTGGACTTGGCCGGAAGTTGAGATTCTTGCCTAGACCAGATCCAAATCCT
ATATATAGTATTTTCCTGTGTGTGAGCGTTGATTGTGCGAGGCGAGCGGCACGAAGCGAAACGTAACGAAACAAAAGACAAATTATAGTATTTGCGAGTCTTTGTTGCCTGA
CGGCAACTGTTGGCCATCGGGATGAGTGGGATGA
(SEQ ID NO: 124)
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Exon: 1001..1412
Exon: 2072..2174

FIGURE SHEET 57

Exon: 2777..2902
Exon: 5189..5366
Exon: 6045..6491
Exon: 6549..6986
Start ATG: 1001

Transcript No. : CT37292
ATGGCGGCGTTGGAACATCCGGATGCCATGCTGCCATACTCCAAATTGTTGTCAACAGCCCTCACTGTGGCCAGTGGTAACTCGAACTCCTCCGATGGTACTTTGCTGCTCA
TCCAGACCAGTGCGGCACCAGGTGGCGATGTGATGGCCACCGGAGCCGGAGCCGGAAAGTTGGGTGTGCCCTCGATGAACTCGTACCTGGTGAGCATGGCGTGGCCCAAGTC
GCTGGCAGTGGCCGTCTTCCTGGTCATCATCCTGGTCACCGTGGTGGGCAACACACTCGTCATCCTCGCCGTTCTGACCACACGCCGCCTGCGCACCGTAACCAACTGTTTC
GTGATGAACTTGGCCATCACCGACTGGCTGGTCGGCACCTGCGTGATGCCTCCATCGGTGGTGCTCTACATAACAGGCACTTGGCGCTTTGGCTGGATACTGTGCGACATTT
GGATCTCGCTGGACATCCTGCTCTGCAGCGGCTCCATCCTCAGCCTGTGCGCCATCAGTCTGGACAGGTATCTCGCCGTCACACAACCACTGACGTACTCCAAGAAGCGCCG
ATCCAAGCGACTGGCCCTCCTCATGATTCTCGTCGTGTGGATAACTGCCCTGTCAATCACATGTCCACCCTATTTGGGCTGGTACGAGGTCGGTCGGCACCAGGCGGAGTTC
GTGGACTGCCGCTACAACCAAAACAAGGGCTACGTGGTCTTCTCGGCGATGGGATCGTTCTTCATTCCCCTCACCGTGATGCTCTACGTTTACGTGAAGATTGGTTATGTCC
TCACGTCACGGCGACAGCGCATTGTGCGCGATGCGTACTCGGAGCGCACGGCAGACTACGATGTGGATGGGGACAACTTCATCTCGGAGTCGGAGCACTATCATTGCACGCC
AACCAAGTGGCTGCCGAACAGGAAGTCCCGCTGGAGGTTCAACTCCCTGCACGACCCACCCACCCAGCGCCGCCACGAATGCAGCAGCGAAGGGACACCAGTCGTCCGTCAAG
TGCTCCAAGTGCTCCAAGTGCTCCTCTGCCACTGGAACTGCTGGAGCTGGAGCTGGAGCTGGTGTGGTAGACAAAACGCTGACGTTCAAACATCAGCCCACCTTTTACGAGC
TGGTCGAGGTGTCGCGTCTCTCGTCGCTCATTCACTGCTCGGCAATTAGCTGCAAGTATGGAGGACCCTGCATGCACTCCACGCCCTCGGGCATGCACTACGTTGGCACGGA
GGCCTCCTTCTCGGACACCTGCCTGGGTGGCAATAAACTGGAGGCGGAGGCCAAGCAAAAGCAACAGCAGCAACGATCCTCCTTCGACCACCATCACCCGCATGCACACCAT
CATGGCTCCCATGGCCAGCAGAGCCATCACAATCATCACCATCGCATGCCGATGCGAGTTTCGACCACGAAACGTGATAGCAAGACCGCCAAGACCCTGACTATTGTGATGG
GCGGCCTAATTGCTTGCTGGCTGCCCTTCTTCGTCTATTATCTGCTGATACCCTTCCTGCCGCGACCCGCCGTCCTCGAGGACCTCATGTTCGGCTTCACCTGGATTGGCTG
GGTCAACTGCGCCATCAACCCGTTCATCTACGCCTTCTACAATCCGGACTTTCGCACTGCCTTCTGGCGGCTCACCTGTCGCCCCATTTGCAAGCAGAAGCGTCCGCCCAAC
CACCTGGCCATGTTCCGTGGCTAG
(SEQ ID NO: 125)

Start ATG: 1

MAALEHPDAMLPYSKLLSTALTVASGNSNSSDGTLLLIQTSAAPGGDVMATGAGAGKLGVPSMNSYLVSMAWPKSLAVAVFLVIILVTVVGNTLVILAVLTTRRLRTVTNCF
VMNLAITDWLVGTCVMPPSVVLYITGTWRFGWILCDIWISLDILLCSGSILSLCAISLDRYLAVTQPLTYSKKRRSKRLALLMILVVWITALSITCPPYLGWYEVGRHQAEF
VDCRYNQNKGYVVFSAMGSFFIPLTVMLYVYVKIGYVLTSRRQRIVRDAYSERTADYDVDGDNFISESEHYHCTPTKWLPNRKSRWRFNSLHDPPPSAATNAAAKGHQSSVK
CSKCSKCSSATGTAGAGAGAGVVDKTLTLTFKHQPTFYELVEVSRLSSLIHCSAISCKYGGPCMHSTPSGMHYVGTEASFSDTCLGGNKLEAEAKQKQQQQRSSFDHHHPHAHH
HGSHGQQSHHNHHHRMPMRVSTTKRDSKTAKTLTIVMGGLIACWLPFFVYYLLIPFLPRPAVLEDLMFGFTWIGWVNCAINPFIYAFYNPDFRTAFWRLTCRPICKQKRPPN
HLAMFRG*
(SEQ ID NO: 126)

Name: Octopamine receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384349
TCCATGCATTTATAATTCAACATTCGCTCGCGGCCTTATGAAAAGCTCATTTGGTTACGAGTGTCCTGGGTCCTTAAGTCCTTTCTACCTCGAAAGTGTTAATGAGCCGGCA
GGCTGCCGTAATTATGCAAATTTTTAATGACTATGAAAATGGTTTCCGCGGAGCAACAAGTGCTCGCGTCTTGGTCCTTGGATCTCTATACCCCTCATACCCCTCTAAAAAT
GCCAGCTAATTCCATTTGACCCCAGAGGCCCCAAAGCAATCCATTTGCATGGCTACCAATAGCTCGTCGCATTCGTCGTACCAACCCAACCATTTTCCATTTAATCCCTACG
ATGTGTGAGAGCTCTGTACTGAGCTTACTGCTGGCATTCGGTCTTTAGATTTATACAGATTTTGTCAAACAAAACATGAATTCGCACTTTTACACACATATGTGTGTCTGTAAA
TGACTGAAAGGGAGAGCGTCGAAAGCCGATTTGGTGCCATTCAGTTGAAGCCCTTTAGGTCGTGATTCGCATATGGTCGAGGCCATTTAAGCTGATATCAGGCACATTAAAT
GTAGTAAAGGAACGTAAGTATGATAAAGGCAGCATCACAAAAGTGTCAAGTAAATGCAAATTAACATTAATTTAAGACTTGAATTCGTCTGTACTGAAACAGTACAATTAAA
ATATAATTAGCTATATATTTGTAACTTTTAAGAACGGATACTTCTGGGACCAATGTTTTTTGAACATAACAGATATCTACCATATGAAGTGAAATAAATAGAATTTTTCGGG
ACCATTTTGTTTCCAGATTTCAAATGAAATGAAACGCATATTTTTGCCAGTTTTTGATAATAAATATCAGGGGACTTGGCCAAATTTTAATACAATCTCATTTAGAAAAATA
AAACAATTGCATGCCGATAAAATAATAAGTGATACCGAAAGAGAGCTTTTGATTAGAGTGAAATATGCTCATGCGGTTCAGTCGAGATCCAAAGTTTGCGCAGAATGCTTCT
GAATATTTTAGCTATAATTCTTGTATTCGTAATTTCAAGCCAATCGGAGGCAGTTATTCCTGGATGTGATTACTTCGACACCGTGGATATATCTCATATCCCAAAGCTAAAT
GACTCCTATGCGTACGAGGAGCTAATCATTCCTGCTCATCTCACGGGTCTATATACATTTAGGCAACTGGCGGATGGATCACAGGAGCCAGTGAAGAGTCACTTAAGAGCAT
GTATCTGCAAACTAAAACCTTGTATCCGATTCTGCTGCCCCCGCAACAAAATGATGCCGAATAGTCGCTGTAGCGATGGACTCACAGAGAATCTGAAGCGGATCAATCCCTA
CTTGAAGATCACACTGGAGGATGGAACTATAGGAAAATATTACCTTCTCACCGACATGATCGTCTTAAGATATGAGTTTCGGTATTGCGAGAAGGTTGTTTCGGTACAGGAG
GATCAAGCTACAAGCTATATGAGGTTAAGATTTCAATCTTTTTGAAGTATCTCAGTATAATTTGATATCTATAGAATGGCAGCTTTATGATTAAACCCGATGTAAACTGGACAT
TGAGCAAGCAGTGGTACTGCCTCCATCCCCGTTTGGAAGATCCGAATTCCATATGGATACTGGAACATGTATATATACCGAAGTCAATGCCAGCCGTACCTCAGGGCAAGCA
CCTACTATATCATCTAATCTCATCTCATCTAATTCTCTGATTTTTCCAGTCGGTACTATTTCCATGGTTGGTTGTATTCTCACGATTGCAGTGTATCTCTACATAAAGAAAC
TGCGAAATTTGCTTGGAAAATGTTTCATTTGCTATGTATTTTGTAAGTTTGTGCAGTACCTTATCTGGGCAGGAGGAGATTTGAACTTGTGGAATAATATTTGCTCCCTAGC
AGGTTAGTTGAATCCATATTAAAGTTTGACTTAAAATATGCGTTTATTCTAAACAGGTTACACTAACTATTTCTTTGCTTTGGCTTCTCACTTTTGGCTCTCTGTTATGAGT
CATCAAATATGGAAAAACTTGAGGTTAATCAATCGGGATGAACGTAGCTATCACTTTCTCATCTACAACATCTACGGTTGGGGCACACCTGCTATCATGACGGCAATTACAT
ATCTGGTGGATTGGGCCTGGGAGGATAGACCTGACAAACTGAATTGGATTCCCGGTGTTGGCTTATATCGATGCTGGATAAACAGTGGGTTTTAGGGTAGAGTGTTTAAGCC
AGTTTAAGACCAGTAATTGATTTTCTTTGAACAGCCTATGACTGGTCTGCTATGATATACCTATATGGACCGATGCTGATCTTGAGTTTATTCAATGTGGTCACGTTTATCC
TGACAGTAAATCACATAATGAAGATTAAGAGTAGCGTTAAGAGTTCTACCCCAACAGCAGCGAAAGTGTATACAGAATGAGTAAGCTTTAAGTATTTATAACTTACTATT
TCTAATTCCATTCTCTTACTATAGTTTTCTATTATACCTACGACTGTCGGTGATGATGGGCGTGACTGGGATTTCTGAGGTAATAACTTACTTCGTCAAGCGGCACAAATTT
TGGCGACAAGTCCTTCGGGTGCCAAATTTTTTCCATTTGGGTTCCGGTATAGTCGTATTTGTGCTATTTATTCTTAAGCGCAGCACATTCAAATGATAATGGAGAGGTAAG
AGCTTTTTGCTTAATAGATTTTAAAGTTACTATATCAATATCATTTTAGAATCAGCGGTCCGAGGAGACAACAACCTGCATCTTGATCAACCTACTAGTTTAAATAAATGCA
AATTATAGATAAGTGAGCTCTTTTTTTTTATAAGTTTAGTATAGAGCAGTCCCTCTATGGTCAATAAATGCTTATAATCTTCTTATTATTGAAAAATTCTTTATTATTGATA
TTTAATCAATAATATATTTTTATTTTTTTTTTTTTTTGTTAGAACAAAATGTCAATTGTCATCAAAAATATGTGTTTGTGAATAAAATCAAGTTCCGTAGGAAAAATATGCACT
TTTATGGAAACTCGCTTTTTCAATTAGTCCTTGCATACGCGCCAGGACCCCAAATCCTTCCCACCTTCCCCACAATCCTCGGCTGGTGTCAGAATGCAAATGCAGATTTTTAA
GCCTTGCGGCAGCTTTTGCGCAAACAGATTGTAAACAAATAAATGCCGCCGGCAGACACACAGATACTCGAACATTCGGTGGTCAGTGGCCAGATTGCAGCCTGAAATTCAT
TCAATACTTTATCTCACATGCATTGCACTTCACTTTTGAGCCACGTTAAGTTCAGTCTGCCGAAACCTTTTTCGCACTTAAGTGGTTAAATTGGCTGTGATAAATTGTTGCC
GAGTCAAAGTTGCTGCCCGCTGCGGGGCACCTCAAGTCACATGTGGTGATGGTGCGAGTGGGTGGTTGGCGTGTGCTTTTCTCCTCGGAAAATGCGTGAAAAGTCCACA
AGCACAAAAAGTCTGGGAGGCTGGCTCTCTCTCATCTCATCACGTTCATTGAGTGCCTGTCGCTGACAGTAATCATAACGCAGTCATCAGCTCGTAATATTACGGCCGCCTG
ACATATGACATCTGGGAAAGCGGAAAATGGGGGCTCAGGGACCAAGGAAAAGGTATGCGTACTATTAATATGCCAGTGTGTGAAGGAGCTTTCATTC
(SEQ ID NO: 127)

Exon: 1001..1636

FIGURE SHEET 58

Exon: 1741..2208
Exon: 2283..2681
Start ATG: 1001

Transcript No. : CT37715
ATGCTTCTGAATATTTTAGCTATAATTCTTGTATTCGTAATTTCAAGCCAATCGGAGGCAGTTATTCCTGGATGTGATTACTTCGACACCGTGGATATATCTCATATCCCAA
AGCTAAATGACTCCTATGCGTACGAGGAGCTAATCATTCCTGCTCATCTCACGGGTCTATATACATTTAGGCAACTGGCGGATGGATCACAGGAGCCAGTGAAGAGTCACTT
AATCCCTACTTGAAGATCACACTGGAGGATGGAACTATAGGAAAATATTACCTTCTCACCGACATGATCGTCTTAAGATATGAGTTTCGGTATTGCGAGAAGGTTGTTTCGG
TACAGGAGGATCAGTACAAGCTATATGAGGTTAAGATTTCAATCTTTTTTGAAGTATCTCAGTATAATTTGATATCTATAGAATGGCAGCTTTATGATTAAACCCGATGTAAA
CTGGACATTGAGCAAGCAGTGGTACTGCCTCCATCCCCGTTTGGAAGATCCGAATTCCATATGGATACTGGAACATTCCATGGTTGGTTGTATTCTCACGATTGCAGTGTAT
CTCTACATAAAGAAACTGCGAAATTTGCTTGGAAAATGTTTCATTTGCTATGTATTTTGTAAGTTTGTGCAGTACCTTATCTGGGCAGGAGGAGATTTGAACTTGTGGAATA
ATATTTGCTCCCTAGCAGGTTAGTTGAATCCATATTAAAGTTTGACTTAAAATATGCGTTTATTCTAAACAGGTTACACTAACTATTTCTTTGGCTTCTCACTTTTG
GCTCTCTGTTATGAGTCATCAAATATGGAAAAACTTGAGGTTAATCAATCGGGATGAACGTAGCTATCACTTTCTCATCTACAACATCTACGGTTGGGGCACACCTGCTATC
ATGACGGCAATTACATATCTGGTGGATTGGGCCTGGGAGGATAGACCTGACAAACTGAATTGGATTCCCGGTGTTGGCTTATATCGATGCTGGATATGGTCTGCTATGATAT
ACCTATATGGACCGATGCTGATCTTGAGTTTATTCAATGTGGTCACGTTTATCCTGACAGTAAATCACATAATGAAGATTAAGAGTAGCGTTAAGAGTTCTACCCAACAGCA
GCGAAAGTGTATACAGAATAATGAGTAAGCTTTAAGTATTTATAACTTACTATTTCTAATTCCATTCTCTTACTATAGTTTTCTATTATACCTACGACTGTCGGTGATGATG
GGCGTGACTGGGATTTCTGAGGTAATAAACTTACTTCGTCAAGCGGCACAAATTTTGGCGACAAGTCCTTCGGGTGCCAAATTTTTTCCATTTGGGTTCCGGTATAGTCGTAT
TTGTGCTATTTATTCTTAAGCGCAGCACATTTCAAATGATAATGGAG
(SEQ ID NO: 128)

Start ATG: 1

MLLNILAIILVFVISSQSEAVIPGCDYFDTVDISHIPKLNDSYAYEELIIPAHLTGLYTFRQLADGSQEPVKSHLRACICKLKPCIRFCCPRNKMMPNSRCSDGLTENLKRI
NPYLKITLEDGTIGKYYLLTDMIVLRYEFRYCEKVVSVQEDQYKLYEVKISIFLKYLSII*
(SEQ ID NO: 129)

Name: mth-like 6
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384207
AGTATATACGAGTATATCCTGTACGACTATATATCAAACCGAAAGTCGAACTGAAAGTGTCCTCTAAGCGGGACTTTCATCGAGGTCGGTGCCCCTCATTATCGTATTCATT
TGTGGGGCTCATTTGATTCATTGTGTCTGTTCGTGTGTGTTGGCGTGTTACTCTGTTAAGTTGGATGCAATTCTGTCGCCGATGGTTGTGGTTTTGTGTCCATGGCCCATCA
ATGGGGATGCTCCATCCATGTGGATGGGCGGTCAGCCAACTAACTTGGAACATTCGTATGTGATGTGTCTGTGGTGGAGGGCGCCGACCTCGAGGCCCGCTAGCTACTGTAT
ACTGTGGGAATCGGAAGGAAGGTTCTGTGTGCCGTGGGTTTTGGTTTTGGGTGGGAGGAAAAGCTTGCTGCTCGTGATATGTGATAGGTTGTGGGAGCAGCCCACTTTGAAG
GACACTACTCTATTCTGGTAAAGCGAATCGTATCCTTGGCGTTTGCTTACGTCTACTTTGGAATCATAATCGCGTGCTTGCTGTGTGTTGATTATATCGCTACTTGGGGTT
TGCTTAATGTAATTGTTAAAAATTGTACCTAGCCTACAGCTTGCAATCCACCGTTCATGCTCCACATAGCATATATGTATGTATGTAGTTTAGTGGTATGTACAGATCTATT
TACATAAGTAGCTAGTAGAACCTTAAAGCTATTGGGAAACGCAACGAACGACAAACGAAACGAAACTGGAGCCCAATTGAGATCTCTGCTGCAACGATGGCCTCCATTTGGC
ACACTTTGCCATCCTCTCCCGGGCTTTAATCCATTCCACAAGGGACCCATCATCCAATTGCCTATTGCTATAACTATTGCTGGTGACGTGCTCGCCGTTGATAATCACCCCA
TGTGCATGATCTTCTTGAAGGCCTTGCGAAACTCGGGATTGAATATTGTGTAGATAACCGGGTTCACAAAGCTGTTGATGTAGCCCAGCCAGGTGGTCATCATGTAGGCGGT
GAGCCCAGGTCGGCAGTCTTTCTTGAACTTGGCGCACATGGCGTCCATGATGTTGCAGCTGAAGAACGGCAGCCAGCAGAACAGGAAGACACCTGTTTGAGGGTTTGAAGGT
TATATATATGATGGCATATGGATTAGAATATGGCAGAGCGCAAGGACGTGGTCCAAAACGGCTGGGGGAGGTGGCTCAACTTGAACTTACCCAAAACAATGGCCAATGTTTT
GGTGGCCTTGCGCTCCTTTTTGGCCGACGATTTTTCGCGTTTCTTTTTCGAGGCCTTGTGCACCTTGTATATCGTGAATCTGTGCGTCACGCGAAGGATAATAGGCCATGGT
GTGGTATATATTGCATTTTCCACAGGCAAAAAAGCAAATGATGAAGACGAGGTAGAGAAGGCAGAAGGAAATGGGGGTGGCATTAGCATCGACTGGCCAACAAGAGCCCAAA
TAACTAATAACTGTAATTAGGGGCAATGGACGGCGTTACTCACCTTGACGCCTGCCGAGTTCTTCTTATCCTTGCGCGAGGACGTTTCGATGTAGTCGATAGCGTCGAGTCG
TTGCGTGCCAAAGTCATGGCCTCCTGCACTCCGTACCGCACAAAGGACAATGGCTTCATGGCGACGCTGCGAACGGAAGTCGGTCGGATTCGGAATGAGAACTTAACTGCGG
CATTACGTACTACTAGTCACTATTTTTGGGCTTGCCGGATTGCCTACATTGCCAACATGCGGCTTCTATTTTGGGGGTTTCGAGGATAAAGTGGCAGGTTTCTCGCTAAACA
CTACGTAATAGGTCTGTGATGAAAACGTGAGCTCTTTTTGCTAAGCAACTTAAATCAAGCGATTGTGCAAGAATGCCACCAAAATAATCAATTGATGATTTCATAAGCCTGC
TGATATGTAAACATGCCGACAATAATTATGAAAAGTAGTGGCAAGTGGCAGAACTAATACTGCAAATCACTATTTAAATGTGCAATTGGATTCAATCTGTTTGAAAAATGT
AATGTGTTAAAAAAAAAAAAAACATGTAATAGTTGACAACAATAACCCGACATATTTAATTAAACTTTGCCATTTGTTTACCAATTAATATTTGGAAGCAAAGATGTTGACA
TTTTTGACGCGGTCAAACTCTTTGTCTGTTTTTATTGAACGAAAAAAGCCATGCGTGTTATACGCATTTATTGTTTTGTTTATAAATAATGACAATTGATGTGTGCAATTTA
AGCAATTTTAATATGCTACGTAATCTAGTGTAAGTAGATAAAAAAAAACATTGCGCAAAAAAACATTGCCGCTATAGCTGAAAAAAGTATTATATTATTCAAAAACTATGTAC
AAAAACTTGAATGGGAATGCTTTATTTTGTCGGGCTGCAAAAACAGTTCATTAAACTTTTAAACTGTTGCGAAAAGTTTCATTTTACCTATGGTACAATCAAAAAGAATGTT
GTTCAATGATTTAGTACCAATGTGGTACAGATATTGGACGGTATTTTGTTTTTTTTTTTTTTCTAAATATTAGCAATTTCTCGAATTTCCGATATAATTGCCGGAACTTTGA
TTTTAAAACAATAACTTGGATGAGGCATTATGTTTTTATCCGTGCACGAACTTCTACTACGCCCCCAACTACTGGGGATGCTATTTCTAAGGTGGCAGGCTTACGGATCTGA
ATGCCAAATACCTGGAGTTATCGACACCGACTGACCTGAGGGCGGGTTCGCCGCGCTTCGGCGAGTCGTCGCCGGTGGGGCGCCGCTGACTGCTGACGCTGGATCGGTGCGG
GGTGGCGCCACTGGGCAGCGGACTGTCCGGCGGCGAGCCGCTGCTCCGCGGAGCGGCTGATGTGGCAGCAGAGGCGGAGGCGGCCGCCACGCCTGCAAGGACATCGTCAACG
TTTGAGGCTGCATAACCAGAATCATGATTACCATTCGGATCGGCGACGACCAGCTGCGGCTGTGTGGTGATTGGGCCACAACGCTGCTGCGAGTGCGTTATGGCAATGTGG
AGCGATGTGACGGTGGGGTTATCCAATTAATGGTGCCGCGACCATATCCATCAATCAATCAATCAATCGGCGATAGACGACGAGTGGGCGAAGAAGCAGCAGAATCCGGCGT
TGATGAAGGACGAAAAGATGGAAAATCGGGGTGCAACGTCAATTAAAGGCAAGGCAAGATTGAGTTTTAATAAAGTGACGCATTAATTGAATTATTGAGAATTATTTTTCTC
TGCCATTGGCTGTGATTTCTTTTGGCGGGTAAAGTTTCGCGGTCTTGTTTGCCATCCATTTCAGCCCATCGGTTCGGTTCGGTTCGGATCGGATCCCATCCCTTTGT
GCATCCAGCCTCCTGTCATTAATGGTTTCATTTCATGTCCTTATTGGATTAAGCAGGCCATCAGGATGCTAATTGGCTGCGCTTAACGCTCGCACTTAATGGCGGTTCGGC
CAGGAATTGGGAGAAAGATTCGAATGCCGTGGGCGGGGACATCCGATTGCAAGGATGATGGGCAAGGGATCCTTTCGGCAGGACCTGATTGAAAGTGCAGCACGCTTTTAT
GTCGGCAATTGAGTGCCGCTGTGTCCGGACGAAGCCTGCCATTAGATTGACAGTTTTCCATGGGCATGCACCGTCTGGGGGTCCATTGCTTTGCTGGTCTGCTGGTCTGGAA
GGAAGTGCAGTCGAGACCACTCAGCAGAAACAGGCTTATCTATTACGTGTTTGGGGCACGTCGTCAGGGTTGTCAGGTTGCAAGTTGCAAGTTGCAAGCGGACA
AGGATATGGACACGGAAACGAAACTGCTGAGCTCCGAACTTTTGCAGGGCCATCGGAGATAGCCCCCAGCCAAACATTCGTTCTCCAGGCGATGGAGTTTTCTGCGAAATTC
GCCGAAAGTTTCCGCTTTTCATACCCCGTTCACGTAAGATGTAAGTGGGTTTGCAAATGTACATATATGTCCAATCCGACTCCATTGGCAACGTGTTTATATTCGTGAAGTA
ACATTAGCCGCCAAAAGAAGGTCTTACACAGCCAAAAAAAAAACTTTGTGAAACGTATATTTCCTTTTTGTATATTCCAAATCTGATTTAAAGCTATCATGTTCTACGCATTT
CTACACAGCACATCAAAGCCCCTAAATGGTATCGTAAAATGAGTACTCACTTGCCCGTCTTCCTCGACAACGGTGGCCAGCATGAACTCGGTGGACTTGTCGTTCACGATGAC
GTGGCAGTCGTCGATGTCCGGCGAGATGGCGTTCTCGTCCTCCTCCTCGTTGGAGCCGCTGGCCGTGTTGGTGGCGGACGTCGTCGGGCAGAATCCTACTGGCGTGGCGACTG
CTGTCCAGGGCCGTCTCCGCCAGCGCCGGGTCTGGGCAATGTTCTCGATGACGCTGCCGCCCGTGAGTTCCGATAGGTGGGGCTTGCGGGCCGCCCGCTGCTTCCGCGCTC
GACTCCTCAGCGCCTGTGGGTGGGTGGGTACGAGATGTAAAATACAGAAAACAGTATACCAAACATGGGACACAGGATACAGACTACGGACGACGGACCACGGACTACGGGC
TGTGGGACACGGGATGCAGGATGCAGGATGCAGGATGCAGTAGAGAGCGGATTAGGCACTGCCATGCTGCGCTTGCATCCTACGGATATTCGCCCCCAGTCAGCAGCAAATG
TGCACAAACAGAAACAGAAACAGGAAGAGAAACAGAAGCATCCCCAAGCCAGCATTGCAGATTATGGATCTGCGCCAGCAATATTCATTCCACTCGACTCGGAGAAATCCGA

FIGURE SHEET 59

60/89

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TTTTAATTGCGGTCTTTTAATAATAGTGCTTGAAATTTTTTTGCGCAATGGAAAGAGCGACAGAAAGACCAAAGCGCGGAAAATTCGCTCTAGGAATTAATGTTTGTGGGAA
GCTTGGAGTGTTCAAAGGAATTAACATGTTTGGAATATATCGTATATATACATATATCGCTCGCTACTCACCTTGAAAATGTTCCAGTAGAGAAACACCATGATGATGCAGG
GTATGTAGAAGCTGCTCAGCGAGGAGTAGAGTATAAAGTCGGCGTTGTAGAAGGCGCATACATCGGGTTCGCGGTTGGGCGTGTTGTTGAGGCCCAGAACTATCGGCGAGCC
GATGGCAGCCGATATGGCCCACACCAGCAGTATCGTAAGGCAAACGCGGCGGCTATTTTTGTGCTTGGCGTACTTTATTGGCTGTGTCACAGCGATGTATCTGTGGGATATA
TCCGTGGAATGTGTGCTTGGGTCATATGGGTCTCCGAAATAGGGGCCGCTGTGAACTCACCTGTCTATGGAGATGGCAACTAAGTTGAATATCGATGAAGTAGAGCATATCA
CATCCATGGCTATATAGAAATCACAAACGACGTCAGGCAGGGCCCAGGCTCCATTTACCTGCAAAACAAAAAGAAGGAGGGGGGGGGGGCGTCAGGTAAGAACGAGGATGTG
TATGTCGATGCGGATGAGGAGCACACTTCATTTGTTCGGCACTTAATCGACTCGGGAATGGAGCTCTATTGGAATGCCCATCCTTTGTCGAATATTAATAACAATATTTTCC
CATTTCCCGTGCTGCTGCCACAAATTAGTTTTAGACTCTATCTCTTCATCGACGTCTCCGGCAGCATCTATGTTATGGCCCAACCCGAATGCCGGACTCCATAAAAACCCCAA
CAAAAACGTCAGGAATTTCCCAAGCCAAACAATTTGTAGCACACAAAGCACATAAAAAAAGGCCGAGTGGGCCACCAGTTCGGTTGGAACTTAATGTGGATATGTTTGGGTG
AACACCCAACCTGTCGTGGTTGCACTCCCCATAGCCCGTGTACGAGGTATACATAATGTAGCGCCAACCGATTCGGTATTAGAATGGCATCGATAGCTTTTTGGATGTGAAT
ACTATTAGTAAGTAGAGGTAGCTGTCACATAGGTATTTGTTGACTGATCTGCGGGTAAGAGGTATCGCATAGTCGAATACACTCGGCGGAGCCAGTTTCCCAGAATCAGTAG
TTTAACATTTTAAGAAGTCAATATTTGAATAATACTACTACTACATATATTGTACTTATATGCCACCAATGTGTGTGCTAACTAAAATGCATGTAGACGGTATCGAATAG
TCGAAGTTAATCGACCCTAACGTACTATCTTGTTTTTCTTCTTCAATCGGTTTTGCGCCTAAATTATACAAACACATTGAAACTTGAAGCGGGGCTCAACGCGTGGGAAGAG
TGTAAAATATTGATACACACGCAACCACACCACACGAAAGTAAAAGTGAAAGTGAAAGTCAAGTGAAAGCAGCATAGAAATGTGCTAAAATAGCTGGGCAGTCGCAGACTTG
GAATTTCTTAGAACTCGGATGAAGACTCCTTAGCCGGAGCTAAGCGAGCATAACAA
(SEQ ID NO: 130)
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Exon: 5552..5437
Exon: 5364..5112
Exon: 4605..4307
Exon: 3111..2836
Exon: 1746..1612
Exon: 1423..1323
Exon: 1212..1001
Start ATG: 5495 (Reverse strand: CAT)
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Transcript No. : CT37739
TTGCAGGTAAATGGAGCCTGGGCCCTGCCTGACGTCGTTTGTGATTTCTATATAGCCATGGATGTGATATGCTCTACTTCATCGATATTCAACTTAGTTGCCATCTCCATAG
ACAGATACATCGCTGTGACACAGCCAATAAAGTACGCCAAGCACAAAATAGCCGCCGCGTTTGCCTTACGATACTGCTGGTGTGGGCCATATCGGCTGCCATCGGCTCGCGC
GATAGTTCTGGGCCTCAACAACACGCCCAACCGCGAACCCGATGTATGCGCCTTCTACAACGCCGACTTTATACTCTACTCCTCGCTGAGCAGCTTCTACATACCCTGCATC
ATCATGGTGTTTCTCTACTGGAACATTTTCAAGGCGCTGAGGAGTCGAGCGCGGAAGCAGCGGGCGGCCCGCAAGCCCCACCTATCGGAACTCACGGGCGGCAGCGTCATCG
AGAACATTGCCCAGACCCGGCGCCTGGCGGAGACGGCCCTGGACAGCAGTCGCCACGCCAGTAGGATTCTGCCCGACGAGGCCGCCACCAACACGGCCAGCGGCTCCAACGA
GGAGGAGGACGAGAACGCCATCTCGCCGGACATCGACGACTGCCACGTCATCGTCGTGAACGACAAGTCCACCGAGTTCATGCTGGCCACCGTTGTCGAGGAGACGGGCAACAGC
GTTGTGGCCCAAATCACCACACAGCCCAGCTGGTCGTCGCCGATCCGAATGGTAATCATGATTCTGGTTATGCAGCCTCAAACGTTGACGATGTCCTTGCAGGCGTGGCGC
CCGCCTCCGCCTCTGCTGCCACATCAGCCGCTCCGCGGAGCAGCGGCTCGCCGCCGGACAGTCCGCTGCCCAGTGGCGCCACCCTCCAGCGATCCAGCGTCAGCAGTCAGCG
GCGCCCCACCGGCGACGACTCGCCGAAGCGCGGCGAACCCGCCCTCAGCGTCGCCATGAAGCCATTGTCCTTTGTGCGGTACGGAGTGCAGGAGGCCATGACTTTGGCACGC
AACGACTCGACGCTATCGACTACATCGAAAACGTCCTCGCGCAAGGATAAGAAGAACTCGCAGGCGTCAAGATTCACGATATACAAGGTGCACAAGGCCTCGAAAAAGAAAC
GCGAAAAATCGTCGGCCAAAAAGGAGCGCAAGGCCACCAAAACATTGGCCATTGTTTTGGGTGTCTTCCTGTTCTGCTGGCTGCCGTTCTTCAGCTGCAACATCATGGACGC
CATGTGCGCCAAGTTCAAGAAAGACTGCCGACCTGGGCTCACCGCCTACATGATGACCACCTGGCTGGGCTACATCAACAGCTTTGTGAACCCGGTTATCTACACAATATTC
AATCCCGAGTTTCGCAAGGCCTTCAAGAAGATCATGCACATGGGGTGA
(SEQ ID NO: 131)
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Start ATG: 58 (Reverse strand: CAT)
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MDVICSTSSIFNLVAISIDRYIAVTQPIKYAKHKNSRRVCLTILLVWAISAAIGSPIVLGLNNTPNREPDVCAFYNADFILYSSLSSFYIPCIIMVFLYWNIFKALRSRARK
QRAARKPHLSELTGGSVIENIAQTRRLAETALDSSRHASRILPDEAATNTASGSNEEEDENAISPDIDDCHVIVNDKSTEFMLATVVEETGNSVVAQITTQPQLVVADPNGN
HDSGYAASNVDDVLAGVAPASASAATSAAPRSSGSPPDSPLPSGATLQRSSVSSQRRPTGDDSPKRGEPALSVAMKPLSFVRYGVQEAMTLARNDSTLSTTSKTSSRKDKKN
SQASRFTIYKVHKASKKKREKSSAKKERKATKTLAIVLGVFLFCWLPFFSCNIMDAMCAKFKKDCRPGLTAYMMTTWLGYINSFVNPVIYTIFNPEFRKAFKKIMHMG*
(SEQ ID NO: 132)
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Name: Dopamine Receptor-like
Classification: G_protein_linked_receptor
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Celera Sequence No. : 142000013384407
TCCATGCCAGGCCTGGATGCACATGGGCCGGATGGGGATCAGGTATATATCGAGAGCGTCGAGAGTTCGGTTTGCGTTTTGCCCACCAAGACGAAACCCAAAAAGGTCGCCT
TTTACGGCAGCAATGGTCAGCGCTACACTTTCCTGTTCAAGGGCATGGAGGATCTCCATCTGGACGAACGCATCATGCAGTTCCTGTCCATCTCGAATGCCATTATGGCCTG
CCGCAGCGACGCACCCGGCAATGGCTGCTATCGTGCCCACCACTATTCGGTTATACCATTGGGACCGCAATCCGGACTGATTAGCTGGCTGGGTGGACGGGGTCACACCAGTCTTT
GCGCTCTACAAGAAGTGGCAACAGAGACGGTCCCAAGTTGCTGGGAATGCGGGACCAGGTGCTGTGGCAAATGTCCCGCGACGTTTCACAGACTTGTTCTACAACAAACTCT
CGCCCCTGTTGGCCAAGCACAATATGCAGGTGAGCGATCCACGACGCCAATGGCCAATATCCGTCCTGCTCCAGGTGCTCGACGAATTGTCACAGGAAACACCCAATGATCT
GCTTGCCCGCGAACTGTGGTGCCAGGCGGGAAATGCCGCCGAGTGGCGGCAATCGGTGCGTCGCTTTGTCCGCTGCATGTCGGTCATGTCGATGATTGGCTATGTCATTGGC
CTGGGCGATCGTCATTTGGACAACGTGCTTATCAACCTGGGAAGCGGCGAACATCGTGCATATCGAGTATCACAACGTGTGCTTCGAGAAGGGCCGCACCCTGCGCATCCCCGAGA
AGGTGCCCTTCCGTCTTACCCAGAATCTAGTGCAGGCCATGGGCATCACAGGAATCGAGGTAAGACTATTGCTCATCCTATACCAATCAATTATCTCAACAAATCGCTGCTG
GGGGTGTTTAAGAAACGGTGCTCCTAAAGATAATGTCCACTTTTATTGCTATATCTCCATTTAATTCTACCAAGTTAAAGCGTTGGGTTTCCCAATTCCGTTGATCACTGAG
TGGCCTTCGGTTTGATCTCCTGAGATGAGGATGTGGCCTCCATGCGGTGCTTGCTGTCCGCCGGCAATTGATCCTCGCACTGCCTCGCCGTTCGGCAGCATAATGTTTGGAC
ATGCTAAATAGCTGGGCAATGGCCACACAGAAGTACGGTAGCCAACAGAGCGTGAAGCAGCCCATGATGAAGACCACAATCTGGACGCTCTTCCAGTCTGGATGGAGCAGCA
GATTTCGCATGGTGGTGGCCTCGTCCGTGTTGTAGACCACCGACTGTCGCAATCGCAGCGCCTGCTTGGATGCCTCGCGCATGATGCGCCAGTAGACGAGGAACATACAGAT
CCAGATGATCACAAAACCCGGCGTTATCACTCCGGCAATGTAACCAGGCGCGAGAACTTCGTCGAATTCGCACGCCTGTGCATCCGGCCATCGATTCCAGAACACTGGCAGC
AGAGCCACCAATGCACCCAAGCACCAATTGAATATGATGATGCTATATGCCACTCGACGGGTCATGTATCTACGGTTTCAAAGGGTTTCACATATGTAGCCATTGAATTAGG
ATTTATCGGTTCGCTTAATACCTTACCTTCTATAGTGCAGAGCATAGACGACTGCTATATACCGATCCACCGCAATCGAGATCAGAGTCAACATGGACACGCAGCAGGCGC
AGATGAGCAGGAAGAAGCGCAGCAGGCAGGGACCTCTCATGGCGCCAATGTCCGAGCCCATGTAAAATACCAGATGATAGGGCAGTGCCAGTCCCACACAGAAGTCGGAGAC
GGCCAGCGACAGGATGAACAGATTGGAGATGACCGATCGCAGGTGGCGGCAGGTGCGCACCGCCACAATGGTCAGAATATTGCCGCCCAGGATAAGGACAAACAAGAAGGCA
TTGATGGCTAGCCACAGCAGATGGCCGGCACCGAAACTGGTCGCCTGGAGGGTTATTTCCGTTGGCGTTTCCGTGGCGTTCTGGTGCTGCCACAGGAACGGGACGACACCCA
ACGCTTCCGGGGAGCTTCGATAATCCCAAGCGGGCGATGAGCTGCTGGTAAATGCCATGAGCCACGATGGTAAACGAAGCGCACGCGACGCCAGTGGTTGGCTATCTGGCAA
CCGTGGGGAGCTGGAGTTGTGCTGACTTTTGGCCAGGACTTCGGCTCGGCTCGGATCGGATTCAGATTCAATTGGGTTTCGGCTCGGACCGTGGGCGTCGTTTGTTTACGTTT
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FIGURE SHEET 60

61/89

CGCTGGTGGCTTTACGACATCGTCATCGCGCCAGTTAACTGATAGCGCGCCCAGATCCACCGTGAGAACTGCAATCCGTTGATAAGCCCTCCACTTTGGCCCAACCACCATT
CACCACCCTCATACCTAACCACTCACCCACCCATCGAGTCAATCCAACCACTCCAACCAGCCAAACTATCCATTGCCCCCGAGTATTTCGAGTGTCCGGACTCCCGGGCCCA
ATGCATGGCCAAACAGATCGCTGGGGGTTTTAGCAGATTAGCCCCAGCTCCGCGGACCAAAATAGATTGATAAAAGGCCAGGGCCAGCAACTGGGATACGTGGTAAACAGATA
CATCATTGATATTCCCAAATTTCCTCGATACATTGCAAGCGAAGAAACTATATGTAAATAGTGATATCATCATAATTGTTATAAATCCGAGACCAACAGTACAACCAGTACT
ATTAGGATTGACATGGTTATCCACTCTTGGTTCTTTTAGAATTAGAAATCAGGAGAATATATAGTATATATAGGTACAACTCTCTGATCTAATCCCATATTTGAATTATCTT
TAAGATGAGATATTAAAGATTTCATGGATCAGAACAGACCAGGAGTTTGCTAAGGATG
(SEQ ID NO: 133)

Exon: 2186..1708
Exon: 1637..1001
Start ATG: 2186 (Reverse strand: CAT)

Transcript No. : CT38338
ATGGCATTTACCAGCAGCTCATCGCCCGCTTGGGATTATCGAAGCTCCCCGGAAGCGTTGGGTGTCGTCCCGTTCCTGTGGCAGCACCAGAACGCCACGGAAACGCCAACGG
AAATAACCCTCCAGGCGACCAGTTTCGGTGCCGGCCATCTGCTGTGGCTAGCCATCAATGCCTTCTTGTTTGTCCTTATCCTGGGCGGCAATATTCTGACCATTGTGGCGGT
GCGCACCTGCCGCCACCTGCGATCGGTCATCTCCAATCTGTTCATCCTGTCGCTGGCCGTCTCCGACTTCTGTGTGGGACTGGCACTGCCCTATCATCTGGTATTTTACATG
TAGCAGTCGTTCTCATGCTCTGCACTATAGAAGATACATGACCCGTCGAGTGGCATATAGCATCATCATATTCAATTGGTGCTTGGGTGCATTGGTGGCTCTGCTGCCAGTGTT
CTGGAATCGATGGCCGGATGCACAGGCGTGCGAATTCGACGAAGTTCTCGCGCCTGGTTACATTGCCGGAGTGATAACGCCGGGTTTTGTGATCATCTGGATCTGTATGTTC
CTCGTCTACTGGCGCATCATGCGCGAGGCATCCAAGCAGGCGCTGCGATTGCGACAGTCGGTGGTCTACAACACGGACGAGGCCACCACCATGCGAAATCTGCTGCTCCATC
CAGACTGGAAGAGCGTCCAGATTGTGGTCTTCATCATGGGCTGCTTCACGCTCTGTTGGCTACCGTACTTCTGTGTGGCCATTGCCCAGCTATTTAGCATCTGCCAGAGCAG
CTCGATGATCTACAAGACGACGTTCTCTCTGGCCATTGCCAACTCTGCTCTCAATCCGATTATCTACTCGTGGAAGAACTCTGGCTTTCGGCGAGCCTTTGTCCAAACATTA
TGCTGCCGAACGGCGAGGCAGTGCGAGGATCAATTGCCGGCGGACAGCAAGCACCGCATGGAGGCCACATCCTCATCTCAGGAGATCAAACCGAAGGCCACTCAGTGA
(SEQ ID NO: 134)

Start ATG: 1 (Reverse strand: CAT)

MAFTSSSSPAWDYRSSPEALGVVPFLWQHQNATETPTEITLQATSFGAGHLLWLAINAFLFVLILGGNILTIVAVRTCRHLRSVISNLFILSLAVSDFCVGLALPYHLVFYM
GSDIGAMRGPCLLRFFLLICACCVSMLTLISIAVDRYIAVVYALHYRRYMTRRVAYSIIIFNWCLGALVALLPVFWNRWPDAQACEFDEVLAPGYIAGVITPGFVIIWICMF
LVYWRIMREASKQALRLRQSVVYNTDEATTMRNLLLHPDWKSVQIVVFIMGCFTLCWLPYFCVAIAQLFSICQSSSMIYKTTFSLAIANSALNPIIYSWKNSGFRRAFVQTL
CCRTARQCEDQLPADSKHRMEATSSSQEIKPKATQ*
(SEQ ID NO: 135)

Name: Adrenergic receptor- like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384675
GCCTAAACGATAAGATTAGAAAATGGAAATGGAAATGAAGACAGCCACCTGACGCAATCTCACATGCCAGAAATTTGTCGTTTGCCATCCAAGGCCCCGATTTCCGAAATCG
AAAATCCTTGATATCCAACTGGACATGACCAGTTTCCGGAGGAATGCACTCCAGTTACACAACTGGCACAAACATTTGTTTGCTGTTTTCTGACCAAAAACAAGCCACACTT
ATGCTGGCACTTTTTTGTTGACAGAAATATGCAAGCAGACACAAGTAAATATTTATTTGATTATTTATTTTAAAGAAATGTGCAAGCTCACCGAATAAATATTATATTTTAA
AATCAATAAGTAGAAACCTAAACAAATACAAGCTGGTGAAGCGATTGCTCTGCAAATTCCACATATTTAAACTATTAATTTACAAAAATAAATGTGGCGGTCAATTTCCAGC
TGAACAGTTCTCAACAATTAATGAAAATAATTGCCACTGATAATAATAGTTTTTTTTTATTATTCGATTACATACTTTAAATATTTTTTAGTTTCCCAATTAGAAAACTTTT
TTTTAACAAAATATTTAATATTCCGTAACAGTATTTATGCTTAATTACCAGATGACAGTTTTTATTTCTTTTGACTATACTTACATTATTTTGAAAAAATAGCAATTATTTT
TAGACTTCTGCCACGAATGCCTTTAATTAATAGCTGATGCAATCGCTTAAACTCAATTAAGTTACACACGCAACCCACATCTTCTGTGTAAAAAAAAATCAATGTATTCGAC
AATACTTACGTATGATGGGGCGCCACACACTCGCACACGCATTTATGAGCTCGGCAAAACCCATTTGATTGACTAACGAAACTTATTTGCCACTTTATTTCAGCGGACGCA
GTGCAGCAGTTCCACGACGACCATGAGCGACCAGATTGGCAACCCCAATGCAACATTCAGTGGCAGTGGCAGTGGCAGTGGCACCAACGTCGCCTCCATCGCCGAAAGTGTG
GCGGAGAGCGGACCGGACTTCGATGCACTTCGGGCCGCCTGCGAAACGCGGCTAAATGCCAGCGGTCAACTGGCGGGTGAGTCGTGCACTGCGAGAAAATATATCACACAGC
TTTTTGCACTGTTTTACTTACATTCCCTTTCTTTATGCCAGTTATTTGTCTTTACTTAAGCGAAAGAAAAAAATTCACTCTGAAATTGTAGCACTAGGGAAATATAACAGTTT
TTGGTATTTCACTACATATTTTTGCCCGTGCTTCTGGCTCTGGCCAACTGCAATTTCGGCGTCCATTATGCACGAGTAACTTTAAATTGCTGACCTAACCACTCCCCTTTCC
TTTTTGGCCCCTTGGCAAACAGGCTCCGGAGGACCAGGCGCAGAAGCAGGAACCCACTGTGCCGGCACCTTTGATGGCTGGCTTTGTTGGCCGGATACGGCTGTCGGCACTTC
TCAGCTGGGGATCTGCATATGACACGAAAAAATATATATATACATACATATATCACATGTATGTATGTTACATATAGGTTAAATAGCATGCCAAAGGGAAATGTGTTTGC
ACGAGGCAATGCGGTTGGATAAGTTGGTTGGGTTGTTTGGTAGGTGGAGTGTGCCAGTCTACCCTCTAATTGGGCTCATCCCCGAGCTCATCGTTATATACACATAAATGGA
ACAGAAAATACGCTCCAAGCCAGGCCAAATCAATTGGAAACTTGTTATGTTTATGCTTTGATTTCGTGTCGTATGGAAACATCAAGTATTCACAAAACCACACGGGCTAAAG
TGTAAGGCAGAAAACACGGCCAAATTGATTGAGGCTGCTGGGCAGAGTAGAAGTCAAATATGTGTGTGGGTATTTAAAGATGCTGGAGCACGAAGAAAGGGGATTTAAATTT
TATCATGTTTGTGAATTTCATATTTTTTTAATCATTAATCAGTGTTCTTGGCAAGGTGTTGATGACGGTCATAATAACATAACTGAAGAAGAAAACCCTTTGAATAGTTTCA
CCAACTCATTGTCGTATCATTAACATATCATAAATAAAAATATCAAAGGTGACTTGAATTATTTCTCAACTTTCTGCCACACTGCGTGTATTTCATTCAATTATAAATATAT
ATATATATAAAATATAAATATAAATTAATCAACTGATTGGCCAAACGCACAAAGAAAACTAATTAATTATGCTTGGCATTAAAGCAAACGTTTAAAAACAAAGCGCACGCTCT
TCAACCTCGTTTTGGCCATGACCAGGGCAACGAAAATAGCGAGAGTTGAATGACTTTTTTTGTTATGACAGAGCGGAGAAAAACAAGGCGAGCGTCAAGAAAGTGCTACTTT
TGCTACATTTAGCTTGTGGTTAGCATGGCGCCACCCCCTTTTTCATCCTTTTTGCATTTTTTTTTTTGCCTTACGGGGTCGCCGCCAGCTTGTACAAGATTATGTGCTTTGG
CACTGCGCCGCCATTAACTTTTATGGCACTTCCGGTCGCCGGATGTCGATGTGGTGAGCTGTGGTCGAGAACTCCCTCACCCCCCGGCTACTTATCTGCCACACAGCGCGTA
TACGTGATTTTCTCGGTCTGCCTGCCAAACGGCGATAAATGGATTCTTGGCCAAGATCATCGGTCGAAAAAAAAAGAAAACGGAAGAGCCGGAAAAACGAACGACCTGAT
AAAACTCACCTTCGAAGTTCCTAACAAAAATTCTCCAGTAATTTTTCTACAAGTGCCACTCGGTAAATTGCATTGCAAACTTGGTAATCTACAATCGAATCGAATGGAAAGT
TTTTGTCACGAACTTCGAATTGATTCGACTTAAACACACACATGACCCAAACAACAGAATGATTATGCAATTTTCAAATTGATATGCTTGCAATTCGAATGCGAACCGCAAT
TCTTTTGCGGTTAACTTGGTGGCAGATGCAATAAATAATGGTTAATTCAATTGAATGCTCGGGCCGACCGCAAAATGTAAATATGAGCCGGAATATTTATGCAGTAGTCAAT
CATGAAATCACACATATTTAGCAAGTGTAAATATTTGTGTGGTGCACAGGATGTGAAAATGTTTGCTAGAAAAAACGGTAAAGAATTAATCGTATATACAATATTTATTGAG
GAGCTGTAATAAGCAGAGTAAACAGCATGGTTAATTTTTTTATTTTTTTATTTATCGCAAACTGACATTGCTTTAATTATGCAGGATATGCCCACAAGGAATGCGGTCTCGATGGCGA
GTGGTTCAAGCATCCGCTGACCAATAAAACATGGTCCAACTACACAACCTGCGTAAATCTCGAAGACCTCAACGTAAGCCGATCCCATACATAAATATCCTATATATCCTTT
ATGTAATTAATTAATCGCAACACTATATATCCAGTGGAGGCACACAGTGAATCTGATCTCCGAGGTTGGCTACGGCACCTCACTGCTGGCCATTCTGCTGTCGTTGGCCATA
TTGGGTTATTTCAAGTGAGTATGGCCAAGGGCTTTGCACTCCTTCATCTTGGCCACAAGTTGACAGCTTCGTTGGGAGATGGCAAAAACACTTAGGGGTAATGAGGCACGCT
GGTGACTTATATTGCGACTTATATTATGACGACTGGCGCCCATAAGTGAAATTTACTGATGGCAAACAAATGCGACAGTGGCTTAATCAACTGCCAACCTGGATGCTGGATGC

FIGURE SHEET 61

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CCAAATGCTCATTGCACTCATTGCTCATTTAATGCGGCACAATTGACGCCGGAAATGGGAAAATACATTGTGTCCCCATCTCCTGGTGACTCGAAGCAGGATATCGATTAAT
TTCCCAGTGCCTGCAGACCAATTAGTGCTCTGGGTTTGTTTATCGCACATTCGAATGGAACTGGGGCTCAAGGATAAAGGATAATGGATGTGCGGACTGAGGGGCGAGATCC
CATAGACGGTTCGGCCAACTGACAGAACTGTTTTAAATTGTGTGCCAAAGGCAAATAAAATGGGTCCAGATACGTGTGGGAATTTGGTCTGCCCTAAAAAAGTGAATAATTA
AAAGTTTAATGACAGAGCAATGGGCAACACCAGCCCCGGAAAAACGCATTCCTCAAACAGCTGTAATGAAAATACCAGAGTTTTCATTCAAATAAAATATAAGAGTATAAAG
GAAATTGAGTCGTTGTGAGCGGCCAAAAATAAATAAAGAAGTATTATTATAAAATATACCATCAGTATATTCTCAGTCAATAATTGTATTGCTTAAAGAAAGTTTAGAAGTG
AAAAGTAGTATATAAAATAATTTATTTAGACAGAAGTAAATTAAGTAAAGTAGAGAAGGGATTAACGAAAACAATCTAACCTATTGAATTAAATTGCTGAAAAGAAATCAAA
CTAGATTCAGTTTGGCCAGATGTCAGCAATCAATGCAATTGAGCAAAGGAGAAACGGAAAATGGGAAAATGGACAAATGAACTTTGTCCTTTTGGTCGCAGGACTTTTTCTG
CCTCTTTCGGCCCTATCCAAGCTGCCTCACATGCCCCTGGCCCCGAATGCAAATGAAGCCATAGACAAACTTGCAAATTTGGCCATAAAAACTTGCCACAAATTGCCGGCCA
AAGTAATTCGATTCGCATATTTGTCTTTCGATTGAACAGATCCCTGAAGTGCGCCCGCATCACGCTGCACATGAATCTGTTCGCCTCGTTCGCTGCCAATAACTCGTTGTGG
CTGGTCTGGTACCTGCTGGTCATGCCGAATTCGGAGCTACTGCATCAGAGTCCGGTAAGTGTGCACACCTGGCGAATGCGTAATGGTGAATCAACCTCGGCTTCCGATTTCC
ATATTCCATACTCCGTGCGAACACCCAGATGCGCTGCGTTGCCCTGCACATAACGCTACACTACTTCCTCCTGTCCAATTACTCCTGGATGCTCTGCGAGGGATTCTATCTG
CACACCGTCCTCGTCGCCGCATTCATTTCCGAGAAGAGGCTGGTCAAATGGCTCATCGCATTCGGCTGGGGCTCCCCGGCCATCGTCATATTCGTCTATAGCATGGCTCGCG
GTCTGGGCGGCACGCCCGAGGACAATCGTCAGTAAGTGAATAATGAATGGGTACAGCTTACACCGAAAGAAAATGAGGAATGCCAATAGTTATCAAAAGTGACCGACAACAG
ACAAGGTGTAACCATATTGTGTTGTCTAGAAGTATCCTAGTTTAATGAAATCCCACAGACTTGAGTATCACAGATTGATATCAAGATATTTCTGTGTAGCTAAGATATTCAG
TCTGTCGAGCTCTTGACCAAATGCTAATCAAATCAATCAGCAATTCACCCACTGACTCATCTCGCATTCCTTCGCCAACTTGCAGCTGCTGGATGAACCAAACCAACTACCA
AAACATTCTTATGGTGCCTGTGTGTATCTCCATGTTCCTGAACCTCCTGTTCCTGTGCAACATTGTGCGAGTGGTCCTTTTGAAACTGAATGCCCCGGCCAGTATTCAGGGC
AGCTGCGGTCCATCGCGAACGGTTTTGCAAGCATTTCGGTAAGTTTTCCCGTCCAAAACAAAAGAAAAAAAAAAAGAACTGTTGGGGGGGAGATTGAAACACTTATAAGCGAA
GCAGAGAACTCTCAACTGGCCCACGGGGGCGAATGCGTAATTATATTTTGTTTCCCTTGTATTTAGACTCTTTCCCATCGGCCATCAGGTCTTTTATTGTTTATTCGCTCTGC
ACTCTGGAAGTTGGGCTCATTTTACATTTTGAATTACGCATACGCCGCGTTGACTTGCATGTTAATACACAGCTGAAAAACGAAAACAAGGCATTATAATTCACCCTCTCAT
CCTGTTTTAGGGCAACGCTGCTTTTGGTTCCTCTGCTCGGCCTCCAGTACATCCTTACGCCCTTTCGTCCTGCACCCAAACATCCCTGGGAGAATACATACGAAATCATCTC
GGCGTTTACGGCCTCATTTCAAGTAAGTAAAATGTTTTCGTTTCGTTTCTGTTCTCGTTTCGTTTTTTTTCGTTTTTTTTTTTGCTTTTTCTTTCCGGCTTTTGTTTTG
CACGCTCTCATAAAATCACTTTACGACTCCGAGCTGGCTAAAAAGTTATGTGATGTTAGTTCGCCTCATGGTGCCATCCACCACTGGGAATGCAAATAAGCCAGCATTACTGGA
ATACCGAATACCAAATACCAGGACTAGCAGCTCATTAGATCGGGGCTCTTTTCAAATCAATAATGAAAATACACGCCATGTGAAATACCCACCATTGGCATTTCACTTGATC
TCAGTTTATTAAATTGCTGGCCGAGATTGGAGCGAAGTTCCCCCGTTGGAAAAATGTAGCAAGTTGAGCATGAAATGCACTCTCGCACACAGGAACTCGTAAAAGCAACTCG
AGCTTGTCCCTCGGCCAACTCAGTCTCGACTAGACCAGCATTTACACATGGTTAACACACATACATATATTCTTGGCCGCAACTTAAAGACAACGACGGCAAACTTCATCCA
GCTACGTTGCCTTCTTGTTTGTTGAATACCCAAAGAATCTTTCAGTTCATGTTTGCAGTACACAGATAAAATAATTTGCATATATTTTCGTGTTTTTGTGCACGAAATGGTT
TTTCATTACAGACTGTTGATATAACAGTTGCCATGGAGGTAGAGGTGCCTAAAAGTATGTTGCAGCTTAGATGGCTTTCCTTTACAAAATTTCAAAAGTAATTTCTAAGGCA
CCCCCTAGCTGTTATTCGAAAATCTTTTAGTTCGATCTAAAAACCCAACTCAATCGGTTCAAAAAGGTAGCCCATTGAATTCATAAACAGCCCTAAAACAACAGGAAAATCCA
TTATCTTGCGAGTAGACATAAAATCATCTTGGGTGCCACTAAGCTGCAGTTGAGCTCTTGACTATTTTCTATAACTTGGCAAACTGAACATTGTCACCTCGGTCTGAGCCTT
TTTTCATCATTGCCAATCGATAGGTGAAATCTTTTATTCGACTGCTAAAAGTTTAAAGCCAGTCGACGGGTACTTTTCCTTTGCATTTTCCTCTTGTCGTATTTATTCACTT .
TTTTTTATGTCGCTGTTTTCCGTTGGCTTATTTGCTGCAAAGA
(SEQ ID NO: 136)


Exon:  1001..1196
Exon:  1590..1727
Exon:  3775..3881
Exon:  3955..4046
Exon:  5156..5318
Exon:  5405..5631
Exon:  5910..6086
Exon:  6395..6659
Start ATG: 1031


Transcript No. : CT38445
CGGACGCAGTGCAGCAGTTCCACGACGACCATGAGCGACCAGATTGGCAACCCCAATGCAACATTCAGTGGCAGTGGCAGTGGCAGTGGCACCAACGTCGCCTCCATCGCCG
AAAGTGTGGCGGAGAGCGGACCGGACTTCGATGCACTTCGGGCCCGCCTGCGAAACGCGGCTAAATGCCAGCGGTCAACTGGCGGGCTCCGGAGGACCAGGACGCAGAAGCAGG
AACCCACTGTGCCGGCACCTTTGATGGCTGGCTTTGTTGGCCGGATACGGCTGTCGGCACTTCCGCCTACGAACTCTGCCCGGACTTCATCACGGGGATTCGATCCAGCAAGA
TATGCCCACAAGGAATGCGGTCTCGATGGCGAGTGGTTCAAGCATCCGCTGACCAATAAAACATGGTCCAACTACACAACCTGCGTAAATCTCGAAGACCTCAACTGGAGGC
ACACAGTGAATCTGATCTCCGAGGTTGGCTACGGCACCTCACTGCTGGCCATTCTGCTGTCGTTGGCCATATTGGGTTATTTCAATAATTCGATTCGCATATTTGTCTTTCG
ATTGAACGGATCCCTGAAGTGCGCCCGCATCACGCTGCACATGAATCTGTTCGCCTCGTTCGCTGCCAATAACTCGTTGTGGCTGGTGGTACCTGCTGGTCATGCCGAAT
TCGGAGCTACTGCATCAGAGTCCGATGCGCTGCGTTGCCCTGCACATAACGCTACACTACTTCCTCCTGTCCAATTACTCCTGGATGCTCTGCGAGGGATTCTATCTGCACA
CCGTCCTCGTCGCCGCATTCATTTCCGAGAAGAGGCTGGTCAAATGGCTCATCGCATTCGGCTGGGGCTCCCCGGCCATCGTCATATTCGTCTATAGCATGGCTCGCGGTCT
GGGCGGCACGCCCGAGGACAATCGTCACTGCTGGATGAACCAAACCAACTACCAAAACATTCTTATGGTGCCTGTGTGTATCTCCATGTTCCTGAACCTCCTGTTCCTGTGC
AACATTGTGCGAGTGGTCCTTTTGAAACTGAATGCCCCGGCCAGTATTCAGGGCAGCTGCGGTCCATCGCGCAACGGTTTTGCAAGCATTTCGGGCAACGCTGCTTTTGGTTC
CTCTGCTCGGCCTCCAGTACATCCTTACGCCCTTTCGTCCTGCACCCAAACATCCCTGGGAGAATACATACGAAATCATCTCGGCGTTTACGGCCTCATTTCAAGTAAGTAA
AATGTTTCGTTTCGTTTCTGTTCTCGTTTCGTTTTTTTTTCGTTTTTTTTTTTGCTTTTTTCTTTCCGGCTTTTGTTTTGCACGCTCTCATAAAATCACTTTACGACTCC
GAGCTGGCTAAAAAGTTATGA
(SEQ ID NO: 137)


Start ATG: 31


MSDQIGNPNATFSGSGSGSGTNVASIAESVAESGPDFDALRAACETRLNASGQLAGSGGPGAEAGTHCAGTFDGWLCWPDTAVGTSAYELCPDFITGFDPARYAHKECGLDG
EWFKHPLTNKTWSNYTTCVNLEDLNWRHTVNLISEVGYGTSLLAILLSLAILGYFNNSIRIFVFRLNRSLKCARITLHMNLFASFAANNSLWLVWYLLVMPNSELLHQSPMR
CVALHITLHYFLLSNYSWMLCEGFYLHTVLVAAFISEKRLVKWLIAFGWGSPAIVIFVYSMARGLGGTPEDNRHCWMNQTNYQNILMVPVCISMFLNLLFLCNIVRVVLLKL
NAPASIQGSCGPSRTVLQAFRATLLLVPLLGLQYILTPFRPAPKHPWENTYEIISAFTASFQVSKMFSFRFCSRFVFFSFFFFAFFFPAFVLHALIKSLYDSELAKKL*
(SEQ ID NO: 138)


Name: Calcitonin receptor-like
Classification: G_protein_linked_receptor


Celera Sequence No. : 142000013384816
ATTCGTTCGGTATTTTCGCATTTGGCATGTTTGTGGCTAAGATATCATCAATTCAACACAATGATCAACAATATTCAACGACAAACACTCGACTTGGGACCCTGGATGCTTC
ATCGGCGGCGCTCGGGAAACTGAATTTGACCCACTAAGGGGAACTAGGCAAAATTGCAACGCTCTGTTGGTAAGCCCACCAAATCGAAGCGTTCAGGGGCGGCCAAAAGGAA
ATGAATCATTCTACCGATTTGAACAACGATCGAAACTTCACACTAGCCTATCATTTCAGTATCATAGTTGTATGTTGTATGGCTAAGAACTACTGGAAATGTCTTTTTGGGC
TTATTTGCTTTTTGGATTTTAACATATTTGCTGTGTTTTATATTCGTTTAGTGGGCCTTGGTTTTTCGTTTCTTAAGCGCAATTCGCAAAGCGTGCGAAGATTGAAGATTTT
```

CCGAATTTTGAATTCTCATATTTCCGGCCCGTCGTCAAGTTTGGCAAATTGTTTAATAAACGCTACACGATTTCATTTTGTAAAATTCTAAATGCTACTTAATATGGACTTTG
AAAAAGGTTTATACTTATGCAATCTTTAGATAATAATCCTGCTGCTCGAGTAGCATATGATTTTCGTATATTGTTTTTGTTGTAGCAAGTTCGAATTGTAAACCGGAAACGG
AAATGTTGCTCTTGCCTAGTGAATTGTCTCTTGTCTACGAATTAGAATTAGAATTAGATCGCTGCTACATATGTATATGTATATGGCTAGAGTTAAGTACAAGTATATATAT
ACGTGGTAAGCTCATAAATACACAATAATAATCGTCAATCAATTCAATCAATCAATCGGTGAATCAATCATAATTGGATACGCTAAAAACTCTTAGCTTAGCTTAGGTCTAG
AAATATGAATATGTCTTTCAACGTGTCTGTGGTTTTGGTGTTTTTGGTGTTTCTGTGTGGTTTGCTGTATGGTGGCTGAGTGGTTGAGTGGTTGCGTTTTTAGTTTTCAGTT
TTTCTGTGGCTGTGACTGTGGGGTGGTGCTTTCATTGGCATGTCGCGTAGCGCCAAACGGCCCGTAAATATGCAACTATATGGCAAACAGGCAAGTAAGTGTTTATATATAT
TGAGAGAGAGAGATATATAGAGAGTTAAGGAAATGGCTCAATGCAATTACAACCAATTATTTACTTGCAGGACTTTGTAGTTCTTCTCAAAGGGATTACGGAGGATGGGTTT
GGGAGGGGGATTTTTACGGATAATTATTGTATTTTTTTTTGAGGAGAATGAAAATCTAAATCTAACTCTAGTCATCTGGGTCCAACCCGATTAGCTCTGCTTGCAAACGGCC
CTTAGTCTTACAACAAATGGTTAAGCAAAATACTCTCAAAGCGATACGGAATTGCGGCGACATACTGGTCATGATCAGAATTTTCAAAACGAATTCAATATGCCGATCCAG
ACGACGGCGAAGTTGATAAGAGTACTTTGGATAACATCGCCCGTGACCACCTCGTACAGACGCAACAGAATCCATGGCAGCCAGGACACCCAGAATGCAAAGACTAATGCGA
ATGACATCATATGACTAGGGTTCGATAAATTTTCAGCCAGAGCAGTTGCATATTCTTTATCGTGTATCGGCTCGCCGGACCTAATCCTTACGCATCATTACAAAGATATAGCC
GTAGTTGTGTACGATTGAAATGAGGCTGGGACCTAAGACTAATATCGCCAAGGTGGCGCTATATGCTGCCATATTCCCCCAGTCCAGCATGCAAATGTGCGTCATGTTGTTC
TCGATGGGCATCGAGTAGCCCAGGATTGGGGGACAGCACAGCAGGGCCGCCGATATCCAAGTGAACACCATCCAGCATTGGCATCTGCACGATAAAGGTCACAAGAGATCAA
AGATTAATCCAGTTTTAATCCAGATGAGGAGGAATTCGGGGTTCCATTGGCGCTACTCACCTCGTTTTCGTCTGCACCGTTTCATATCTGAGTGGCTTCCGCACCGCAAGAT
AGCGATCCACTGATATCCACATGAAGGTGTATACCGATACCGCCCACAGAGTGACCTCCAGATAGCCGGTGAAGCGACACACGATGTCGCCGTACATCCATTCTCCGGTCAA
AGCCGGGATACACGGAGAAGGGCACCACCAGGAGTCCGCAGAGCAGATCGGCGATGGCCAGGGACAAGAGGTAGTAGTTGATCACCTCTGTGGGTCCTGCGATGACAGCAATA
TCGTTAGAAAACGAAGTAGAGGTGTATTCAAAAATAATAGGCAAATGCAAACAATAATATTTAAATGGATCATTCAATAATTTGGGCGAGTCTATTTGTACGACATTCACTA
GAACTATTTAGAAACCTAAGGTTCTTAAATTTATCCAATAACAATCAATTTATAGGATAAAAGTTTAGGTACAAAAAGGGGAAAGAAATAATATGCTTAAGCACAATTGGTT
TTTGAATTTTTTCAAAGCAATTAAGACAACAAGAAAACAACACATTTGAATTTTTGGGGAGGATGCCGTGTTACTTCATTCCTTTCACTTTCACATCAAAATCATGGATGCA
TTTTAAGTATAAACATTGGACTTAAGTGGTCAAAATAAATTATATTCAACACATATGTAGGTTACTTATGAAAATATTATGCTTGAGGCCAAACCCAACCGCGAGATTCGAG
CGATATGGAGCCACCGCCTTGGTGAGGGCCTCCACCTTGGAATTATCCTGTAGGTAGCTCATTTCCTGCATTTTTACGGGCTGGCACTGTCGGTTGAAATGGGCGCTCCTGTGC
TCGTTGTATACGCTCCCTTAGCTCCTTGTCCGTTTCCCTCCTCCTTGGCTCCTCCTGCTTTCACCTGCTTTCGCTGCTGCTTTCACCCGCTTTCTCCGCACCTTCTTGGCGG
GCTGATTGTTATGCAAAGGCCAGTGGACGTGGACGTGACCGTACTTTACTTCCGGTCATGGCGGACGCCCATGCAATTGTCCTGTGCCTTCGGTTGTGTGTGTCGGTGTGTC
TGTGAGTGTCTATGTGTGCTTAGGTGAGTGTGTCGATGTGTGAGTGTGTGTGTGTGTCTGGGTGCGAGTGTTGGTGGCGTCCTTTATTGTGCAACGAGGCTTGCACACGCGA
AGGTCGTCGGAGTCCTTGGCGCTGTTTTTTCGTCCTTTCTCCAACGTTGGCGCCAAATTTGTATAAATTTTCTACTGCCTACTTTATTTGGGCTGCAACTTCTACTACTGC
CCACCTTTTGGCGCCGAGCCAAGCATTTGATTGTTACCCTCACAATCCTGGCGTCGTGGTTAAGGTTAAGGATAAGGTTGTGCTGGTGTGTGTGTCTATGTGTGTGTCTG
AAGCTCGTTTAAAATGCTGCTTGGGCTAAAATCTTACACGTAAAATCTAGTAATTGCGTACAATTTGGTTTCTATCTTAGAGGATCGTTAATGATTTAAAGAATTCGTTTTG
TTTTGCTAAATTCACAACGCTCTTTGCTAAGTTTTAATGAACGTCAAAACTGTTAGTTGTATGCTTGAATAATTCGCTACTAGTTTTAATATCGATTTAAAAAATGTACACAT
TTCAAACTCGCAAGTGGAAGAATAATGATTATTAATTTAACTATTTAATGTGTAATAATTACGCGGTTTTCAGGGCTCTTTTTCTTTCGGGGTTAGTTGAAATATCTTTCGA
CTATAATTAAAGCACAGCACAAATGGTTTTGTTGTTTTGTAAGGCTTCTGTTGTGCTACATTTAAGTTTGTTAAAATAGTTCGATAATAGTTCGGTTGTTAAGTATCGGTTT
.TGCTATTTAATTTCGCTGCTTGGTGATTGTGATTATCCTTTTGCTTGTAAATTCTGGCTCTTGTTGCTGTTGTTGGTGTTTAAACTCCACGTCCTGCTGTCGTTTTAAGCTA
ATTGTGCGCATCTGAAAGGACAAAGGATAGCAATTGTATGCCTTTAGCGCTTCATAAATAGTTTACAGAATCTTCCATCTTGAGCCAATCAATAAATTATCCCACATACGGC
AGCAGGCGGAAAAGCCTTTTAGCTGCACAAACGCTTTACA
(SEQ ID NO: 139)

Exon: 3185..2737
Exon: 2223..1965
Exon: 1876..1001
Start ATG: 2869 (Reverse strand: CAT)

Transcript No. : CT41076
ACACACTCACACATCGACACACTCACCTAAGCACACATAGACACTCACAGACACACCGACACACACAACCGAAGGCACAGGACAATTGCATGGGCGTCCGCCATGACCGGAA
GTAAAGTACGGTCACGTCCACGTCCACTGGCCTTTGCATAACAATCAGCCCGCCAAGAAGGTGCGGAGAAAGCGGGTGAAAGCAGCAGCGAAAGCAGGTGAAAGCAGGAGGA
GCCAAGGAGGAGGGAAACGGACAAGGAGCTAAGGGAGCGTATACAACGAGCACAGGAGCGCCCATTTCAACCGACAGTGCCAGCCCGTAAAAATGCAGGAAATGAGCTACCT
ACAGGATAATTCCAAGGTGGAGGCCCTCACCAAGGCGGTGCTCATATCGATACTGGGCGTGGCCATCGTCCTGTCCAACCTCCTCATTATCGCCACCTACGAACTTCAAG
GGACCCACAGAGGTGATCAACTACTACCTCTTGTCCCTGGCCATCGCCGATCTGCTCTGCGGACTCCTGGTGGTGCCCTTCTCCGTGTATCCCGCTTTGACCGGAGAATGGA
TGTACGGACGACATCGTGTGTCGCTTCACCGGCTATCTGGAGGTCACTCTGTGGGCGGTATCGGTATACACCTTCATGTGGATATCAGTGGATCGCTATCTTGCGGTGCGGAA
GCCACTCAGATATGAAACGGTGCAGACGAAAACGAGATGCCAATGCTGATGGTGTTCACTTGGATATCGGCGGCCCTGCTGTGCTGTCCCCAATCCTGGGCTACTCGATG
ACAACTACGGCTATATCTTTGTAATGATGCGTAAGATTAGGTCCGGCGAGCCGATACACGATAAAGAATATGCAACTGCCTGGCTGAAAATTTATCGAACCCTAGTCATAT
GATGTCATTCGCATTAGTCTTTGCATTCTGGGTGTCCTGGCTGCCATGGATTCTGTTGCGTCGTACGAGGTGGTCACGGGCGATGTTATCCAAAGTACTCTTATCAACTTC
GCCGTCGTCTGGATCGGCATATTGAATTCGTTTTGGAAAATTCTGATCATGACCAGTATGTCGCCGCAATTCCGTATCGCTTTGAGAGTATTTTGCTTAACCATTTGTTGTA
AGACTAAGGGCCGTTTGCAAGCAGAGCTAATCGGGTTGGACCCAGATGACTAGAGTTAGATTTAGATTTTCATTCTCCTCAAAAAAAAAATACAATAATTATCCGTAAAAATC
CCCCTCCCAAACCCATCCTCCGTAATCCCTTTGAGAAGAACTACAAAGTCCTGCAAGTAAATAATTGGTTGTAATTGCATTGAGCCATTTCCTTAACTCTCTATATATCTCT
CTCTCTCAATATATATAAAACACTTACTTGCCTGTTTGCCATATAGTTGCATATTTACGGGCCGTTTGGCGCTACGCGACATGCCAATGAAAGCACCACCCCACAGTCACAGC
CACAGAAAAACTGAAA
(SEQ ID NO: 140)

Start ATG: 317 (Reverse strand: CAT)

MQEMSYLQDNSKVEALTKAVLISILGVAIVLSNLLIIATYANFKGPTEVINYYLLSLAIADLLCGLLVVPFSVYPALTGEWMYGDIVCRFTGYLEVTLWAVSVYTFMWISVD
RYLAVRKPLRYETVQTKTRCQCWMVFTWISAALLCCPPILGYSMPIENNMTHICMLDWGNMAAYSATLAILVLGPSLISIVHNYGYIFVMMRKIRSGEPIHDKEYATALAEN
LSNPSHMMSFALVFAFWVSWLPWILLRLYEVVTGDVIQSTLINFAVVWIGILNSFWKILIMTSMSPQFRIALRVFCLTICCKTKGRLQAELIGLDPDD*
(SEQ ID NO: 141)

Name: putative adrenergic receptor
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384685
TAAATATGCATATTGAACGAGGCAATGCAATGCGATTGAGGTCCGGCTGTGCGTTTCAGTTGCGAAATGAGTTGCGAACAGGATTTATATTCAGATTTAGCCATTAGCCAAA
TGCAACACCTTCGACGACGTGTGGACACGTCGACTTTGATTCGGCCAACTGAGTGATCCGGGTAGTAGTGTCAGATGCCAACATTACTTATGCACTGAAAGAAATAAATAA
AGGATTTACATGTGTAGTAATGTATAATTGGGCTGCATGACATGCATGATAATGATCAACTTTCAAGCAATAATAATTCTATGACATCACGACATTCATACGGACAGAAAGA
CGAACATGGATTTACCATTAAAATGTAATTATAATATAATATAATAAAGTATCTAAAGAATTTTTTACTTGGATCTCCTAGCAATTTTAACCATATTCTCAAATGCAAAATG
TGAAGTTCTTGCAAATAGATACACACGACTAATGGGTCCGCATTTGCCAATTAATTGCCTACAACGCCCAGGTTGCTTTGAATCACAGGTGGACATTTGGACAGGTTTGCTCA

GCTCACTGGCAGCTCCACTTTGGCCATTCAAAATTGTTTATCGCTTTGACGAGTTGCAGTAGCAATTTCGACACCGTATGCCCATAATGAAGAAACGGCATTGATAATAACA
AAGTAATGATAAATTAGATGCTGTTGACGTCTAATTCATTTTTGATGATAGTATTGATTTTATACATAAATGACACAATTTCCCTTTTATTTTGTAAAACATTATGGCATTT
TCACTTTTAATGGTCCTGTAAAACACAAGTTAGTTGTAAAGCACAGAAAAACTTTCCATTTCGATGACAAGAAGTCCTTTAAAATTCAAATAAATATATAATTCTAATTCTAA
ATAAATAATTCTAAGCAATGGTTTATGTATTTAAACTCCTTAAATTTTGTTCCAGTTTTTAACTAGCACATATACATCAAAAGAGCGGAACTAGATAGTCTACAATGATGCA
AGAGACCGGCAATCAAATGGGACAGACCCATATGCACCAGCGGGTTCCTTTCAACGACACGGTTCTGAAGGACTATCATCTCACGAGCACCGATATCGAGAAGTTTGTAAAG
CTATGGCAGGAGTACCAGATGAAGAACATGACCCCTCAGGTGGATGAGTGCCAGGGCTATTGCCAGGGGGAAATATACAACTGGTTGCGAGCCTACAACAGCATCCATGGAT
ACGTTTCGCTGATGGTAAGTAATACTCGTGATTACAACTCCCCCTGGGCACGAAACCCGCAATGTTGGCCAAAACAAAGGAATCGGTTGACTAATGATGAGCAAGGGAAGCC
AAGACGATACACACAGACCTTCGCCGACAGACCACTGATGAATGTAGGGGACTTCTTTACCTTTGAACTCTTGCCAAAGTCGTCCTTTTTTCGAATTAAAGTTATAGCATGC
GCTCAGCTTAACCATCAAAATCACAAATGAAATTAGTGGCCGGGAATCTCGGTCTTTTGTTTATGTCCGGGTTTCCCTTTTCAGGGCTTTTTTGAAAAGGATATAAATTATA
TTAGATGTAGTTAAGCCGTTGAGGCGTTAATGTGCTATTTTTTCATTATAATTTTCAGTCGTAAGTCATTTTGCGTTGTAGCAGACGGCCTTTACCACAGGAATTGGGTCAGAA
AATACCGAGAATCCATTTCCATCAAGGCTAGTTCATAGCCCATCTTTTCAAATAAATATACAATAAATCAAATACAGTTGAAAAATGTAACTTTATTGCTTTCCTTCGTTCG
CACAAAAAATAGTTTACCTCTTAAATTGAAATAAAATTCTGAACCAAACTTCGGTTACTGTAGTTCCATTTTTTTTTTTTTTTTGCTTGTGTGAGCAATGTTAAGAAATGTAA
ATACGAGAGGTCACGACAGTTGAGTTGCTGCTCACGAGCTGAATAAATAAAATATTCATCCACTTTGGTGTCCAAGGGGAGTGCATTCAGTTGAAAGTATGTGAGCGCTCAC
AGTTTCGATTTGACAAAGGACGCATTTTATGTTGATTCTTCTTGTTCTTTAAATCACCTAGATTTGCATTTTCGGGACAATAGCAAACATCTTGAACATAATGGTCCTGA
CCAGAAAGGAAATGGCCAAGACGCCCATAAATAATATACTTAAGTGGCTGGCGGTGGCCGATATGTTTGTGATGCTGGAATATATACCCTATACATCGTATCAGTATATATA
TATGGGGCCAGGTAAGCATACATTTAGTAATAATATTTAATAATAGTCTTGGTTATAGCTTTACTTGTTATTTATTTATTAGTGTTATCAGCTAGATTATTATTATAAAGGT
ATACTCTTGATCAGGATCTACACACGTCTGTCTGTCGTTTCTAAGGGTATATTTTGTTAACAATTTTGTTAACAATTCCCATATATCCTTTCCCCTTTGCACTTACTTTTA
GTTGAGTAACGAGTATGTGGTAGTCGAGGCAATCGGCTATGACCTTCTCTGTAGGTTTCCTTTCTTTTTTAATTTTAAGCCGTTTAAATTTTTTTGAATTATTTAATATTCT
TTGTATGGCTGTTGCAGGTGAAAAAGATTTGAGCTACACCTGGGCGGTTGTCTGCTGGTTCACATGCACTTCACCCAGATCCTGCATACGATTTCCATCGGATTGACTGTC
ACGCTGGCGGTGTGGCGGTATGTGGCTATCAGGTGAGATGATCCTTCGGCCAGCTATGCATGACTTATTCCGGAATTCGCCGTCATCCATGTAGAGTTTGTCTCCGGTTCAC
ATTCATGATAATCCACATCCGCAATTCGAACAGACATCCGGCTAATCTGATTACCACATCATTGTGGCAATGTGGCTTCTCTTCTCTTCCCCCGTCTTTTGTTTATAGCCAA
ATGTTACCGTCTCTATTCCACAGACATCCGAACGGGGGCTGTGCCAATTTCCTGCTAGCACATTCCCGGGAGGCGATCCTCCTGCCCTTCATCCTGTCGCCGATCCTCTGCC
TGCCCACGTACTTTGTGTTCCAGGTGCGTGAGACGTACGACGTGGACAAGGTCAACTCGGAGGCCATGTATCATGTTTATTCGACAAGGACTCGGTGCTCTACAGGTGCGC
TTAGATAAGAAGTCTGATGTCATTTATGCATCCTGCGAAGAACCAATTGTAAAATATTTCATCGTGAAAATCCTTAACAGATTCAACTTCTGGATACATTCCGTGCTCATCA
AACTTCTGCCGTGCGGCATATTAATTGTGATCAGTGCAGTACTTATGCACGTTTGTGCGAGGCATCGAGACGTCGCTTGAAGCTGAGGGATTACAACAATCCCGCCAAATA
TGCCATCCAGCTTAATCTGAATGAAACCAAATCCAAGAAGTAAGTACGCACTTGACTCGTTTAGTGCTTAAGAATTCGCCTCATTTGCAGTTTGCCTTGTTAGTTTCATGAT
CTTTGATTTTTCTGTTTTTGAATGGTCTCGGATTTTGTCAAATCTCTTCTTAGGTTCCTTTTTGCCATCTTTTTTATAAATTTGTCTTTTTGTTTTTGTATCTTAGGCCGCC
TCGCTGTGATCGCCGTAACGATCGGACTACCCTTTTGCTGGTTGCGGTACTGGTTTTGTTTCTGATCACGGAGTTTCCGCAGGGATTACTTGGTCTGCTGTCCGGAGTGATG
GAGAAGTGCTTCTTCGCCCACTGCTATCCGCGTTTGGAGAGCTGATGGATCTGCTGGCACTGATCAACGCCGCCGTCGGGATTCGTGCTGTACGGTCTGATGTCGAAACAGT
TCCGGACCACCTTCCGATCGCTGTTCATGAAGCGGCACTTTGGCAGCACCGAAATGACCAGATTGACCCGCGTAACCACGACTTGCGTCTAGTTGGGCACATCTAAAGATGT
GATCATGGGCAGGAGCAAACACTAGTGAGGGATGAAGTAGGTGAGGGACATCCAAGATGTTCCGGCCCGGCATTGAATTTGAATTTTCTAAAGCATAAACTTTATAAAGTT
TCGTTGACTAAACAAAGCCTAAATATGAGAAACTGTGAGTGTGGAATTATTGTACGGGCTGACCAGTTGATCAGTTGATTTCCACAATGGTTTACTTTTAGGTGTAGTCCTA
AGGCGTTGACTGGTGCATCGATCGGTTTAGAAATTGATTCTGCTTGTGATCTGGCTGTTTCGCAAAGTGCCATTTCATTTCCAAATAATTACATTGATTAGTTTACCAGTTG
GTGTTTCAAATTCGTATTAGTATATAAGTTTCATAGGCTAAGTCAGCTGTACAAAGCTGTACAAATACGAGACATTTACTTTTCCATAAGATGCAGAAAAAAAAACAGGAAT
CCATCATCAGCAAAACTGTAGCCATGCTAAGAGGACTGAAGAACTCACTGAGCCCCGAGTTGCTCTCTCTTCTTAGCTGGAATCACGAAAGAATTCTATTTTGATTGTATGG
CGTTAACTGGTTTTCAACAAAGTGCCAATGCATTTTAAATTGGCTAATTGAATAACCATATTTTGAGTACTTTTTAAGTCGCTTATACTATTTATAAATAAATGTGAACACT
TTCAAAAAAAAATATGTTTGATGTGAGTTGCATACAAATGAAACGTTTATTGCTTTCCATTACCGAAAAATGAACATCTAATTCTGACTGACAACAGCATTCACCTCCAGTGG
CAATTCGTCCGGCAGAAGTTCCGTGGCCCGATTGTGTCCCAAATCAGACTCGCCCATATCCGCGGAATCCAGCAGGATGCCATTGCCCTGATTCGAGATGCGCAGCAGGCAT
TTCAGCTTGGTGGCTTGGAATTTGTACTGCAGGATAATGAGATTGATAAAATCTGCTCTCGAGGGAGTTTCGACCATAATGTAA
(SEQ ID NO: 142)

Exon: 1001..1246
Exon: 2080..2251
Exon: 2594..2720
Exon: 2936..3130
Exon: 3217..3399
Exon: 3579..3900
Start ATG: 1001

Transcript No. : CT32473
ATGATGCAAGAGACCGGCAATCAAATGGGACAGACCCATATGCACCAGCGGGTTCCTTTCAACGACACGGTTCTGAAGGACTATCATCTCACGAGCACCGATATCGAGAAGT
TTGTAAAGCTATGGCAGGAGTACCAGATGAAGAACATGACCCCTCAGGTGGATGAGTGCCAGGGCTATTGCCAGGGGGAAATATACAACTGGTTGCGAGCCTACAACAGCAT
CCATGGATACGTTTCGCTGATGATTTGCATTTTCGGGACAATAGCAAACATCTTGAACATAATGGTCCTGACCAGAAAGGAAATGGCCAAGACGCCCATAAATAATATACTT
AAGTGGCTGGCGGTGGCCGATATGTTTGTGATGCTGGAATATATACCCTATACATCGTATCAGTATATATATATGGGGCCAGGTAAGCATACATTTAGTAATAATATTTAAT
TTTGTCTGCTGGTTCACATGCACTTCACCCAGATCCTGCATACGATTTCCATCGGATTGACTGTCACGCTGGCGGTGTGGCGGTATGTGGCTATCAGACATCCGAACGGGGG
CTGTGCCAATTTCCTGCTAGCACATTCCCGGGAGGCGATCCTCCTGCCCTTCATCCTGTCGCCGATCCTCTGCCTGCCCACGTACTTTGTGTTCCAGGTGCGTGAGACGTAC
GACGTGGACAAGGTCAACTCGGAGGCCATGTATCATGTTTATTCGACAAGGACTCGGTGCTCTACAGATTCAACTTCTGGATACATTCCGTGCTCATCAAACTTCTGCCGT
GCGGCATATTAATTGTGATCAGTGCAGTACTTATGCACGTTTGTGCGAGGCATCGAGACGTCGCTTGAAGCTGAGGGATTACAACAATCCCGCCAAATATGCCATCCAGCT
TAATCTGAATGAAACCAAATCCAAGAAGCCGCCTCGCTGTGATCGCCGTAACGATCGGACTACCCTTTTGCTGGTTGCGGTACTGGTTTTGTTTCTGATCACGGAGTTTCCG
CAGGGATTACTTGGTCTGCTGTCCGGAGTGATGGAGAAGTGCTTCTTCGCCCACTGCTATCCGCCGGTTGGAGAGCTGATGGATCTGCTGGCACTGATCAACGCCGCCGTCG
GATTCGTGCTGTACGGTCTGATGTCGAAACAGTTCCGGACCACCTTCCGATCGCTGTTCATGAAGCGGCACTTTGGCAGCACCGAAATGACCAGATTGACCCGCGTAACCAC
GACTTGCGTCTAG
(SEQ ID NO: 143)

Start ATG: 1

MMQETGNQMGQTHMHQRVPFNDTVLKDYHLTSTDIEKFVKLWQEYQMKNMTPQVDECQGYCQGEIYNWLRAYNSIHGYVSLMICIFGTIANILNIMVLTRKEMAKTPINNIL
KWLAVADMFVMLEYIPYTSYQYIYMGPGEKDLSYTWAVCLLVHMHFTQILHTISIGLTVTLAVWRYVAIRHPNGGCANFLLAHSREAILLPFILSPILCLPTYFVFQVRETY
DVDKVNSEAMYHVYFDKDSVLYRFNFWIHSVLIKLLPCGILIVISAVLMHVLCEASRRRLKLRDYNNPAKYAIQLNLNETKSKKPPRCDRRNDRTTLLLVAVLVLFLITEFP
QGLLGLLSGVMEKCFFAHCYPPFGELMDILALINAAVGFVLYGLMSKQFRTTFRSLFMKRHFGSTEMTRLTRVTTTCV*
(SEQ ID NO: 144)

Name: TRH receptor-like
Classification: G_protein_linked_receptor

FIGURE SHEET 64

Celera Sequence No. : 142000013384808
GTTAAATGATTTACAAACAAGCCGACATCTCGGGAACCATTAAAGAGACATTTAAAGTCAAAAAGTGGCCAACTGAAACCCGTTAAAAATCCGCTTGCGACCGCAACTTGGCC
CGACTAAGGCAAAAAATAACATAATCCTGTCAAGTCATGCAGACAGGGCGATTTACATTATAATTTTAAATGGCAATGGATTAGTCATCATCAGTACCTGCTTATCTGGTTT
TCCTGATTTTTAAATCAAATCTGTGACTGTATCTCTTACCTTTCCTCTTGTACCTCGTTATTATAAAATGCGAAAACCCTCTGCCAAAGGACACTATAAAACGAATTTTTA
AAAGACGCCAAACAAAATGGCACTTTTTGTTGAGAAGAAAATATGCCGATAAGAACGTTTTACTTGTAAGACGCTGCAGAAAGATTAGGAACGAAAACTATCGACAATGTTT
ACTTGTATAATCTGAGCTTTCTAAAACACAAAAATAGTGTACTTTTACCATACGCTTAATTTCGAAATTAATCCGGGATATACAGTTGGGGATCCAGATTTTAAATTCGTGA
ACACAGCTGCTGGAGTAGGGCATTTCCTGATCGATCTGTTAGTTTTCGGACTTTTACTTTGGTTGTTGTAAACAATATCCGCAAGTTTCTCGCAAAGTGGGTTGCGTTGTGC
CGTGCCTCAGTAGAGCACTACACACTACCTTCGATTGAGTTCGCTGGGATTTGGATTTCGTTCACAGTCCAAGTTTGGACCGTGCTAGGAGAAGATAATGATCCGATCACTC
AATTAACTTCATGCACCCAGTGACGTCATCAGTGCTTTACTATTCGGTGTCTATATAGTCTATTTTGTTTAATTTCTTACACCCTACATTTCGATACGATTCGATTTTCGTT
TGGAAATTGTCTGAAGGTAAACAAGCATAAATTGGACGTTCAAGCGTAAACAAATCGGTTTTCGGAGCAAAATACAAAAATCGTCAGTTGAGAAAGTCTCTCAAATGGCGCA
GTTCTGCATTCTTGGAGTCCTCCTCATTCTTTCTGGAACACACTGCTCGTGGGGATTCCATGAAGAGACACATTATCCGTGTGCCTTTATCGATACGGCAAACATAACGGGG
AGCTACGGCTTAGATGGCCCATTTGTGCACAACTGGACGGTGATTCCCCGTCACTTCGTAGCCGTGTACGACTTTGTCATCGAAAATGGCATCCGCATCCCCGCAAGCAGGC
ATCTCAGAGCCTGTGTCTGTAAGACCAAACCCTGTGTACGGATTTGCTGTTTACGGGGAGAAATCTACGACCTGGAGAAGAGGCAGTGCTTAGTCCCTGTGGCCGGGGTGTC
CAGCCTTCCCTCCCATAGCCATATGGAGGTGGAGTTGGGCAACGGCAGTCTGCGTCTAGTGAAACTGCAACCCCGTTTTAGCATCCACGTGGAAACACCATGTGAGCACATG
AAAGCCGTAACCAAGGGCTCGGAATACGTTCACTGGACACTTCATGAGGTCGGTTGTGAAATAAACCTTCCATCACATTAATGGCTTTACATCGCCTTTTCAGAACGGAACC
ATCAGCCACCGAGGACACATATTTTCTAAGCATTACTGCTTCACTCCGCTGCTCCATGGGAACTCCACCTGGGAGTGGCAGCCATTGGCCTGTGCACCAGAAAAACTATATT
TCGTCTTGGGGGTGCGGGAGTGGACATACGCCATATGTAAGTAGCAAGAGGAAACATTTTTCCAGCAACTTTCAGCAATTCATTATTCCAAATATGCACAATACTGTTTATC
CAACAATACATAAAAGTAATTGCTAAAGCACCAAAAAAACAATCGATGATAGCATTAATAGTTTGATAGTCAGAATTTAATTTACCCAGCGTATTCACTTTCCAGGTCTCTTG
ATAGCTATTCTATCAATGTTTATCGTGCTGATGGTCTACCTTATGTGTTCGGAAATGCGCAACAGTTTCTACGGTGTGGCCATAAAGGCGTACGCCATTTGTATGATCTTGG
CCCTTCTTTTTTTTTTTTTTAGCAAGTTTGGCGTTGATGAACTTGGTGCTTTCCTTTTACATTCTGAGCTTTATTGCATTTAAGCTGTACTTGAGCTTTTATGGCGTTGTCTTC
ACAAAACTGATGTTTTGGCTAATATTTACTCCCATCGTACTGGTAGCCGTGGGCTGGTCTTTCTTTGTGGGTTTCAGTTATTACGGCTCTAGGCTCATCTTCGGAGGCGATA
CATGCTGGTTTGATCGTAAGCACTGCCAATCCATATATGTTTATAATAATTAATTGGTATTCCACATCGCTAGCACGCAATTGGTCCGTTATGATATATTTTTACGCTCCT
GTTTTCGTGGCTTGCGCCATTAGCGGTTTCTTCTATGTCCTGAGCCAGATCTACATCCGTGATCAGCCAGATATCGAGACGGAGAAGAGCTTCGAGTCCATAGAGAAGAACC
GATTCAAATCATTTTGGAAGTACTTTGGCTACACGGCAGTCGTATGGGTCGTTTGCATATGCTCCTTTGCCTTTAACTACTACTGGGGAGAACAGATCCCACCTTAACTACGC
TGTAAGCTTCTCGCATGGCCTTCCACGGGTTTGCGGCCCTCTATGCGCTGATTGGAAAGAATCAGCAAATCCAAAATTTTCTGCGGCGCATAGATAATGGCGAAGATAACTAT
GAATTTTAAGTACTACTGTTAATATATACTGTTGCAGTGGCGAAGATACCTGTGAAAACTCAGTTCCGCTCTCGAGTTTTGGTTAACTTTTCTTGTTGTGCCCACTGTAGCG
TTAGTGTAACTGGAAGCAGTTGAGTGTATCGACAATATCTGTGCAATGTTTTTAAAATCACTTATCAGCATAGACAAAAACCATGTATTTTAAATGTAAAATTTTGTAGGAT
GTGTGTAAAATATATTTGTAAAATTTGAACTCGAACAAAAAAGTACACTTCTACCCTTTAAACGAAATTACGATAATAAAGATACAAAAAATAAATATATCTGAAAAAAAAA
TCAGGTCTGGAATTTCTACAATTGTTAAAATATGATAACAAGTCCCAACAATCCTTTCAGTATAGAACAAAACATGGAATATACTTAAGCCATGTGAAAGAACACATAACATA
TTAATATTCTAAACAATTTGAGCAGTTTTCTTGAGTTTACGCCTCCAACAATTTATCCTTCACCTTTCTTGAGTTCCAAATTCCTGGACCGTGATCAAGTTTCTCCAGTCTT
ATTTCAAGTCCCGATTTTTACTGTACCCTATCCGCATCGCCAAGCCCGGTGTTACTTCCCCGATCTCTCTATATTATAAATGTGCGCCGATTTTATTTAACATCAGAGGTCAA
TGGCCGCAAAACAGACAGAGAGAGAGAGAGAGAGAAAGTTGGTCAGAGCCACGAGAACTGCATCCCGACAGGGGGCTGTCAAGAGCAAGGAATCAAGTGGAATGTTGGTGGTGC
TCTTTTGAAAAGGCTTCGCAAACTTTCCCCCTGTACACCCCCTTGCCAAGGCCTAATCGCAGAAAACCCACCCGGGTCGGAGTCCCCAATTCATTTTCATGCCGATTATGCT
TCGGGTTTTGGTCCTGCTCTTTTTGGCTGGGCGTACAGCAGCAGGACTCGGGGTACACACTAAGAGAGGTCTAAGAATATAGAGATAGACAAGGAAAGCAGATGGATCGATA
AAACGTAGTAAAAATGCTCGTAGTAATGGAAGCTGGAAATAACATGGCACAAACAGGCCCCAAACTGCATCGACAACACCATCACAATCCAGACGTGCGCACTGGAAAATCC
CGAGAGGTAGGACATGTTTGGCGCGTTTTTCGACTGCATGTGTGCGAGTGTTCTGTTTTGGTTAGATACGTATGAAAAAGTGAAAAAGCCTATATTGACCGCGCCCGGTAGA
TCGCATAGGCAATATCGATATGGGAAATCATTGACTAACATTTGCAGACATTTAGTTTGGGACACATTAAAGTTAATTTGACTC
(SEQ ID NO: 145)

Exon: 1001..1504
Exon: 1560..1716
Exon: 1897..2088
Exon: 2149..2367
Exon: 2427..2784
Exon: 2838..3116
Start ATG: 1001

Transcript No. : CT32762
ATGGCGCAGTTCTGCATTCTTGGAGTGCTGCCCATTTGTGCACAACTGGACGGTGATTCCCCGTCACTTCGTAGCCGTGTACGACTTTGTCATCGAAAATGGCATCCGCATCCCCGC
AAGCAGGCATCTCAGAGCCTGTGTCTGTAAGACCAAACCCTGTGTACGGATTTGCTGTTTACGGGGAGAAATCTACGACCTGGAGAAGAGGCAGTGCTTAGTCCCTGTGGCC
AGCACATGAAAGCCGTAACCAAGGGCTCGGAATACGTTCACTGGACACTTCATGAGGTCGGTTGTGAAATAAACCTTCCATCACATTAATGGCTTTACATCGCCTTTTCACTCC
GCTGCTCCATGGGAACTCCACCTGGGAGTGGCAGCCATTGGCCTGTGCACCAGAAAAACTATATTTCGTCTTGGGGGTGCGGGAGTGGACATACGCCATATGTCTCTTGATA
GCTATTCTATCAATGTTTATCGTGCTGATGGTCTACCTTATGTGTTCGGAAATGCGCAACAGTTTCTACGGTGTGGCCATAAAGGCGTACGCCATTTGTATGATCTTGGGAT
ATGCCCTACTGGCTTATCTCACGCTCCACAACCCAGCAAATCTCTCAAATGCGGCTTGTCGTATTCTACCAAGTTTGGCGTTGATGAACTTGGTGCTTTCCTTTTACATTCT
TTTGTGGGTTTCAGTTATTACGGCTCTAGGCTCATCTTCGGAGGCGATACATGCTGGTTTGATCGTAAGCACTGCCAATCCATATATGTTTATAATAATTAATTGGTATTCCACATCGCTAGCACGCAATTGGTCCGTTATGATATATTTTTACGCTCCGTGTTTTCGTGG
CTTGCGCCATTAGCGGTTTCTTCTATGTCCTGAGCCAGATCTACATCCGTGATCAGCCAGATATCGAGACGGAGAAGAGCTTCGAGTCCATAGAGAAGAACCGATTCCAAATC
ATTTTGGAAGTACTTTGGCTACACGGCAGTCGTATGGGTCGTTTGCATATGCTCCTTTGCCTTTAACTACTACTGGGGAGAACAGATCCCACCTTAACTACGCTGTAAGCTTC
TGCATGGCCTTCCACGGGTTTGCGGCCCTCTATGCGCTGATTGGAAAGAATCAGCAAATCCAAAATTTTCTGCGGCGCATAGATAATGGCGAAGATACCTGTGAAAACTCAG
ATCAGCATAGACAAAAACCATGTATTTTAAATGTAAAATTTTGTAGGATGTGTGTAAAATATATTTGTAAAATTTGAACTCGAACAAAAAAGTACACTTCTACCCTTTAAAC
GAAATTACGATAATAAAGATACAAAAAAT
(SEQ ID NO: 146)

Start ATG: 1

MAQFCILGVLLILSGTHCSWGFHEETHYPCAFIDTANITGSYGLDGPFVHNWTVIPRHFVAVYDFVIENGIRIPASRHLRACVCKTKPCVRICCLRGEIYDLEKRQCLVPVA
GVSSLPSHSHMEVELGNGSLRLVKLQPRFSIHVETPCEHMKAVTKGSEYVHWTLHENGTISHRGHIFSKHYCFTPLLHGNSTWEWQPLACAPEKLYFVLGVREWTYAICLLI
AILSMFIVLMVYLMCSEMRNSFYGVAIKAYAICMILGYALLAYLTLHNPANLSNAACRILPSLALMNLVLSFYILSFIAFKLYLSFYGVVFTKLMFWLIFTPIVLVAVGWSF
FVGFSYYGSRLIFGGDTCWFDPRNWSVMIYFYAPVFVACAISGFFYVLSQIYIRDQPDIETEKSFESIEKNRFKSFWKYFGYTAVVWVVCICSFAFNYYWENRSHLNYAVSF
CMAFHGFAALYALIGKNQQIQNFLRRIDNGEDTCENSVPLSSFG*
(SEQ ID NO: 147)

FIGURE SHEET 65

Name: mth-like 8
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384832
AGTCAGTGCCTGGACGGATCGCACGAGTCCTTCTACTAAGCGCTACCAGTGGTGGTCGTAATCCCCCAATCCAAACCCATACCCAAAGCTTCGCTGCATTTTCGAATACAAA
CACTGAACTATCCGTCGTTGTAAAGCTACCTTATCCACTACGATTACTACACTATCCTACAAAAAACTATGCTGGTTAAAAGACTATACACCTAGCTCCATATACTATATAT
ATATATACAATATCGAGGCATGTGTTGTGTGGGCGAGTGAGTGTGTGCGTGTGACTTCTGATTGAGTTGCCATTTGATTCCAAGTATTTTCGAGTGCTTAGTTTTGTAATTT
GTAGCTAGCCGTTAATGTTTGTATAAACTGTTTCATTGGTTTCCCACTCCGCTTTATTCGATAAGCTCGTTTTCTAGATTTTAGCTTTAGCACTCTTAGTTTAATGTTTAAA
GTTAGTTTCGCTGTTAAGTTTACACCGTAGTCGAGGCGTCTTGAGTAGTTCTTTTGTACATTAAGCTTACACTTAGCTCTACATTAGATATACCATGTCGAACCTACGAGTC
TACGAACATACGAACATATATATGTGCGTTGAAAGCGTTGTATTTTTTGAAGCCGAACTTATGCAACCGAAAGGAGACAATAAACAAATGTGCTATAAAGGACGAAAGTGTC
GCAAATAAATGTGAGCCACTGCTAAAGAAGACCGATTTGCGCAAGGTGTTTTACTCGGCGGCGGCGGCCAAGAAGCGTTTGGGGCACAAACGACGGATGAGTGATTGCCACTC
GTACCATCATCATGACGATGGCGTGTGGAACGACGTGCGCATAGTAATGACAGCGGATGGCAATCTGAACGATAAGCGGCACCCGATAATGAAACATTAAACTAAACCGTCG
GTAGTCGCTGGCCATAAATCTGTCGGCAGTCTGCTCGCAGAAGCTTTTAGGTGCGGACCCCTTGCGCGGCATACTTTCGGGCTTCCGTTCCGTTCCGTTCGCCAATGGCCCT
GCTCCACTACACCTTCGACCAGCTCGAGTTGTACCTAGAATGGGCGTTCGCCCAGCACGGAGAGGCCACGCCGATTCCCTCGATCCAGCCGTATCCGGGCGTGTTCGTGGGC
GATCTCAGCCAGCTGAACCGCTTCAAGCGACATGCCTTCTCCGCCGTCGTGGGCACGCTCTTCGTCCTCGCCTTCTGCGGCAACCTGAGCACCCTCTATGTGAACAGCCGCC
GGAAGCTGCGGCCCTTCTTCCGGGCCTGCCTCATCTCACTGGCCTGCAGTGACCTTGTCTCCAGCATATTCTGCACCGTATCCTACATGGCCCAGTTCCAGGCGCAGTATCT
GCAGCTCTGGGTGAGGCGGCAGGGATTGAGCAGACTCAACACAAGCTAATTACAAATCTCCTTAGACAATTGGTGGCTTCATGTGCAAGTTTGTGCCGTTCATAACCACCAC
GTCGGTGTTGTCCGGCAGCCTGACCCTGGTGGCCATCGCCTTGGACCGCTACTTGGCCGTGATGCGACCCGTGCTGGGGTTCTGGAGTCCCGACAAACGCTTCAGCACTCTG
AGCATGCTGCTCATCTGGGCATGTTCGATAGGATCCTCTGGCCCGCTGCTGGGCATCTACGACTACCGAAAGATCTATCTCCTGGATGTGGAGGACTCCAGCGAGGAGAGCG
AGGAGGTCGTGACCGCTGTGCCCGAGGAGCTGGTGGTCACCGAGCTGGAAATGGTTCACATGTGCCTGGCCGGGGACGTAAGTCAACGACTGGATTATCGCTTAATACAGTT
GACAGCGATTAAGGGGATTGGACGGGGGGGGATGTCAAGTTGTTGAATCAATGTTCCGATTATCTTATCAGCCGCGTCGAAAACAATTTATGCAATTCTATAAATATTCCGTT
TTAGCACGACGTCGGACTCTACTACGTCATACTGTTCACCCTGATCTTCCTGCCGTGCATTGTGTCCTTCCTATGGCTGAATGCCGTGATTGCGAGGCAGCTCTGGCTGCGG
AGACACTACCACCAGGAGCAGCAGGAGCAGCATCAGGAGCCCAAGGAGGGTCAGTTTAAGACCATGGCGAATGGCGGGGATCTCTTGATGCCCTCCACCTTGGTCAGTGCCA
TGGGAGTGGCCGTTCCCTTTGCGCTGGACAACACTCCCTTGCCGCCCAAGAGTACCGTCAACGCTCCTGGCAAGAAGAAGACCACTGCTGCTGCTCTAGCCAGGGAGGCCAGG
CCGCAAGATGGTGGTGGTGGTGCTGCTAATGATGGCGGTTTTCATATGCCTTCGACTGCCCGCCTGGGTCTTCCTGATCATGCGGCTTTATGGATCCTACTCCGAGCCCATC
GACTGGCTCCTGTACTTCAGCTTCGGCATACTGAACCTTTTCAGTTGCGCCCTAAATCCCATCTTCTACACCTTCCTCACCCAGACCATTAGGACCTTGACGCTGGTGAAAC
ACAAAATTCAGGGATTTCTTGGCTGTCCGCCTGGTAAAGTGCCGGATGGTATGCCCACGGATCAGATGGACAAAAGCGGGTGCTGCTGCGGCCTGAGGCCACCCACCTTCAC
ATGGAGGTGCCATCCCAGCCGCGATAGGGCAGCAGCCACCGTAATCCGGGATGTGGACCAGCCAGATCCGCCCTCCGACCAGGTGCAACCGGATCCGAGTAGCCTACGGCGG
TTCCTCAGCTACAAGCAGGAGGTGTTCACCATTTACAAGCAGTGCGGTGACTCGTCGAGTGCGTCAATCGAGTCCTCCGCCTGATAGGCGGTGGTCATAAATCACCCGGGTG
CATTTGTCGGATACGGGGGCCAACGGTTAGCAGAACCCCAGAACTTGATTGATGGATGGATCCAGCCCCCATTCACTCTGTACAGGCGCAAAAACGGTTTGTCACGGTGGGT
ATATCACCCACGAATACACTAGCACGCATATAAGATATAAGCTCACATATTATGTACCTCATCAAATGTGTAAATATGAGGAATAAACGAATGGGTGTTGGCAGCTAACTAA
CCATTAACACATGGCGCAATCGAAATCGGGAAGGTCTCAGCTATTATTGTGACGAAAACCTAAGACCTTTCAAGTACCACTTAAAACTATATTTAGAGAACTTAAGCAAATT
GTGAGATTAAAATGCAATGCAACTCCTAAAGGTGCGAATATACCTATTCTTAAATATTTTTACTCTAGAAATACTGACATCTTTATGTGCTTAGTTTTCGTTCAGACAGACT
ATCTTTGTTATTTCTAAGAACGTAGTAATTAGTTAATGGAATTAATTAGTAACCGAAACTTAAAATTGAGTCATGCCAAAAAAAAGAGAATTGGCCTGACAAGACACACATTA
TAGAGTCAGCAGATCGTGGACGAGACAATGAGCCCGCAATGCAATGGAACTAGATTGTATCATATACTAGATACTTCCGCTTGGAACAATGGTTAACAGATCTCGTGAGAGA
TGGGGCTGAAAGCAGTTGTTAATTGTCAAATGTTGAGCACGCCAGTTAAATTTAGCTATGCAGCGAAAGCTCTCTCCCATACTCTCTTCCCATGAACTTTTTTAAGCCGCAG
AGCCCGAAGCTCGACTCAAAGCTGAATTCTGCGTTTTCTGGCATTCAGTGTCGGCGGTTTGCGGCGAGCGGTTGGATTCGGATTCTTTGGTCGGTAAAACGCGAAATCTTCT
GTGCGGCGGGTGAAATCTTCGGCAGAAGAAACAACAAAGCGACAAGTGTGGAGTGTGGAGTGCATACCGTACCACG
(SEQ ID NO: 148)

Exon: 1001..1354
Exon: 1410..1757
Exon: 1909..2772 ·
Start ATG: 1001

Transcript No. : CT32957
ATGGCCCTGCTCCACTACACCTTCGACCAGCTCGAGTTGTACCTAGAATGGGCGTTCGCCCAGCACGGAGAGGCCACGCCGATTCCCTCGATCCAGCCGTATCCGGGCGTGT
TCGTGGGCGATCTCAGCCAGCTGAACCGCTTCAAGCGACATGCCTTCTCCGCCGTCGTGGGCACGCTCTTCGTCCTCGCCTTCTGCGGCAACCTGAGCACCCTCTATGTGAA
CAGCCGCCGGAAGCTGCGGCCCTTCTTCCGGGCCTGCCTCATCTCACTGGCCTGCAGTGACCTTGTCTCCAGCATATTCTGCACCGTATCCTACATGGCCCAGTTCCAGGCG
CAGTATCTGCAGCTCTGGCAATTGGTGGCTTCATGTGCAAGTTTGTGCCGTTCATAACCACCACGTCGGTGTTGTCCGGCAGCCTGACCCTGGTGGCCATCGCCTTGGACC
GCTACTTGGCCGTGATGCGACCCGTGCTGGGGTTCTGGAGTCCCGACAAACGCTTCAGCACTCTGAGCATGCTGCTCATCTGGGCATGTTCGATAGGATCCTCTGGCCCGCT
GCTGGGCATCTACGACTACCGAAAGATCTATCTCCTGGATGTGGAGGACTCCAGCGAGGAGAGCGAGGAGGTCGTGACCGCTGTGCCCGAGGAGCTGGTGGTCACCGAGCTG
GAAATGGTTCACATGTGCCTGGCCGGGGACCACGACGTCGGCTACTACGTCATACTGTTCACCCTGATCTTCCTGCCGTGCATTGTGTCCTTCCTATGGCTGAATGCCGTGATT
TGATTGCGAGGCAGCTCTGGCTGCGGAGACACTACCACCAGGAGCAGCAGGAGCAGCATCAGGAGCCCAAGGAGGGTCAGTTTAAGACCATGGCGAATGGCGGGGATCTCTT
GATGCCCTCCACCTTGGTCAGTGCCATGGGAGTGGCCGTTCCCTTTGCGCTGGACAACACTCCCTTGCCGCCCAAGAGTACCGTCAACGCTCCTGGCAAGAAGACCACTGCT
GCTGCTCTAGCCAGGGAGGCCAGGCCACCGCAAGATGGTGGTGGTGGTGCTGCTAATGATGGCGGTTTTCATATGCCTTCGACTGCCCGCCTGGGTCTTCCTGATCATGCGGC
TTTATGGATCCTACTCCGAGCCCATCGACTGGCTCCTGTACTTCAGCTTCGGCATACTGAACCTTTTCAGTTGCGCCCTAAATCCCATCTTCTACACCTTCCTCACCCAGAC
CATTAGGACCTTGACGCTGGTGAAACACAAAATTCAGGGATTTCTTGGCTGTCCGCCTGGTAAAGTGCCGGATGGTATGCCCACGGATCAGATGGACAAAAGCGGGTGCTGC
TGCGGCCTGAGGCCACCCACCTTCACATGGAGGTGCCATCCCAGCCGCGATAGGGCAGCAGCCACCGTAATCCGGGATGTGGACCAGCCAGATCCGCCCTCCGACCAGGTGC
AACCGGATCCGAGTAGCCTACGGCGGTTCCTCAGCTACAAGCAGGAGGTGTTCACCATTTACAAGCAGTGCGGTGACTCGTCGAGTGCGTCAATCGAGTCCTCCGCCTGA
(SEQ ID NO: 149)

Start ATG: 1

MALLHYTFDQLELYLEWAFAQHGEATPIPSIQPYPGVFVGDLSQLNRFKRHAFSAVVGTLFVLAFCGNLSTLYVNSRRKLRPFFRACLISLACSDLVSSIFCTVSYMAQFQA
QYLQLWTIGGFMCKFVPFITTTSVLSGSLTLVAIALDRYLAVMRPVLGFWSPDKRFSTLSMLLIWACSIGSSGPLLGIYDYRKIYLLDVEDSSEESEEVVTAVPEELVVTEL
EMVHMCLAGDHDVGLYYVILFTLIFLPCIVSFLWLNAVIARQLWLRRHYHQEQQEQHQEPKEGQFKTMANGGDLLMPSTLVSAMGVAVPFALDNTPLPPKSTVNAPGKKTTA
AALAREARHRKMVVVVLLMMAVFICLRLPAWVFLIMRLYGSYSEPIDWLLYFSFGILNLFSCALNPIFYTFLTQTIRTLTLVKHKIQGFLGCPPGKVPDGMPTDQMDKSGCC
CGLRPPTFTWRCHPSRDRAAATVIRDVDQPDPPSDQVQPDPSSLRRFLSYKQEVFTIYKQCGDSSSASIESSA*
(SEQ ID NO: 150)

Name: Neuropeptide receptor-like
Classification: G_protein_linked_receptor

FIGURE SHEET 66

Celera Sequence No. : 142000013384832
AGGACACATTGGCGTACTTAGTCTAGACCACTGGGTGAGCTTAATGTTTTGCCGTTCGGTTATATATCATGCGGTGATTTGTGGACTTAGCATAAAACCTAACTGAACGGCC
CGGCGACATCCCGACTCTCTGGCGACTTTGGACGGGCCACGATAAATCAAGGCGCAGATCCGGGAGCCCGGCATATAGTGGATATAGTATGCGTGGCGAAACTTAATAAGAG
ATGCGACAACAAACAAATGATACAGATAGACAGACGGCAGGCGACAGTCGCGGTGGTGCGAGAGGTGGGTAGGTGGGTAGGTGGGAAATGGGATTGTGGAAAGCGGAAAAAT
CTTTAAAGCAATGCCGCTGCACAGGACATTTTTCACCGCGCATCCATTCGCAGACGGATCGCCAAAGAGAGACATCAACGTGACTCGCGGGGAGAACAAGTGTTTTGATTT
ATCGCCAGCAATGGCAATGGCAGGGCGGACGGGGATTGCCATCCAATTATACTGCTAACTTTCATTATGTCACTGTGCTATTTCGGGACCGGATTCGCCGCCATATTGGCCC
ATTGTTGCGGCCATTGTCTATGCACAGCTCTCTGTTTAGCAGTGACACACTGCCGGTTTCGGTGGCAGGACTCATCTCCATCCTGCCGCCTGCCTTAGTCGTCCCTTGCCGCTT
CCTCGGTGGACTCCGTCTGATAAATCGTCAGCGCGGCTTCCCTTTTCACATGCTTTGACTTCATTATGGCGTAACAAATCGTCGGCATTTTGCATTCCTCGCTGCGGAAACGG
AAGCGGAAGACATCCCCGAAAGAAACTGCGAACTGGGCCTTTGTGGCCACACGACGAATTGGTCACGCGCCATATAGACAATTCCATCTCAGTTTTCCACATGTTTTGATTG
CTCAACGTTGTCAAGGGACTTTGTGCTGCTGTACTTTTTTCGCTTACACTTTAATAGCTTCCGAAGAGACTCATATCCTTCATATCCTTTCTTGCAGCTCTGCCATGGGATCT
AAAGACTGGCTCTCTCCTGGTAGCACCCGCCGTGAAGAACTCCAGCTGCTCGCATCCGCGCTACTCCGGCCACAATTTCATCGCCCACATAGGGATTGCGGAGACCATCGAG
GCGGTGCTCATCCTGGTCCTCACACTGGGCGTCATCGGGGCCAACTGCCTGGTCATCTTCGTCATCAACAACCGCCGCTATGCGGCCTACATACACCAACAGGTGGGGAGGCT
GAGTCACTGGCTTAACACCTTGTACATCTTATGTCTCTCCTTGTAGCCCCGTTATCTGCTCACCTCGCTCGGCCCTGAATGACCTGACAATTGGTCTGCTAATTACACCATTC
GGTCTAATGCCGGCATTGTTCCACTGCTGGCCATACGGAGAGATCTTCTGTCAGATACAGGTGAGCGGGTCAAGAGTGGGTCAACACCAGGTCAACAAGTGGGGCGGAAGTG
CGATAATTTGTTATGGAACACCCGTCTCCCGTTTGCGGCTGTTGCCACTGCGGTCAATTAACTCTCTCTTAACAATGCACAGTAATTACTGGACATAAATGGCGGTGATGGA
AACGGACAATCCCGATTAACGGGCGGAACAATGTGTAATGCTAGTATTAACGTGGTCGAGAGTGTGTAGGATTCTGCGGTAAGAGTCAGGGTTCCGATGCAGAAGGTGTGAC
AAGCGGAAAGTTATCCCAGCCATATGGTTAGGAAGCTAGTGCACATGGAAAAACCATTGTGCCATTAATTATCATGACGGTGGACAGGGGGCATCGTGGTTAGGGTGTGCAA
CAGAAACTGTTAGTTTATCACTTATCAAGTGTCAAAAAGCATGCAACGAAATCACCTAGAATCCATCACAACAATTGTTGCATACATGCTTAAAAAGGTTGGGTTTTTATGA
AAATCAGAGTTGTAAACATTGTAATAAAAATCCAGTTAACACTCATACAACTATTTTCATGGGAACCAGACTCTTGTTATATATTTTATACGATGTCGTTCACAAAATTTGA
ATTTTTCCAACTGCCACTTTAGGGTTATTGGTAAAACATGCACGCATTCCACGCATAACTCTCACAAATATTGAAACACATACTGACGATTAATAATTTTATTAAAAGTTTTT
CGATTCGCCTCGACAAGCGAAAAAGTTTGCCGAAAGCAATAATACAAATAATAAACTTCTAAACGAGCACTAACGCATTTTCTGGCTTTTTCGCGTTTTCCAGGCCCTGCTC
CGAGGGGCGCTTTCCCAGCAGAGCGCCGTCATCCTGGTTTGCATGGCAGTCGATCATACATGTGTGCCCTGCATCCGCCGCCTACTACCAGCACTCCAGCAGGAAGGTAA
GATTCCACGTCCTATCGCCTCGCATCGATAGGGAACTTCTATTTTGGGTTGCCCGGATAAGGCACGCTCCTCGGCGATCCTTATCCTGTTGTTCTTGCACTCGCGCTCGCGC
TCGGAAGGACAATAAACAAAGCTCCGGCATAATGACGAGAAATCACGCGCCAATAAAATCGACTATAACAATGGGAAGAGCACCGCACAGCAACTACACAATATGGTCGGCG
AGCCAATTACGCAAGCATAAATAAGGATAATGGGCTTTAAGCAGCTTGACAGTCATTAAACAGGCAAAAAATGGGTGGGCAGCGCCAAAGAGCAAGTGCAAAACAAAGCATC
ATGGAGAATGAAAAAGCAAAGTTGGCAAAAACCAACAAAACCGAAAAAAAAAAACAACGGGGGCCAAGTCGAATAGACATTCGAAAAGTGTATAAAATGTGGATAAAAAAAG
GGAGCAAAGTTGGCCTAGAGATTTTTTTACGCGCAATGACTTCGGCACAGGGCGACGACCAGCAAAGTCCTTTTCCAGGACGCAGGCAGGCAAATGAAGCGGCACCTCCCA
CGGAAACCGCAGCCAGGACCAAAGAGCAGCAAAGAGCTCTCAACCAACCCTATTTCCCATTCCCCCCTTCGTAATTTATGGCTCCCGGACTGTAAACAAACGAAAACTAGG
AGGCCAACAGTCGGCTAAGAACACCGAAGTCCGAATGTCCTTGTCCCAAATGAACGGGACTGTTTCAGCTGAAATTGGCGATCAATAAATGTATAGTTTAGAATCCATTTCC
AATTACTAAACTAACTAAAAAAGGAAAATGCCATCAGGCCAAATAAAACAATTGGAAAACGGGAAAGTACCAATAGTGGAAAATAAATTTACATAACAATTTTGTATGCTCC
GAAAATCGGCGCCATTTCGGTTTTTTCATGCCATCTGGACGAGTGGGCGAAATTGGCGCACTGCCACGCCCCATTTGTAAAAATGATGGGCGCAGTGTCGAAAATTAATAAA
TAAATTCAAAGCCAGTCTTGGACATATCTCTTTATTTATAGTGAATTTAACAGCTTAACTCGTCTTGTTGTTCGCCACTCACAATTTGTATTAAATGCACTTGAA
AATTCAATTATTTTGTTATCTAGGATATTTGCTGACTATCCTTACAACTTCAGCAGTCGCCGGGTTGTGCTCTACGAAAAACTCCTGCAATCCTGCAAAAAAAAAAAAATAAT
ATTTACATTTCAAAAATTGTACCCAACTGTTTGAGATCGCCCTGCTTGTTTGTTCGTTCGGGAAAAGTTTTAAATGTGATAGCGTAAATTAAATTAATCACAGCCATGGT
CCGTTTCAAAGAGACACGGACAAAAGTTGAGCTTCCCTTTTTTTCCATGACTTTTTGGCACTTGGGATGGGGCCATTTTCATTTTTTCAGGTGGACAGGTGGACAACATTTTC
CCCTTTACCAAGTGATTTTGGCATAATCAAAAGTTTGTAATTCTATTTTTGGCCTCTTTGGTGAATGTCAGACGAAATGTGCAGTGAAGCGAGTGGAATTTTA
GCAAATTAGAAAGTTGAAGAGGGAATTTCCGACTTATCTGCACGCCTTAGTGTGATATAAGCCACTTCCGGCTAAATAAACACTTAATATGAATTACCCAACCTTCATTCAT
TTTCAATTCAGTATTGGCCATATTGGCCTGAAATGCAGGGAATACGTGCCTGAAGCCCTTCGCCAGTCATAAATCAGACCGCACCTGGCGGAAATGTGCTCCACTAATTGTG
TATTCATTTTGCAGGGCTGCGTGGCCATACTGAGCTTAACCTGGATTATCAGCCTGACGGTGTTTGGCTTTCTGGTGCTGCCCAAAGGTGAGCTGCCCGAGATTGGCCCGAC
ATCAATGCTCTCGAACACGTCAAACCATAAACTATATGCGCAGGTTACTACTTCAACAATACGGGTCTAATGGCCTGCGAGCCCTTCTACAGCAAGCCATCCTACAGGAT
ACTGTCCACGTGCGCCCTCTACTTTCCCACGACGATGGTGCTGATGTACTGCTACGGCTCCAGCTTCCACATGAGCCGCTTCCGGCTAAACGATCCGACCATGCCCCTCACG
GCGGCCGCCCACCACCCCCATCCGCACCCACATCCCACCGCCGCCCAGCAGCTGCAGATGCCACCAGCACCAGCAACATCACCAGCAGGCGGGAATGCACTCGCACCTCTACC
ACGGCCACTCGCATCACCCCAGCCACCCCAGTCACCCAAACCACCCCAACCACCACGGCCACCCCCACCATCATGGACCGCCCGTTATGGGCCATCTCAGCATGGCCATGAG
CATGGGACTGGCCGGCATGCCGAACATGCAAACAAGGATTACCAAAAAGGTGAGCAGCTGAACGGGGTGACTGAGGGAAGGCCAGGTGGCCTGCTGGCCAAAAGGATGAAGA
TGGATGAAGGAGGATGAAAGAGGATGAAGTGGGCGGGCTCCACAACAGTTTGCTCAGGCGGGCGATTGGGGATTAAGTTAGCAGTAAATAGAATTTTCTCGGCATCGCCAA
CCAGAACTCAGGTAAACTAAACTAAAACTCACTTAAAAAAGAACTCGAGTTGTGCAAGTTACTTTACTTACTTTCCGTGCATAAAAATATTTCCAGAAGCCAATATTACATT
TTAGCAAAATAGAAAGCAGCAAAGTTGCATTTGAAAATATATAGAATACTCAACTATATTGCTAATAAACAGGAATAGAAATTTCGTTTGGGCAGTATCTACACATAATTG
AATCAACAATAGTCACTTTAATTCAATCGCCGCAAACATTCCCACAGATTGTTCCCATCCAAGAGAAGAACTCCAGCGGATCCACCTCGCGCTCGATGGCCGCCATTTCACT
GGGCTTCATAGTGATGGTCACTCCGTGGACGATTCAGGAAATAGTCACCGCCTGCACGGGATCCAAGGCAAGTGTCCTGTACAAAGGATTATTGTGTGACCGCTTTGTGCTC
TCACCTGGACGGCGCTGAGCAATAGTCTGTGGAACCCGTTCATGTACTGGCTGCTGAACCTCCGATTTCCGCCGCATGAGTCGCCAGCTGATGCCGAACAAAGTGACTATCGG
GTATCCAACAGTGGGAAGATGAATCTCCTCTTCTGGCGCTAATTTACTGCATCTCTGATCTGGAGCGATGTTCACTGTCCGTTTCAGCAGCAAATCTGCCATAAGCCCTGAT
TGATTGATTCGCTTATCCCTATTCCAAACACCACGTGCACACTTTCATTGACCTCCCCGAACGCCAATCCCCAAGCCCAAATATGGGTATTTCGCCCAAGTGCATCCTGCAG
CTCGCAAATTTTCCTCCTGCACAGCGCAAAGTTTGCAAAAACAGGAGCTACATCCTCCCGAAAGCCCCCATAAATCCGTAACCGAAGGTGTAAGCTCCAGAATGCTGGCAGA
GCCCCACAAACCCCATCCCATAGGTCCTGATTCCATTTTGGTAAACGCAGTCAAGTTGCATGATTTACTTCCGGAGAGCCGGGGTCAGTCTGTGGAATATTTATGGCCCAAC
CTTGTGCTCTGCCAGAATAAATGCGCATTTAAAATCCTTATTAATTTTTGTGCGAGTCGGAATTTATGATGCCTCCCTGCCGTTTCAGTGCTTCCCCCACGAGGATACGCCC
GAGCACAAATCAGGCTGTTGTCACATCAATGCTAACGATTTCGAAATCACAACGCTTCCGATTCCCCCGGAGCCGCCATCATCCCGTCCTCCGGGCGGAGCAGGAGGAGGAG
CGCCTCCCAGTACATCCGAGGGACAATGGGCGGAGGAGTCCACAATCACCAGGCCACGGAAACCTTCTCCACCACGAGGCCTGACATTGAGGGCCTCTCCGGAAGTACTGG
GGCGAGATCCTGGAGAGAACCGTCAGCTCGGGCAACCTGAATGCCATGCAGAAGCACCTGCCGCCCCACCTGCCCTACGCCTCCACCACCTGGTCCACCAGATCCACCAGCCGC
AGCAGCACCACCAACAGCAGACCACCTCCTTCAGCAAGGCCAGCGATCTGCAGCTGAACCTGAACCTCAGCCAAGCAGCCACGGCTGCCGAGCTGGGCAAGTTCTCCAACTC
GGAGCCGAAGCTGTGCGAGCACCTCTTTCACGACGTAAACTGCGCCAAGAGCAAGGCCGCCAACGGGGATGGGGAGTCCTCCGGCAAGCTGGCCTGCGGTCGCAGCATTCCG
GACATCTAGTACGCCGAGGACGTGATCCTGGCCAAGAACCAACTGCTGGCCAGGCAGGCCAAGTGCTCGCACATCCGCTGCACCAGCCAAGACGCGTCTCCATTCCC
ACACGGGCAGCCTGCGCTTCAGCCGGATTCCGCGCTGCCTGCCCCACAGTCCGCCGCCGGAGAAGTCCGCCTTTCCAATGCCCGAGTATCCGCAAGTAGGATCACAGAGGGCACTG
GGATCAAGGATGCCGGGATACGGTACTCCAGGATGTCCAGGATATGGTATAACCATGCACAGAATAGGGAGTGAGAGCGAGCGAGTATCTATAAGATTCCATAGGTGTATGT
GCGTGTGAGTGTCTATATAATACCGCATGATCAAACCATAATATGTGTGTTTTCTATTAGGCTTAAGATCTAGGAGGTCCTTTGGTTGGGTTTTCAATTTAAAGTCTCTGAG
GGTTATAACTCGAATGATTGCTGTCCATCTGAGAACTTTCAATACCATTAGCTAGACTTTCTTTACTATACATGGATCTGGGGAATCGGAATTAGCCGAGTTAAGCAGAAGT
TAACCATAGTAAGTGTTCATTCAATGTTTGTGATACCCTAAGTTTCCCAGCCCAACATACATACCTACCAGTAACATATAATATAATCCTAGTTGTTGTGCGTGCGTCGGCT
AAATTAAACGTAGGATATATGGAAACAGAGATATCAGACTTTCCTATCAGAACCCGCTCGACATTCGGAAGCCCTTCGCCAAATTCTCCACCCACTTAGGGACTAAGGATCTA
CGTAGACTCTGATATCGGCGGACCTTAAAGCGTTGTGGTTAATCATAGTTGTAGTTCCATAGCTCGAGTCGTATACACCAAATTACTCACTGTTCGACGAATCAAAATCAAA

FIGURE SHEET 67

68/89

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TCCTAACTTTGTGATTGTCAAGAATTTAAGTCGGTTGATGTGGACATTGCTGTTAAATTAATTTTTATTTGTAGCTAAGTAATTGACTAGTTAAAGCCAAATAAATTTACCG
TTTAAGTAAGTCTAACTTTAGTTAAATAAACGAGCGGTGTGTAACAAATGTATTTCATAGGCAGAGGATTCAAATCGAAATAAATAA
(SEQ ID NO: 151)
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Exon: 1001..1222
Exon: 1279..1404
Exon: 2232..2348
Exon: 4495..4567
Exon: 4638..5107
Exon: 5648..5818
Exon: 5912..6037
Exon: 6697..7314
Exon: 7402..7599
Start ATG: 1001
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Transcript No. : CT32961
```
ATGGATCTAAAGACTGGCTCTCTCCTGGTAGCACCCGCCGTGAAGAACTCCAGCTGCTCGCATCCGCGCTACTCCGGCCACAATTTCATCGCCCACATAGGGATTGCGGAGA
CCATCGAGGCGGTGCTCATCCTGGTCCTCACACTGGGCGTCATCGGGGCCAACTGCCTGGTCATCTTCGTCATCAACAACCGCCGCTATGCCGGCCTACATACACCAACAGCC
CCGTTATCTGCTCACCTCGCTGGCCCTGAATGACCTGACAATTGGTCTGCTAATTACACCATTCGGTCTAATGCCGGCATTGTTCCACTGCTGGCCATACGGAGAGATCTTC
TGTCAGATACAGGCCCTGCTCCGAGGGGCGCTTTCCCAGCAGAGCGCCGTCATCCTGGTTTGCATGGCAGTCGATAGATACATGTGTGCCCTGCATCCGCGCCGCTACTACC
AGCACTCCAGCAAGAAGGGCTGCGTGGCCATACTGAGCTTAACCTGGATTATCAGCCTGACGGTGTTTGGCTTTCTGGTGCTGCCCAAAGGTTACTACTTCAACTACGGG
TCTAATGGCCTGCGAGCCCTTCTACAGCAAGCCATCCTACAGGATACTGTCCACGTGCGCCCTCTACTTTCCCACGACGATGGTGCTGATGTACTGCTACGGCTCCAGCTTC
CACATGAGCCGCTTCCGGCTAAACGATCCGACCATGCCCCTCACGGCGGCCGCCCACCACCCCCATCCGCACCCACATCCCACCGCCGCCCAGCAGCTGCAGATGCACCAGC
CCATCATGGACCGCCCCGTTATGGGCCATCTCAGCATGGCCATGAGCATGGGACTGGCCGGCATGCCGAACATGACAAACAAGATTACCAAAAAGGTGAGCCAGCTGAACCGG
ATTGTTCCCATCCAAGAGAAGAACTCCAGCGGATCCACCTCGCGCTCGATGGCCGCCATTTCACTGGGCTTCATAGTGATGGTCACTCCGTGGACGATTCAGGAAATAGTCA
CCGCCTGCACGGGATCCAAGGCAAGTGTCCTGTACAAAGGATTATTGTGTGACCGCTTTCTGCCGCCGTTCCTCGATTTCCTGGTCACCTGGACGGCGCTGAGCAATAGTCT
GTGGAACCCGTTCATGTACTGGCTGCTGAACTCCGATTTCCGCCGCATGAGTCGCCAGCTGATGCCGAACAAATGCTTCCCCCACGAGGATACGCCCGAGCACAAATCAGGC
TGTTGTCACATCAATGCTAACGATTTCGAAATCACAACGCTTCCGATTCCCCCGGAGCCGCCATCATCCCGTCCTCCGGGCGGAGCAGGAGGAGGTGAGGTCCATCCA
GTGGAGGTCCCAGCTCTGGCGGCGGAGTGGCCAGTTCCATTGGCGGCTCCGTCCTTGGAATCTGCGGCCGCTCGCGCACAAACAGCCTCAGCCGCAGCGCCTCCCAGTACAT
CCGAGGGACAATGGGCGGAGGAGTCCACAATCACCAGGCCACGGAAACCTTCTCCACCACGAGGCCTGACATTGAGGGCCTCTCCGAGAAGTACTGGGGCGAGATCCTGGAG
AGAACCGTCAGCTCGGGCAACCTGAATGCCATGCAGAAGCACCTGCCGCCCCACCTGCCCTACGCCCACCACCTGGTCCACCAGATCCACCAGCCGCAGCAGCACCACCAAC
AGCAGACCACCTCCTTCAGCAAGGCCAGCGATCTGCAGCTGAACCTGAACCTCAGCCAAGCAGCCACGGCTGCCGAGCTGGGCAAGTTCTCCAACTCGGAGCCGAAGCTGTG
CGAGCACCTCTTTCACGACTACGCCGAGGACGTGATCCTGGCCAAGAACCAACTGCTGGCCAGGCAGGCCAAGTGCTCGCACCATCCGCTGCACCAGCAGGCCAAGACGCGT
CTCCATTCCCACACGGGCAGCCTGCGCTTCAGCCGGATTCGCGCTGCCTGCCACAGTCCGCCGCCGGAGAAGTCCGCCTTTCCAATGGCCGAGTATCGCAAGTAG
(SEQ ID NO: 152)
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Start ATG: 1

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MDLKTGSLLVAPAVKNSSCSHPRYSGHNFIAHIGIAETIEAVLILVLTLGVIGANCLVIFVINNRRYAAYIHQQPRYLLTSLALNDLTIGLLITPFGLMPALFHCWPYGEIF
CQIQALLRGALSQQSAVILVCMAVDRYMCALHPRRYYQHSSKKGCVAILSLTWIISLTVFGFLVLPKGYYFNNTGLMACEPFYSKPSYRILSTCALYFPTTMVLMYCYGSSF
HMSRFRLNDPTMPLTAAAHHPHPHPHPTAAQQLQMHQHQQHHQQAGMHSHLYHGHSHHPSHPSHPNHPNHHGHPHHHGPPVMGHLSMAMSMGLAGMPNMTNKITKKVSQLNR
IVPIQEKNSSGSTSRSMAAISLGFIVMVTPWTIQEIVTACTGSKASVLYKGLLCDRFLPPFLDFLVTWTALSNSLWNPFMYWLLNSDFRRMSRQLMPNKCFPHEDTPEHKSG
CCHINANDFEITTLPIPPEPPSSRPPGGAGGGGGGPSSGGPSSGGGVASSIGGSVLGICGRSRTNSLSRSASQYIRGTMGGGVHNHQATETFSTTRPDIEGLSEKYWGEILE
RTVSSGNLNAMQKHLPPHLPYAHHLVHQIHQPQQHHQQQTTSFSKASDLQLNLNLSQAATAAELGKFSNSEPKLCEHLFHDYAEDVILAKNQLLARQAKCSHHPLHQQAKTR
LHSHTGSLRFSRIRAACHSPPPEKSAFPMAEYRK*
(SEQ ID NO: 153)
```

Name: Biogenic amine receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384618
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GATAAAGCCCAATTACAGAACCTAATACATACACCTAAAATGACTAATTGACATCCATTGTGCGTATTACATAATAATGAATAATTTAAGTGATAGTTGTTTGAACTTACAG
AACACTTCTTAGTATTGCGGACTCATCCCATCCAACTGTTGACTCATTTCAAATTCTATTTAATTATATTTCTGGTCCTGGCACGAACAATAAATTGAGTTTATATGTATTA
CGCCCCTTCTTGTGGTCTCACTTTATGAAAAAGTTAATTGCGTGTAGTTGTTGGCTTTGCTAGATGGATTTTTATTGTGCCGCTTTACTGTCTGCTTTTTTCTTCATTTTCC
ACTCGCCTTTCATTTTTCATCCGCCGGAAAGCGAATCATTTTTTCGCACGCTGAGCAGTGCAAAGAAAGCAAACACAAGCAAACGAGCAGAATTTCATATAGTTGATTGCAT
TGTCTGCAGGAAGATGTTCGCACGATGATGCAGGACATGCAGGACTAAGGACTTCGAAGCGAATGGTGTGAGCTGTGGGCTGGGGCAGGGATAGTCTCATGAAATGCTGATAGCATGCG
CTCAATATTGTCAGTAAATAATACGCGCTTGTTAGAGCCAACTGCATACCAACTAAACTGAACACAGTGAGAATAAACATAACAGAAAGTTGAATTTGCTTAATATATAATT
TCATAAATTTGTCACACCAAAATTCGGATTTAAATTAAAAGTATAATTATATTAATAACATTATTTAATATAATTATAATTATATATAAAAATATATTTTTATATGTATGTT
TCATTTGGTTGCTGAAAACCAGTAACTAACTAATCTTTGTGGGCTATCCAAATCTCTTCATTGCAGAAACCGCAGCGTGCAACATGTGACGTCACAGGCATAAAGTATGGAG
AGCATATTAAAATATTTGCCATTTAGCTGGTTTAGCATGCATTGTTGCATTGACTGCCACATAACAAGTGGAAATTAGCAGGCAGCTACTGTAGACGAATCGAAATGGAAGG
TGGATGGTGGCGAGGAGGAGGAGGACAGTTTGGGCGGGAAAGCCATCATGGAAGGACACTCGACACCAAATGGGGCAGCTGCAAGCCACAGAAACAACAGCACAAGG
ACCAATATCGCGACCAACGGCTGTGCCCATTCGGGCATCCTGTTATTTGTGCTGACAGCTATGACACTAACGAGCTTAATAACGCCCACAGAGCAGCTGGCAGTGGCGCCAA
ATGGCACCACACTGCATCAACTGGAGTCCGTGGAGTCCGAGTCGTATCCATCCATAAATGGCACTCAGAATGAAACAATGGTGACCAGTGTGCGACCCCACCTGGACCACAG
GAATCGACCGACGCAGCAGAATGGCAGTCACTATTTGGAGTACGACGATGATGGCCCGGACTGTTCGTACAGCTACAACTTCATCCTGAAGCTCATCACGATGATCCTGTAC
GCACTGGTCTGCATCATTGGACTCTTTGGCAACACCCTGGTGATCTATGTCGTGATGAGCTTCTCCAAGATGCAGACCGTAACCAACATATACTGAATGCTGGCTATCG
CGGATGAGTGCTTCCTGATCGGCATTCCCTTCCTGCTCTACACAATGCAGGTGGGCAACTGGCCCTTCGGCAACTATATGTGCAAGGCCTACATGGTGAGCACCTCGATCAC
CTCCTTCACCTCCTGATCTTCCTGTTGATCATGTCGGCGGATCGCTACATAGCCGTTTGCCATCCCATATCCTCGCCTCGCTACCGAACGCCCTTTGTATCCAAGTTGGTT
TCGGCCTTCGCCTGGATGACATCCGTGCTGCTGATGCTGCCGGTTATCCTTTTTGCCAGCACCGTGCAGTCGAGCAACGGCAATGTGTCCTGCAACATCGAGTGGCCAGACA
CTCAGAACTCGCACACCGACTCCACCTTCATTTTGTACTCGCTGGTCTTGGGATTCGCCACTCCACTGACTTTTATCCTGGTGTTCTACTGCCTGGTGATCAGGAAACTTCA
CACCGTGGGACCGAAGCACAAGTCTAAGGAGAAGAAGCGCTCTCACAGGAAGGTCACCAAGTTGGTGCTCACGGTAATAATATATGACATTTCGATTAGTTGTGGAACTAAC
TACTACCTGACCACTCTTGTGTTCAGTTTGATAAATATTATTATTACATTATAAATATATATTTTTTTTGACATTTTGAATTCGACTATAAATTAATTGTTTTAAATTGAT
ATATAGAAAGAATTTTATAATATTTATTCAATACAATTTATGGTTTTTTGATTTCTCCACAGGTCATAAGTGCGTACATATTTGTTGGCTTCCACACTGGATTTCACAGGT
AACTAATTGTATACATTACAGTCTAAAAACATTTATCTTTGTGTACTTTAAAAGGTTTTAAAACCATAAGCTATTTGCCTACTATTATCCTTTTGGATTGATTTTTAAATTA
TTATAGCTAAAACAAATTACGAGATTTGTGGAAATTGACATGAACTGGACTTCTTTGGCAGATCATTTGTAGATTCGCTTTTTATTGACTATTTTCCAGGTGGCTTTGATCA
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FIGURE SHEET 68

GCTCCGCTCCTCAACGCTGTGCATCTCGTCTGGAGCTGGCCGTCTTCCTGGCCTGCGGATGCCTCAGCTACTCCAACTCGGCCATGAACCCAATACTGTACGCCTTTTTGAG
CGATAACTTCAAGAAGAGCTTCATGAAGGCCTGCACGTGTGCTGCCCGCAAGGATGTGAATGCCCAGTTGCAGCTGGAGAACAGTTTCTTCCCCAAGTTTGGCAAGGGCAGG
CAATCGGAGCGTCTTCTTGGTGGCAATGGAAAAGGTGGCGCCCAGCGTGGGGCATTAACCAAGAAGAAGTGCTTGGCGACGAGAAACAACAATGCTCCGATGGCCACTACAA
CGACGACGACAACCACCACAACGGGCACGGATGCAGTGACCTGTCTCCAGCCGCCAGTACACCAGGTGCCAGCCGAGATCCAGGTGGGAAATCCGGCCACCGTGCTGGTGGT
CAATGCTGAGACCAACAACTGTAAACCGCCCGTGCTCCACACGGACTTATAAGACCGGGCTCCCTCGATGCCCCTGGAAACGGTGGTCTTCATCGCGCGGAGGTGAGACCAT
CAGGTTGAGCTGGACCTCGATACGGCCATCGATTGCCAGGCAATAGCGAGGCAGCCGGAATGCTTGCTATAGGTCGCCTAAAATGATATTAACATTTTATACCAATATGGCA
GAGCTTTGCAAAAACGGGTAAACTTAATCCCATTTTTATATGATCGAATCTCAGCAAGAAGAAATTTTTAAAAACCCGAATAAA
(SEQ ID NO: 154)

Exon: 1001..2332
Start ATG: 1001

Transcript No. : CT33159
ATGGAAGGTGGATGGTGGCGAGGAGGAGGAGGAGGAGGACGTTTGGGCGGGAAAGCCATCATGGAAGGACACTCGACACCAAATGGGGCAGCTGCAAGCCACAGAAACAACA
GCACAAGGACCAATATCGCGACCAACGGCTGTGCCCATTCGGGCATCCTGTTATTTGTGCTGACAGCTATGACACTAACGAGCTTAATAACGCCCACAGAGCAGCTGGCAGT
GGCGCCAAATGGCACCACACTGCATCAACTGGAGTCCGTGGAGTCCGAGTCGTATCCATCCATAAATGGCACTCAGAATGAAACAATGGTGACCAGTGTGCGACCCCACCTG
TCCTGTACGCACTGGTCTGCATCATTGGACTCTTTGGCAACACCCTGGTGATCTATGTGGTGATGAGGTTCTCCAAGATGCAGACCGTAACCAACATATACATACTGAATCT
GGCTATCGCGGATGAGTGCTTCCTGATCGGCATTCCCTTCCTGCTCTACACAATGCAGGTGGGCAACTGGCCCTTCGGCAACTATATGTGCAAGGCCTACATGGTGAGCACC
TCGATCACCTCCTTCACCTCCTCGATCTTCCTGTTGATCATGTCGGCGGATCGCTACATAGCCGTTTGCCATCCCATATCCTCGCCTCGCTACCGAACGCCCTTTGTATCCA
AGTTGGTTTCGGCCTTCGCCTGGATGACATCCGTGCTGCTGCTGATGCTGCCGGTTATCCTTTTTGCCAGCACCGTGCAGTCGAGCAACGGCAATGTGTCCTGCAACATCGAGTG
GCCAGACACTCAGAACTCGCACACCGACTCCACCTTCATTTTGTACTCGCTGGTCTTGGGATTCGCCACTCCACTGACTTTTATCCTGGTGTTCTACTGCCTGGTGATCAGG
AAACTTCACACCGTGGGACCGAAGCACAAGTCTAAGGAGAAGAAGCGCTCTCACAGGAAGGTCACCAAGTTGGTGCTCACGGTAATAATATATGACATTTCGATTAGTTGTG
GAACTAACTACTACCTGACCACTCTTGTGTTCAGTTTGATAAATATTATTATTACATTATAAATATATATTTTTTTTTGACATTTTGAATTCGACTATAAATTAATTGTTTT
AAATTGATATATAGAAAGAATTTTATAATATTTATTCAATACAATTTATGGTTTTTTGATTTCTCCACAGGTCATAAGTGCGTACATATTTGTTGGCTT
(SEQ ID NO: 155)

Start ATG: 1

MEGGWWRGGGGGGRLGGKAIMEGHSTPNGAAASHRNNSTRTNIATNGCAHSGILLFVLTAMTLTSLITPTEQLAVAPNGTTLHQLESVESESYPSINGTQNETMVTSVRPHL
DHRNRPTQQNGSHYLEYDDDGPDCSYSYNFILKLITMILYALVCIIGLFGNTLVIYVVMRFSKMQTVTNIYILNLAIADECFLIGIPFLLYTMQVGNWPFGNYMCKAYMVST
SITSFTSSIFLLIMSADRYIAVCHPISSPRYRTPFVSKLVSAFAWMTSVLLMLPVILFASTVQSSNGNVSCNIEWPDTQNSHTDSTFILYSLVLGFATPLTFILVFYCLVIR
KLHTVGPKHKSKEKKRSHRKVTKLVLTVIIYDISISCGTNYYLTTLVFSLINIIITL*
(SEQ ID NO: 156)

Name: Somatostatin receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013383997
GATAAAAGCATTACATTTTCGAGTCTGCACGATCGTATCATCAGTTGTTTGCAGGACCTTGAGTTCTTCATACAAAGTTTTAGCTGCTCATTTTTAATCTGTTCCTTGTGCA
GAGATTACACTTCTCCGAAAAGAGCCGACACGTAAATTGGAAAAGGGTTAGTGCAACTGTTGTTGCAATTACAATTCATCACATAGCCCGTAGTTCCTCTTCCTGCTGCACA
GAAAGAAATTGGTATGTGGCGATCGTTGCAATGCCATGCAATTCAATGCCCAATTCAAAAATATTTGAAATGTGTAAACAACTCACTTGTTTTCTTTTCTGCGTGCATGTGG
TGCTCCTGGCCATTTGCCATTTCGCCAGGCATAATCCCGACAATCGGTGCGATGTGGGTGATACGAGTGCGAATGCGAATGCGAATGCCAATGATATGTGTATTGTATGTAT
GTGCATACATATGGCGTCGTAGCGTGTGGGCGTGATGTTTGCACTCCGGTGCAGCGGGACTATAAATAAGCCGGGTATTTATTAGGGGCAATCATAAACTGCGTTAACGACG
GGCACTCTGCCAACGAGAATAAGATCCGGTAAACAAAGGCACCGGTCGACGTACGTCTCATTGTGCGATAAGCTTTCAATTAAATCTGACCCGGATAACGGGGCGCATGGGT
GCGGGAAATCGGAAATCGGAAACGAAAACGAAAACGGAAGCGGAAATCGAAATCGAAATGGAAAGAGATCAATTTTCAATTGCAGCCAATGCATGCATGTCCATGGGTCCAA
TGCTAATATCGAAAGACAAAGCTCCGTGTTCTGGAGGTCGTGTTCGCCATGCAGACTCATTGGTTGGTTGGGTTTAACTCGTACAAAGTTTGATGGGTTTGGGATTGTTTTT
TTTTTTTTTTTTAGAACGATATAACTCGATATAATGCTGGTGCGTAAATAACAACGATGTTCATTGTTCGCTTTGCAGCACATTTACTATGCGGTCGATGGCAAAATGACCCT
CCTGTCGAACATTCTCGACTGCGGAGGCTGTATTTCCGCCCAGCGCTTCACCCGCCTGCTGCGCCAGTCCGGCTCATCAGGACATCCCCATCTGCACCGACGGCCGGAACGTATG
TTTGAATCAAAATCCATGCTGGAGCCAACATCCTCGCACAGCCTGGCGACCGGACGCGTGCCACTACTGCACGATTTCGATGCCTCGACAACGGAATCGCCGGGAACGTATG
TCCTCGACGGTGTCGCCAGGGTGGCCCAATTGGCCCTGGAGCCCACCGTCATGGACGCACTGCCCGATTCGGACACGGAACAGGTTCTCGGTAATCTCAACAGCAGCGCGCC
CTGGAATCTAACGCTTGCGTCGGCAGCGGCCACCAATTTCGAGAACTGCTCGGCGCTTTTTGTCAATTACACCCTACCACAAACAGGTACCTAAAGCCTAATAACTTTTAAA
TCATATTGCAGTATTTTTTTTTTTTTTTTGTTGCCGGGATAGGACTCTACTGCAATTGGACCTGGGACACATTGCTCTGCTGGCCACCCACTCCGGCTGGAGTCCTTGCAC
GGATGAATTGTCCTGGCGGCTTTCATGGCGTAGATACGCGCAGTAAGTAACTGAAATACACTCTAAAAAAAAAGCAGCCGAAAAAGAACATGCTGAGTACAATTAGCATAAT
TAATCGTTGAAGCTGTTTAGCTGTTTAGCAGCCACAAGAAGCTTTATGACTTCTGCCGGCTTATTAGGAGTCAAAAGACATGTCCTACGGTGTTTATCCCATCCACACGGCA
TATCTGGCGGTCACAATCATACGGATCATTAGCTGGGAAACGGTTCAAGTGGTGCACGGCAAACAATTACTTGATTCCGTATTCATCGAAAGGATGTCAATATTTACATGCA
TGACTGGGGGCGTCCAATCAACCGCACTCCCAGTCGGGGCCGCCCCTCCTTGGCTTCCATCGCCGGGGGCTGTCCAGGTGTTTCATGTGCACCCTCGAGCTCCGCCAGTTGA
ACAGGGTTTAAAACACCAGCCAATCGATTGCTTAATTACGATCCTAAATGCTTGCTCTACCCCTCCGATAAATTAAACGTTCTGCAATGGGGAATTGCTATTTAATAACCAT
GGGCGATATACACTGAGCGAAAAGATTCTAAGTAGCTGACTTACCACCCAATATTTTACAAACTTAAAATGCTCTTCCATTATCACTAGTGAATGTATTATCTGCGCTTGTG
GTGCAAAATCTAGGCATATCGAACTATATCTGTTAAGAAATAATTATTCGAGTGCATTGTTGAGCTACGGCCTCATTTCTCCGGGCCGTGTCTAGATTTTTAGCCCCAATAT
TTCGCAGAATTCGCCATCCGAAAGTGTGAACTGCATGGTCGATGGGGCAGCAGGCCAAATGCCCACGGAGGTGAATCCGCCCGGGATGGACGGACTACGGGCCGTGTTACAAGC
CGGAGATTATCCGTCTCATGCAGCAGATGGGCAGCAAGGACTTCGATGTGAGTTGAATTCTTTCCACACTACATCATAATACCTGTTTCAGTTATAGTTAAGAGCATTGCTT
AAATGCCAACCAAAATCCCAAATCAAGGGTATGGTTTTGAAATTACCTAATAGGGTTCCAAGTTTTTTAGACACCCTAAAAAGTGATTTCAAAGGCCTGATTACATTTGTTG
ATAGTGGTTTATAGTAGTAGTTTTAATTCCATTTCTTCCAACTGGTTTGCGATATCCCTTAGGCCTACATAGACATTGCCAGGAGGACTCGAACCCTGGAGATCGTGGGCCT
CTGCCTCTCCCTGTTCGCCCTTATAGTTTCCCTGCTGATCTTCTGCACATTTCGCTCGCTGCGAAACAATCGCACCAAGATCCACAAGAATCTTTTCGTCGCCATGGTGCTG
CAGGTGATCATTCGGCCTGACCTTGTATCTCGACCAATTCCGGCGGGGAAACAAGGAGGCGGCCACCAACACGAGTCTCTCTGTCATTGAGAACACGGTAGGCTTAATATTCC
CGCATAAGGATAAGGTATAAGGCTTATGTTCGATATTATATGTTATGTTCTACAGCCCTATTTGTGCGAAGCATCCTATGTACTTCTGGAGTACGCTCGTACCGCCATGTTC
ATGTGGATGTTCATCGAGGGCCTTTACCTGCACAACATGGTCACCGTGGCCGTTTCCAGGGCAGCTTTCCCCTCAAGTTCTTCTCGCGACTCGGCTGGTGTGTGCCCATTC
TGATGACCACCGTGTGGGCGAGATGCACGGTCATGTATATGGACACCTCGCTGGGCGAATGCTTGTGGAACTATAATCTCACGCCCTACTACTGGATCCTCGAGGGGCCACG
ACTAGCGGTCATACTGGTGGGTAATATCAACTGTTGATCGCTTTAATCACCTATTCACCCAACTGAAAACATCCGCATGCAGCTAAACTTCTGTTTCCTGGTGAACATTATC
CGAGTGCTGGTAATGAACGCTGCGTCAATCGCAGGCCAGCGATATAGAACAGACTCGCAAGGCAGTTAGAGCGGCTATAGTCCTACTACCACTTTTGGGTATAACCAATCTCC
TGCACCAGCTGGCTCCTCTGAAAACGGCCACGAACTTCGCGGTCTGGTCGTATGGCACCCACTTTCTCACCTCGTTTCAGGGGATTTTTTATAGCGCTAATTTACTGCTTTCT
AAATGGCGAGGTAAGACATCAAGTCACTCAGTTGTCCATTTGCCTAAAACCCTCACTATTTCCAACCAAAATATATATTTTTTAGGTTCGTGCCGTGCTACTAAAGAGTCTG
GCCACCCAGCTGTCGGTGCGAGGTCATCCGGAATGGGCGCGCCGAAAAGGGCATCTATGTACTCGGGTGCTTATAACACGGCCGCCGGATACGGATGCAGTGCAGCCTGCAGGAG

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ATCCATCGGCCACTGGAAAGCGGTAAGCATCCGCTTTGTGCACACCCCACCTTGAAACTCCTTACATCAATTTAAAACTCCCAGAATATCACCGCCGAATAAAAGGCTGAAT
GGAAGAAAGCCGAGCAGTGCCAGCATTGTGATGATTCACGAGCCTCAACAGCGCCAGCGACTGATGCCCCGGCTGCAAAACAAGGCGCGGGAAAAGGGCAAGGACCGGGTGG
AGAAGACGGATGCGGAAGCGGAGCCGGATCCGACCATCTCCCACATTCACAGCAAGGAGGCGGGCAGCGCGAGATCGCGAACTCGCGGCTCCAAGTGGATAATGGGCATCTG
CTTCCGGGGTCAAAAGGTACTAAGAGTACCGTCAGCGTCATCCGTGCCACCCGAGTCAGTTGTATTTGAGTTGTCAGAGCAGTAGACCAAAACCTAGCCTAACTAATAGATG
TAGCCATAGCCGTAGCCAAATAGCCGTAGAAGTAGCCAACGCCATGTAGCCCACCACCACAGTAGCCAGCACCCACACAATCGGACCGGAAATGATCCCAAAGATAACCCAG
AACCCGACTATTCCTGCATCTCCCATCGACCCACCAAGCAAGCCAGCTGGAAACAGCACATATGTAAAATACCCCAACAAAATATCGCAGTTCTTATACCCAAGATCATTTT
GAACAGAAAGTAAGCTCATTGTTTTGTAATTCAAATTAAACCAATAGACATTTAATTTAAATAGTTATTTTCGCTTGCCTTCGGTTCTTGCTCCACTGTACTTATGTAAATA
CATACATACCTTTATTTGTGTAAGCCATATCCAAACCCTTTCCAAAATCTAGAAATCTCCTATCCTTTCGAAATCGGCTAATCCTACGAAAATTCAAATTTCCCTACAAGTT
TTACAAAATATTTTTGATGACAATAAATTTCCAATAGCGTCACCTTCTGTTCTGGACACGCAAATACATTCAAAAACACTCGCACACGGTTCTTACTCGATGAATTTTTCAG
CAAAACTTCAGCGGCATGTTCTTTTACTTCTACTATTCATATTTAAATATTAGATTGAAATATTTAAGTGAATTAACACAAACTTGCGGTAACTGCGCAGTGTGGCCAGGCT
TTGTGAGCCATTAGAACTTATTACATAACATAATTGAAAAGTGACATTGTTTAAAGGAACTCACCTTTAATCAACTGTTGAACTTGCTGTTCATCGGATTCCGTTATTAAGT
TTTAAGATTTGGGTTTACTTGTATTTACATTTCTTTACCACTTTGATTAGCTTACACTTTCCGTTCCTGAGCTGGTCACACTGCCAGCTACAATCGATCACGTTCACTGCA
ACTGCCTTGAATTTTGCTAGCTGCGCTTTGTTGTGCAACAAAAACTTTGCCACAATCGATATTTAACTAATGGGGTC
(SEQ ID NO: 157)

Exon: 1001..1322
Exon: 1500..1610
Exon: 2472..2623
Exon: 2863..3120
Exon: 3192..3488
Exon: 3555..3818
Exon: 3894..4054
Exon: 4117..4453
Start ATG: 1001


Transcript No. : CT33238
ATGACCCTCCTGTCGAACATTCTCGACTGCGGAGGCTGTATTTCCGCCCAGCGCTTCACCCGCCTGCTGCGCCAGTCCGGCTCATCAGGACCATCCCCATCTGCACCGACGG
CCGGAACATTTGAATCAAAATCCATGCTGGAGCCAACATCCTCGCACAGCCTGGCGACCGGACGCGTGCCACTACTGCACGATTTCGATGCCTCGACAACGGAATCGCCGGG
AACGTATGTCCTCGACGGTGTCGCCAGGGTGGCCCAATTGGCCCTGGAGCCCACCGTCATGGACGCACTGCCCGATTCGGACACGGAACAGGTTCTCGGACTCTACTGCAAT
TGGACCTGGGACACATTGCTCTGCTGGCCACCCACTCCGGCTGGAGTCCTTGCACGGATGAATTGTCCTGGCGGCTTTCATGGCGTAGATACGCGCAAATTCGCCATCCGAA
AGTGTGAGCTGGATGGTCGATGGGGCAGCAGGCCAAATGCCACGGAGGTGAATCCGCCGGGATGGACGGACTACGGGCCGTGTTACAAGCCGGAGATTATCCGTCTCATGCA
GCAGATGGGCAGCAAGGACTTCGATGCCTACATAGACATTGCCAGGAGGACTCGAACCCTGGAGATCGTGGGCCTCTGCCTCTCCCTGTTCGCCCTTATAGTTTCCCTGCTG
ATCTTCTGCACATTTCGCTCGCTGCGAAACAATCGCCACCAAGATCCACAAGAATCTTTTCGTCGCCATGGTGCTGCAGGTGATCATTCGCCTGACCTTGTATCTCGACCAAT
TCCGGCGGGGAAACAAGGAGGCGGCCACCAACACGAGTCTCTCTGTCATTGAGAACACGCCCTATTTGTGCGAAGCATCCTATGTACTTCTGGAGTACGCTCGTACCGCCAT
GTTCATGTGGATGTTCATCGAGGGCCTTTACCTGCACAACATGGTCACCGTGGCCGTTTTCCAGGGCAGCTTTCCCCTCAAGTTCTTCTCGCGACTCGGCTGGTGTGTGCCC
ATTCTGATGACCACCGTGTGGGCGAGATGCACGGTCATGTATATGGACACCTCGCTGGGCGAATGCTTGTGGAACTATAATCTCACGCCCTACTACTGGATCCTCGAGGGGC
CACGACTAGCCGGTCATACTGCTAAACTTCCTGTTTCCTGGTGAACATTATCCGAGTGCTGGTAATGAAGCTGCGTCAATCGCAGGCCAGCGATATAGAACAGACTCGCAAGGC
AGTTAGAGCGGCTATAGTCCTACTACCACTTTTGGGTATAACCAATCTCCTGCACCAGCTGGCTCCTCTGAAAACGGCCACGAACTTCGCGGTCTGGTCGTATGGCACCCAC
TTTCTCACCTCGTTTCAGGGATTTTTTATAGCGCTAATTTACTGCTTTCTAAATGGCGAGGTTCGTGCCGTGCTACTAAAGAGTCTGGCCACCCAGCTGTCGGTGCGAGGTC
ATCCGGAATGGGCGCCGAAAAGGGCATCTATGTACTCGGGTGCTTATAACACGGCGCCGGATACGGATGCAGTGCAGCCTGCAGGAGATCCATCGGCCACTGGAAAGCGAAT
ATCACCGCCGAATAAAAGGCTGAATGGAAGAAAGCCGAGCAGTGCCAGCATTGTGATGATTCACGAGCCTCAACAGCGCCAGCGACTGATGCCCCGGCTGCAAAACAAGGCG
CGGGAAAAGGGCAAGGACCGGGTGGGAGAAGACGGATGCGGAAGCGGAGCCGGATCCGACCATCTCCCACATTCACAGCAAGGAGGCGGGCAGCGCGAGATCGCGAACTCGCG
GCTCCAAGTGGATAATGGGCATCTGCTTCCGGGGTCAAAAGGTACTAAGAGTACCGTCAGCGTCATCCGTGCCACCCGAGTCAGTTGTATTTGAGTTGTCAGAGCAGTAG
(SEQ ID NO: 158)


Start ATG: 1

MTLLSNILDCGGCISAQRFTRLLRQSGSSGPSPSAPTAGTFESKSMLEPTSSHSLATGRVPLLHDFDASTTESPGTYVLDGVARVAQLALEPTVMDALPDSDTEQVLGLYCN
WTWDTLLCWPPTPAGVLARMNCPGGFHGVDTRKFAIRKCELDGRWGSRPNATEVNPPGWTDYGPCYKPEIIRLMQQMGSKDFDAYIDIARRTRTLEIVGLCLSLFALIVSLL
IFCTFRSLRNNRTKIHKNLFVAMVLQVIIRLTLYLDQFRRGNKEAATNTSLSVIENTPYLCEASYVLLEYARTAMFMWMFIEGLYLHNMVTVAVFQGSFPLKFFSRLGWCVP
ILMTTVWARCTVMYMDTSLGECLWNYNLTPYYWILEGPRLAVILLNFCFLVNIIRVLVMKLRQSQASDIEQTRKAVRAAIVLLPLLGITNLLHQLAPLKTATNFAVWSYGTH
FLTSFQGFFIALIYCFLNGEVRAVLLKSLATQLSVRGHPEWAPKRASMYSGAYNTAPDTDAVQPAGDPSATGKRISPPNKRLNGRKPSSASIVMIHEPQQRQRLMPRLQNKA
REKGKDRVEKTDAEAEPDPTISHIHSKEAGSARSRTRGSKWIMGICFRGQKVLRVPSASSVPPESVVFELSEQ*
(SEQ ID NO: 159)


Name: Calcitonin receptor-like
Classification: G_protein_linked_receptor


Celera Sequence No. : 142000013385192
GCTTACAAAACCAAAAACCAGATTTTGTGCTTCAAATCACAAACATAACGAAAGAAATATGAATGGAAAACAGAGGATTTTATCATCACTTGAAGGCTGACAAAACATTTGG
CACAATTTACATTGTCCGGCGATTTATTGCCGTCTAGAGACAAAAAATACTCCGGAAAATTGTCACTTTGCTTGCAGTAGAAAGTAACTTTTAATTAGAGGTTACTGCAGC
TATGCAGCTGCTACTGCGGTTGCTACTAAAAGCAAAAGTGAAGATATATCCTTTGAATCTCAGCACAAATTGCATTCTCCGTATTTTCTCATTTGTCTAATGGAGTTATGTC
ACCAAGAAATGCGTGAGTGTTACACTCACAAAATATGTTCTATTCCCAAGAAATTCTTCTCTGTAAGTAAGTGTAAAAGTGTGTACACTAACTCTGTTTGTATTAAAGACAA
ATGCATAAGAATGCCTTAAATTCGTCTACGTGTAACATGTAAGCCAGAATTTTTGTTGCATGTTACACGTTTTCCCACAAATTGCCAAAATCATCTGCTTCTGCCGGCCCAC
TAGTCGTATGCGTATTATTGATTACGGAACGAGGCCTTGTTTTCTTACCATTTCGGACAAATGGTAATGACATTTCATTGTTGATTCGTTTGAAATCGTACCTTTGACCTGC
CCTGAACTTGGACATCGTTCTTTGCATGTGGCATGCAATGCCATTGTATTTGGGGAATTTCGAAGCTTAAATTCTGGTAAAATTCAAACCACAACACTGAATTCGTTTTTTA
TTCACCTAACGCCTGATGTTTATTTGCAGGTAGCAGGTAGCACTTTCGCCACGCAGCCTGCATATTTGAGTGTTGGAATTTCCGAAAAGGGAATTTAAATGAAACGCCAGAG
GAGCAGCGGGGCGCACTGAGTTGGCAGCCGGACACCGCGGTCAATCAAACGGAGTCCTTGCAGGACATCCCACCACCGACTACCATCTGGCCTTCATTGACACCATGGTCAC
ATATTAATTAGTTTTTTAAGTGTAATTTACATAATGATTTGCCAGCCGGGGGCGCATAATGAAATCATGTGTGTAATTGCCTACGGCGTGTGGCAAAAGGCTAACGAA
GTGTGCCTAATGTGGATGGGCCCCTTTCGGATTAAACTGAACAAATACTCGCATAAATCCATAAAGCAGATGTTAAAGGTCGGAGATGAACATTTTGAAAAATATATTGAGT
TCAATCTAACCAACCATGTTGTTTATTCGGTTTCTTTCTCTACATAAGCTCTAATTACTTTAAGAATTTAATCATACCCAATTTTGTGCTCAAGTGAAACTGGTTTTAAATA
TTTATCCCAATTTTTTTGTCTTTCTCCCCAACAGCTACAAATACTTTCACGGTTACTTCTCGCTGATTGTCTGTATCCTGGGAACCATTGCGAATACCCTAAATATCATAG
TGCTGACCCGACGGGAGATGCGCTCCCCCACAAATGCCATACTCACGGGTCTGGCTGTCGCCGATCTGGCTGTGATGCTGGAATACATACCCTATACGGTGCACGACTATAT
CCTCAGTGTAAGGCTGCCGCGAGAGGAGCAGCTCAGCTACAGCTGGGCGTGCTTCATCAAGTTTCACTCGGTATTTCCCCAGGTGCTGCACACCATCTCTCATTTGGCTAACG
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GTGACGCTGGCAGTTTGGCGGTACATAGCGGTAAGCTATCCGCAAAGGAATCGCATCTGGTGTGGAATGCGAACTACTCTGATCACCATAGCCACGGCCTATGTTGTCTGTG
TCCTGGTAGTGTCACCTTGGCTGTACCTAGTCACAGCCATTGCCAAGTTCCTAGAGACTTTGGATGCCAATGGCAAGACGATTGCCTCAGTGCCATTGAGTCAATACATTCT
GGACTACAATCGGCAGGATGAGGTGACCATGCAGGTCATGTCGAGTACAACGCCAGATGTTCCTGGGCGATACCAAGTGATTCGGCCAATGGAACTGCAGTTAGCTTGCTA
AGTCTAACCACAGTGATACCCCTAACCACATTAAGCACTGGAGTAACCACATCCTCGTCGTTGGGTGAGCGCAATGTGACTGTCTATAAGCTGTATCACAGCGCACTGGCGC
TGCGTGATCGGCAGTTCAGGAATGCGACCTTCCTTATATACAGTGTCCTGATCAAGCTGATACCCTGCTTCGCACTGACCATTCTGTCTGTGCGGCTCATCGGTGCTCTGTT
GGAGGCCAAAAGGAGGAGGAAGATCCTGGCCTGTCATGCAGCCAACGATATGCAGCCAATTGTCAATGGAAAGGTGGTGATTCCGACGCAACCCAAGAGCTGTAAACTGCTG
GAGAAGGAGAAGCAGACCGATCGCACCACGAGGATGCTTCTGGCCGGTACTGCTGCTCTTCCTGGTCACCGAGTTTCCACAGGGCATTATGGGTCTGCTGAATGTGCTCCTGG
GCGATGCCTTCTTTCTGCAATGTTACCTAAAGCTGAGTAAGTATTTTAGGATTAAGACACCCACTCCTCCGCTGTCTGTAACCCGTAATTGCTTTATTGGCTATGATAATTG
ACTGAATTTATGGTTGGTGTTTAGGTGGGCCCAGTTTGGCACATTCATCAATCATACGCACCCGTTGGCTGCCATAATTGCACCACAAATTTGAGGCTTCAATGAAGGCCTGG
CATTGACGTGTTCAATAAGTGTACATTTTGTTTATCTCGTACACCCAAAATAAAGTAGTCTTACATTTAAAACTTCGCAGATACTATTAAATTGAGAGATTTTTTTCTTTAA
TTTGAGTAAAAGTATAAAATTGAAAAAAAAAATATTTTAAACATTTAATATGTAGTTTTTAGCTAGCATATGTTTTTTCAAGTGTAGGAGGTATAAAATCTAATCGCCCTTGA
ACTTTATGAAAGCCCTGCCCATAGATGGCGTGTTGGTGGAACCCGACATTTATGGCATTTCGATTTTTTCGTTTCAGGTGACCTTATGGACATCTTGGCGCTTATTAATTCG
AGCATCAACTTCATCCTGTACTGTTCGATGAGCCGCCAGTTCCGGAGCACGTTCGCGCTCCTCTTCCGTCCGCGCTGGCTGGACAAATGGCTGCCGCTGTCGCAGCACGACG
GCGAAGGGAGGGTGGGCGGAAGTGGCGGCCTGGGCGGCTACGGCGGATATGGACGGCAGCGGTTGCTGCACACGGATGCCGTTAGCAAGAGCATGGCCATCGATCTCGGGCT
GACGACCCAAGTGACAAATGTGTAGCAGGAGAGCAGCGGCCGGGCGGCGATGTCAGCCGCAGCCGGCGGAGCAGCTGCATCGGTGGCTCTGGCCCTGGCAGCCACTGATGTT
ATCGAAGGCGGCGCAGTGGGAGTGGCACCAAGTGCATCTGGCCCACGACGGACTGGCTGAGAAAGCTGCGTAACCAGAAGGCTAGAGAAACGGAGCAATCCTCCGAACAGGA
CATAGAGCTGGGCAAGAGCTCCATCAACAGGCGCAGCAGTGTTCTTCTAATGGTATTACTAAGCAGCTCCGATGAGGTTAAAGCCAAGGCGGTTTTGGTCAGTGAACAGCCG
CCGAGTCCAGCGGACGAGGATGTGGAAGACGCCATTGACGCCCCTCTGGCTGTGAGACGACCCCTCACTTCCATTTTGTACGCCCTGTAAATTATCCAAGTACCCACTAATAT
TTAACTACCGTGTACAGACCAATTATTGAGACAAATTGTTATGCGCTGATTCCATTATTTTCCCGCCAGTGTTGTCTTGGCGAATCGAGAGCCCCTTTCGCTGAGACTTTGC
TTTGCTGGAAAATGAGTGGATTTTCCTTGAAAGGACTCCCTGGAAGCAGCCTGCAACACTTTGTGACCACATTTGATAAGTGATATACTTGACTAAGTTTCCCCCCTTAATA
GTTGTGTAAGTGCTAAGCGCGTCTCTAGATATAAACGAATTAGTCATAGTCTAACTATTAATTAAGATATATTGATGAAATAATTCGGAAGCTAAGAGATTAAATTTCTTTT
TATATTGAATAAATGTTTTTTCGAAGTAAACTTGATTCAATTCACTTATTGTAAGTGTTATTGCGACACTTTGTTTTAATTAAACGGAATTTATATTGAACTTTGATAAACG
AATGCTTTTGAATGCAT
(SEQ ID NO: 160)

Exon: 1001..1062
Exon: 1492..2093
Exon: 2172..2612
Exon: 3102..3385
Start ATG: 1001

Transcript No. : CT33298
ATGGTCACGAACATGTCGCAGCCGCCATTATTGCGGCACCGGCATCGGATGATTTCCACACAAACTACAAATACTTTCACGGTTACTTCTCGCTGATTGTCTGTATCCTGGGAA
CCATTGCGAATACCCTAAATATCATAGTGCTGACCCGACGGGAGATGCGCTCCCCCACAAATGCCATACTCACGGGTCTGGCTGTCGCCGATCTGGCTGTGATGCTGGAATA
CATACCCTATACGGTGCACGACTATATCCTCAGTGTAAGGCTGCCGCGAGAGGAGCAGCTCAGCTACAGCTGGGCGTGCTTCATCAAGTTTCACTCGGTATTTCCCCAGGTG
CCATAGCCACGGCCTATGTTGTCTGTGTCCTGGTAGTGTCACCTTGGCTGTACCTAGTCACAGCCATTGCCAAGTTCCTAGAGACTTTGGATGCCAATGGCAAGACGATTGC
CTCAGTGCCATTGAGTCAATACATTCTGGACTACAATCGGCAGGATGAGGTGACCATGCAGGTCATGTCGAGTACAACGCCAGATGTTTCCTGGGCGATACCAATAACCACA
TCCTCGTCGTTGGGTGAGCGCAATGTGACTGTCTATAAGCTGTATCACAGCGCACTGGCGCTGCGTGATCGGCAGTTCAGGAATGCGACCTTCCTTATATACAGTGTCCTGA
GCAGCCAATTGTCAATGGAAAGGTGGTGATTCCGACGCAACCCAAGAGCTGTAAACTGCTGGAGAAGGAGAAGCAGACCGATCGCACCACGAGGATGCTTCTGGCCGGTACTG
CTGCTCTTCCTGGTCACCGAGTTTCCACAGGGCATTATGGGTCTGCTGAATGTGCTCCTGGGCGATGCCTTCTTTCTGCAATGTTACCTAAAGCTGAGTGACCTTATGGACA
TCTTGGCGCTTATTAATTCGAGCATCAACTTCATCCTGTACTGTTCGATGAGCCGCCAGTTCCGGAGCACGTTCGCGCTCCTCTTCCGTCCGCGCTGGCTGGACAAATGGCT
GCCGCTGTCGCAGCACGACGGCGAAGGGAGGGTGGGCGGAAGTGGCGGCCTGGGCGGCTACGGCGGATATGGACGGCAGCGGTTGCTGCACACGGATGCCGTTAGCAAGAGC
ATGGCCATCGATCTCGGGCTGACGACCCAAGTGACAAATGTGTAG
(SEQ ID NO: 161)

Start ATG: 1

MVTNMSQPHYCGTGIDDFHTNYKYFHGYFSLIVCILGTIANTLNIIVLTRREMRSPTNAILTGLAVADLAVMLEYIPYTVHDYILSVRLPREEQLSYSWACFIKFHSVFPQV
LHTISIWLTVTLAVWRYIAVSYPQRNRIWCGMRTTLITIATAYVVCVLVVSPWLYLVTAIAKFLETLDANGKTIASVPLSQYILDYNRQDEVTMQVMSSTTPDVSWAIPITT
SSSLGERNVTVYKLYHSALALRDRQFRNATFLIYSVLIKLIPCFALTILSVRLIGALLEAKRRRKILACHAANDMQPIVNGKVVIPTQPKSCKLLEKEKQTDRTTRMLLAVL
LLFLVTEFPQGIMGLLNVLLGDAFFLQCYLKLSDLMDILALINSSINFILYCSMSRQFRSTFALLFRPRWLDKWLPLSQHDGEGRVGGSGGLGGYGGYGRQRLLHTDAVSKS
MAIDLGLTTQVTNV*
(SEQ ID NO: 162)

Name: TRH receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384809
ATAATTCTTATGAAAAATATAAAAATGGGCTGATTAAAATGATTGGTATTATGGAAATTATTATTGAAAAAATATGAAATTTACATTTTAAAAAGTGTTATTCGCGTTATTA
CTCAGTTTGTAAATAGCGGGCATCAATTGTGCATAGTTTGAAGGTAAGTTGCCCAATAAATGGCGCAAAGCTCGTAACCGCGAATTATATATGTATGTACATATACGATAAA
AATAAAGTGTGGCCTTTGCTTGGATAAAAAAATCGTCCGAGTCGCCGGATATCCATATTATCGCTTTCAGAAAATTCGATATCATCGATAGGTGTTTCCCTTTCAAAAGTCT
TCGTCCGATTTGGTCCGTTTGACTACTTTTATCTGGTGCATACCCGATTTGACTGCTTGGACGGAGTGGGATGTGTGAATGAACACTAAAACGCTTGAAACTTGAGAAATTA
GGGAAGTAGACGGGTAGCGTCAGTTTGTTTGAGAAGATTAACAAGCCCACAAAACTTGCAAGGCCATTTTATTATTTGTCTATCCATTTTCGATCGATATGGC
AACAACATTTAAGCCATGCCCACTCTAATGCGTCAATAAATGCGACTAATCCAGGCGGGCCCCCAAGTTAACTTGGCCCTCCTCATCGAGTCAAGCGGCTTCCTTCGAAGAAT
GATTTACCGTTGATCATACCGGGAAGCCTTTTTTGGTCTTCAGGGGAGGTAGAGACTACATGTGGTATTAAGATGAAAAAACTAAATGCGTACATCAAATCAAAAGTATTCT
·TATTAATCCAAGTGAATTATAATATTTATTTTGGCACCTTGTAAATGTGACAAGTGATTAGAAATGTGGTTCTTCTTAAAGTATAAAATGTACATCATAATATGCTAGAGTA
CTGCAGCGACTATTATTTATATACTCTCCCCGTGTCGCACGACTAAATGATTCATAATGAATATGAATACCAGAGTTCACGATGAGCAATAATCTCAGTTCCTGTTAAAGTG
ATGTCACTGTCGGCTTGTAGGGAGAGTCTGTGAAGGAAAAATATCAATGTTAAAAGAAGATAAATTAAAGCAATAAGATGAACACCAACCTGAAGATTTTAGATCGCCTTTCT
ACTTACACATTAATGGCCCACCAGGATTTGACGTGCAAATTCTTGCCAAGGAGCAGAATAAAACCAGCTATGGCCAGGCCCAGAATGCAAATTCCACTCCAGAAGTCAATGA
TGAAGAAATGCTCTCTCACTCTGGCCATTATATACACGACTATTTCTCGGATCCAGACCGCAAACACGCCCACTATGTAAGCGCTAAAGGCATAGAAACTGCAGGAATATAA
AAGATAAATAGGTCTATAATAAAAACAGCTTTTAGGAAATCTTACTGCGTCTTGACGATTTTCAGTTGAGTGCCCAATATGTACTGAGTATCTCGGTGGCAGTTCGTAGATGG

72/89

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AAAAGTACGCCTTGAGACAGCATACAATGCTGAATATCAGGAGGAGTGCAATGGGTCCGTAGTAGTAGATCAAAATACCCCAGGTGCGAACTGAAAATGCATAGATAATTCG
AAATTAGACTTTGTTGTACTTTCTTATTCAACCTACCATCGAACCAGCAGTAATCTTCTCCCATGCCTGGCTTGAAGTGCTTGGGCAGCTTGGAGTCCTGGGCTAAGGAGAC
GCCAGAAAGACGAAGGAGAGCATGATGCAGAAGTAGGCCAGAAATCCTTTTGGGATGCATAGAACAAAATAAGTTATCCAGTTGAAGTAGACAAAATTACTCAACCTATGTT
TCTGCAAGCCACATGCGAGAGCTTCATGGGATTCTTCAAGGCCAAGTAGACCAACAGGGAGTAACCAACGATCATGGACAGCAAGTAGTAGATGATTAACTGGCCATAGTGG
CTTTTTACGGGCATCTCTCACAGATCCAAGTAGGGAGAGTATGAAAATGTTTATAATGATGGCTATAATACTGCCTAGAAGGGAACAAGAGTTAGAATCTTCTTCGAAAGTATT
CAAACAACACGACTCACAAATGGCGTAAATCCAAACCCGGTACCCCGTTTGAAAGCGTTCGCAGTTGAGCGGAGTGAGCTCCCACTGCTCCGGATTGTGCTCCAACGGGCTA
AAGCAATACTCATCCGTTGACCACAGACGATTGTCCCGCCGCAGAGTTCCATTCTCGAAGAGGTCCCATTGCCAGAAGTTATCGTGCTTTTTGTCCACGAATTTGTTCCGGC
AACCCAGCTCTGTGCGCACCACAAAACGATCGCGTATGCGTACTTGATCCACAGTCCTGTTAGCGTAGGTGAGCTCCACGTGAGTGGACTCGCGGACTTGGTGTGGCATTGT
GCAGTTCCAGTGCTTGGCATCAAAGACGAGGTTCTCCGGACAACAGAAACTGATGCAGGGCTTCAGCAGACAGACGCAGCCGCGCAGATGTTTCTTGGCCCGGTACTCCACT
CCATCGATCACCTTGAAGGAGTACTCCGCCATCAGATGCGGTGGGACCACTACTCCAGCGTATGAGTAGGAGCCATCCTTCATCCGCAGTCCATCCGTAATGTTGACCGTGT
GGGCGTAGGCACAGGGATGGTTTATACTGGCGATCTCCACTGACTTTGCGCCCACGGAGAGCCAAATAATTAAAAGAATTATCAATGGCGAGACCATGGCTAACTGATCCAC
GCTTGTTGGATTTTTGGTCGATTCGTTCGTCGGCCTGACGTCACACGCTGTTCAGCTCGATAATTAAGTAAACAAATATGAGAAGCGATCGCCGTTCGCTTTGAGCAATGCA
CGCACACTCGCCGAGTCAGAAATCTGCACCAACAACAATGGAAACCCAAAATTGACAACGAATGTGACGCGGGTCTAAAAACGGCTGCGATTGCGACAACGACACCGACAAC
ACCAAAAAGAACAACCATAAACATAAAAGTTTGGTGGAGAGTCTCTCCTAGCTAGTCGTCTTGCCTCTCTCTAAACGACAAACCGGCAACCGCAACGGAGCTCCATGCTGGC
CAAGAATAAAAAACAGACTAACTGATTAGCCGTTCCCAAAACCAGACGCGACCACAAGCAGCTGGCAAAAAGAGCGATTGGGAAGACTCACAACCCGTCCCGCCCCTCCTCC
TAGAAACCGGCGTGGAATCTCAACCAGCTCGGAACTTGCACATGCATACCTTAAGTTGTAAGCATATAATCCATTCGAGCCATTTCCAGACTTATCTTGAGATAGATATAAA
AGTTAAGAATATTAGATTAGATTATTTCCATCCATTTTCTATAATTTATTGCCTTTGCGACCGTAAAGAAAATCCAATTTTTAACCGACAATCCAAATGGCCCAAACGAATT
TACCCACAGCTTTAGTTTTTAAATATTTAGGTGCATTTCCAGGCTATACAAAGTTTGTCTACATGTAGGTGTGTGACCTGGCTTGATATCGTTTACGGTCTTCAAGAATATTC
GAAAAGATTCGTTGATTTTTGACAAACAGATCCGCTGAGGAAAAAACGACGTTCATTTTATCTTTGGCTTTATTAAGCTTGAAATACAATTATAATTCTTGTATTGTGTTTT
ACATTAGTTCAGAGATAATGCAGATATGGAGAATGGTACATTTATGCAAAGAGGGTATACAATCAACACCAATCTCGTTTTTAACAAGGCACATCTGTATGTTACGTATTTTT
TGCTGGATGTTTACCTTGGACTTAGGCTAATGGAGAATTACAAATTTGATCTCTCAGCTGGGTTCGGAGAACCTTACAATTTTGCTTGCATAAACAGTAGATATGGCTCTGC
ATAAAATTTCTTATACAACTAATCAGGTTGTTCGTGGTCACATGGCATTAAAAAATGAAAGAGAATTGGGCGGGGTGGGGTGGGTAAGGGTTTTCGTGGTAGTTCTGGGGGAT
AGGGACTTTCTCTTATAGTAGTGTCTTTCATAAAGTTCTATCCGTATGTGGATGCTACTTCGCGAATTTA
(SEQ ID NO: 163)
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Exon: 3214..2258
Exon: 2201..2010
Exon: 1950..1717
Exon: 1658..1502
Exon: 1442..1239
Exon: 1176..1097
Exon: 1035..1001
Start ATG: 2897 (Reverse strand: CAT)
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Transcript No. : CT33414
TCGTTTAGAGAGAGGCAAGACGACTAGCTAGGAGAGACTCTCCACCCAAACTTTTATGTTTATGGTTGTTCTTTTTGGTGTTGTCGGTGTCGTTGTCGCAATCGCAGCCGTTT
TTAGACCCGCGTCACATTCGTTGTCAATTTTGGGTTTCCATTGTTGTTGGTGCAGATTTCTGACTCGGCGAGTGTGCGTGCATTGCTCAAAGCGAACGGCGATCGCTTCTCA
TATTTGTTTACTTAATTATCGAGCTGAACAGCGTGTGACGTCAGGCCGACGAACGAATCGACCAAAAATCCAACAAGCGTGGATCAGTTAGCCATGGTCTCGCCATTGATAA
TTCTTTTAATTATTTGGCTCTCCGTGGGCGCAAAGTCAGTGGAGATCGCCAGTATAAACCATCCCTGTGCCTACGCCCACACGGTCAACATTACGGATGGACTGCGGATGAA
GGATGGCTCCTACTCATACGCTGGAGTAGTGGTCCCACCGCATCTGATGGCGGAGTACTCCTTCAAGGTGATCGATGGAGTGGAGTACCGGGCCAAGAAACATCTGCGCGGC
TGCGTCTGTCTGCTGAAGCCCTGCATCAGTTTCTGTTGTCCGGAGAACCTCGTCTTTGATGCCAAGCACTGGAACTGCACAATGCCACACCAAGTCCGCGAGTCCACTCACG
TGGAGCTCACCTACGCTAACAGGACTGTGGATCAAGTACGCATACGCGATCGTTTTGTGGTGCGCACAGAGCTGGGTTGCCGGAACAAATTCGTGGACAAAAAGCACGATAA
CTTCTGGCAATGGGACCTCTTCGAGAATGGAACTCTGCGGCGGGACAATCGTCTGTGGTCAACGGATGAGTATTGCTTTAGCCCGTTGGAGCACAATCCGGAGCAGTGGGAG
CTCACTCCGCTCAACTGCGAACGCTTTCAAACGGGGTACCGGGTTTGGATTTTACGCCATTTGCAGTATTATAGCCATCATTATAAACATTTTCATACTCTCCCTACTTGGAT
CTGTGAGAGATGCCCGTAAAAGCCACTATGGCCAGTTAATCATCTACTACTTGCTGTCCATGATCGTTGGTTTACTCCCTGTTGGTCTACTTGGCCTTGAAGAATCCCATGAA
GCTCTCGCATGTGGCTTGCAGAAACATAGGATTTCTGGCCTACTTCTGCATCATGCTCTCCTTCGTCTTTCTGGCCATTTGCAGTCTTGACTTTCTGCTCAAATTTAAACAA
AAGGCTGTCAGGAGCTCCGTCCGTCGATTGTCCCTTGCTCTGGCAGTTCTGGCGGTGATTGGTCTTCGGTTTTTGGTCTCCTTAGCCCAGGACTCCAAGCTGCCCAAGCACT
TCAAGCCAGGCATGGGAGAAGATTACTGCTGGTTCGATGTTCGCACCTGGGGTATTTTGATCTACTACTACGGACCCATTGCACTCCTCCTGATATTCAGCATTGTATGCTG
TCTCAAGGCGTACTTTTCCATCTACGAACTGCCACCCAGATACTCAGTACATATTGGGCACTCAACTGAAAATCGTCAAGACGCATTTCTATGCCTTTAGCGCTTACATAGTG
GGCGTGTTTGCGGTCTGGATCCGAGAAATAGTCGTGTATATAATGGCCAGAGTGAGAGAGCATTTCTTCATCATTGACTTCTGGAGTGGAATTTGCATTCTGGGCCTGGCCA
TAGCTGGTTTTATTCTGCTCCTTGGCAAGAATTTGCACGTCAAATCCTGGTGGGCCATTAATGTGGAATCAAGTCAGACAGATCTGAGTATTATTAATGCTCGCGTATACAA
GTTCGATGAGAAAGGCGATCTAAAATCTTCAGACTCTCCCTACAAGCCGACAGTGACATCACTTTAA
(SEQ ID NO: 164)
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Start ATG: 318 (Reverse strand: CAT)
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MVSPLIILLIIWLSVGAKSVEIASINHPCAYAHTVNITDGLRMKDGSYSYAGVVVPPHLMAEYSFKVIDGVEYRAKKHLRGCVCLLKPCISFCCPENLVFDAKHWNCTMPHQ
VRESTHVELTYANRTVDQVRIRDRFVVRTELGCRNKFVDKKHDNFWQWDLFENGTLRRDNRLWSTDEYCFSPLEHNPEQWELTPLNCERFQTGYRVWIYAICSIIAIIINIF
ILSLLGSVRDARKSHYGQLIIYYLLSMIVGYSLLVYLALKNPMKLSHVACRNIGFLAYFCIMLSFVFLAICSLDFLLKFKQKAVRSSVRRLSLALAVLAVIGLRFLVSLAQD
SKLPKHFKPGMGEDYCWFDVRTWGILIYYYGPIALLLIFSIVCCLKAYFSIYELPPDTQYILGTQLKIVKTHFYAFSAYIVGVFAVWIREIVVYIMARVREHFFIIDFWSGI
CILGLAIAGFILLLGKNLHVKSWWAINVESSQTDLSIINARVYKFDEKGDLKSSDSPYKPTVTSL*
(SEQ ID NO: 165)
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Name: mth-like 9
Classification: G_protein_linked_receptor
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Celera Sequence No. : 142000013384809
CGAGCCATTTCCAGACTTATCTTGAGATAGATATAAAAGTTAAGAATATTAGATTAGATTATTTCCATCCATTTTCTATAATTTATTGCCTTTGCGACCGTAAAGAAAATCC
AATTTTTAACCGACAATCCAAATGGCCCAAACGAATTTACCCACAGCTTTAGTTTTTAAATATTTAGGTGCATTTCCAGGCTATACAAAGTTTGTCTACATGTAGGTGTGTGA
CCTGGCTTGATATCGTTTACGGTCTTCAAGAATATTCGAAAAGATTCGTTGATTTTTGACAAACAGATCCGCTGAGGAAAAAACGACGTTCATTTTATCTTTGGCTTTATTA
AGCTTGAAATACAATTATAATTCTTGTATTGTGTTTTACATTAGTTCAGAGATAATGCAGATATGGAGAATGGTACATTTATGCAAAGAGGGTATACAATCAACACCAATCT
CGTTTTTAACAAGGCACATCTGTATGTTACGTATTTTTGCTGGATGTTTACCTTGCACTTAGGCTAATGGAGAATTACAAATTTGATCTCTCAGCTGGGTTCGGAGAACCTT
ACAATTTTGCTTGCATAAACAGTAGATATGGCTCTGCATAAAATTTCTTATACAACTAATCAGGTTGTTCGTGGTCACATGGCATTAAAAAATGAAAGAGAATTGGGCGGGGT
GGGGTGGGTAAGGGTTTTCGTGGTAGTTCTGGGGGATAGGGACTTTCTCTTATAGTAGTGTCTTTCATAAAGTTCTATCCGTATGTGGATGCTACTTCGCGAATTTATAGAT
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FIGURE SHEET 72

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ATCGACTTTAAATGTTGATTACAGAATAATCTCATGATAGGAATATGTAGTCCTAAAAATATGAATAAGTGATCTTTATCTACAGAAAGGAACGCAGTGTTCGCAATAATGCG
AGGATCCGATCGAAATGAATATAAATGCGATTAGTCCTTCCTGATCTGCACGCATCCCGAGGTATTCAATGCTCTGCCTATGGCGGCAACTGCGAGTGCTGTGATCAGCGGA
AGATGGTGGTTTTCTGAGGATCCACGCTCGAGCTGATCACTAGCGGCTTCTCCACCGATGGCTTCTCGTGCAGCGACAGATTGGCCACGCTGCTCGACGTGGTCTTGGTGGA
GTACTGGCTCTGACGTTGGTTGCTGCCATCGCGAACACTCGAGCATCTGTGTTTGTGTGAAGTGGTGGAGTGGTTATGACGTCCATTGCGTGGGCAGCGTGGAATAGACAAT
GGCGGTAAATCTGATTAGAATTGGTTCGTTTGAGTGCTTGGATTTTAAGTTAGGGAAAAGCAGACACATTAAGCGATCCTACAGGATATAAACAGGTTACCTTCACCAAGAC
ACAAAAGTGGATGGTCATTATGATTAGTTTTCGAGGGGTTAGAGGTTATCAGGGTTATCTAATGGTTTCTTCCAACTGGGGTTAACTACAATGTCAACTACTTCTCCATTTC
CAGAGGATTACCTGTGACCATTTTGATTAGATGGCTATCTTCGGGGTCGGACTCGGGTCGGTGGCATTGCTACCGGCCTTGTCAACAGCCTTAAGGTGCAGCTTTCTTGGCA
GCACATTCGCGTCAGAAGTGATGGAAGTCGAGGTAGTGGTCGAGCTCAGGCCATTCGAGCGCCTTTTCTCCAGGAGTCTTCAATGAATAGCGATCGATGATGATCAAATTGA
TGTTGAGACACATGCACATATGGACACACATGGTGGATGCAAACATAAGTTTGTGTTTAGATCAGGGCAATTAGGAATGGTACTTCTGTTTAGTAGCTACAAAGACGCGACC
GGACTGAGTCACCGAGCTAGGCGGCTGGAGATTCAGTGCTGTGTTGGCTGTCAGTGTTCGGTTTAGAGTTAGTCTGCAGGCAGTGTCTGTTGGTGTTGAGCTTGCTTTTAAG
CAATATCGAAAGCAGTCTGACAACGAAAATAAGTACAACATATAAGGTTTAAAATAATCACAGATTGCGCGCTGTCAGAACTCGAAGTGCATATGTATTCCCATAATCTTCA
ATGGGTCTTCCATCTTAGTGCAAGAGATTTAAGGAACGTGGAATTAGACAGGAATCATATAACCCGAAATTTTCAATATTCTTGATTTAAGCGCGGGTTAGCAAAGGCCACA
ACAAACGAGCAACCGAGCTAAAGGAGACCTTCTTACTGAAATCGACGAAATCGATTTAGACTTCGTGTGAATGAATACCACTGGTGGACCCATTGGCAAATGCGTTGCGGAT
CACCCACCAGCTTGCGGATCTGGTTGGAGGCGTCCATAAACCGCTGCTTCATCGAGAACGAAGTCGGTCCCATCGTTACGCTCTCAGTCTGCCGCAGACTGCGCACACGTATC
GTTCTGAGAATAGTCGGGGTTACAGATATGATGGTGGACAGAGTCAGAGACACGACACACAAGAGGGAGTCACGAGTCGTGTGAATGGACAAACGCCCAGTGGGCGGGACAG
GACATAACGTGGAGTTAAGAATAGAGCAACACTTACCTGTTTGTGATCAAGTGCTTGACCTTCTTCTTCATTACAAACAACATGAAAATGAGAAAGCCCTGCATCGCATTGG
CCAGATCCGAGATATAAAAGAGCTTAGACCATCCCTTGTCGCTGCCCACGAAGTACGAGATAAGCTCCGTGAGCCAGGTGATGCCCATTATGAGAAAGAGGCGTAAGAACAA
GCCGAATCTATAGTTGGACCAAGCACGATAAAAACGTCTTTAGGGGAAGGTGGATAAGAAATACTGAAAGGATGACACTCACTTGTCCTTCTCGGTTCGTAGGTTCTTGGTG
CTGTTCTCACTCGCAATTATCCGGGCCATCTCGCGCTGCACGCCGTGAATCTTAATCGCCGTCATTATGAACATGATGGTGTTGGCAACAACGATCGCCAGAATGGGACCGT
AGAAATAGATCATGGCTGCCCAGTTGCTCATATCCAGCCAGCAGTATACACCATCACCAATACCTGGCTTTAGGTTCGCGGGCAAATTGGTAAGTTGCTGGGCGCAATAGGT
GAAGGCTAGGAAAACTAGGGCAATACCCCAAGAGTACAGCGAATAAAACAGGAAGCGTTTCTTCTCCTGGAATCGGTTAATTCCTCTCCGTCCCTCGGAAATTGGTGCCACAAG
TCAAAGCTAATGACACTTAGCCACATGTAGGCACCCATAAAAAAGAAATATGCTGTGTATCCAAACACTTTGCATGTAACACCAGTGGCATCAACTTGATAGAGTTGCACGT
AGCACAGCGAGGAGTAACCCACGGAGAGCCCTATTAAATAGCAGACCAAGCTCTTTCCGTGCTGGTTGCGGAGCTCGGGAATCAATAGGTAAACGGCTATGGTAAGCATCAT
GAAGGGAATGGAGAACATCATGGCTAGTGCAAGGAATTTCGGTCGGATTAATAAAATGCTGTTTACAAGAAGTAAAGGTGATCGTTTCACTTACCATACGAATTGATAATCT
TTACCGTGCTATGATCGTCCTGCATGTCACAATTGGCCGGATGTATGGTGTAGAACATTGTGTCCGGTAGTAATCATAGCTTCCGTTGGGAAAGAGCCTATGGCCCGTCAGATTCCTGATTAG
CAGTTTATCGTCCACACGGAGCATGGATCCGTTCTCAAAGAGTAGATAATAATCATCCCAATTGTTGGTCTCTGGCTGCAGAGAAAACATCTTGGGGCAGGGTCTGAAGCTTTGG
ATAGCAAACTGCGTAAACATGTTGACCAATATCGTAGACTCGTTGCGGAAGGTTATATTGAGCATAGGCGGATCTGGCCACGTTCGGTTGTCCGAGTGGTCTATTATGCATC
CGTCAACTTCAGAGTTAAAGACCTGCCGCCACGGGCAGCAGATATTCAGGCAGGACTTGAACTTGCAGACGCATCCCCTAACGTGTTCCCGAACCTCTATGCGCTCCGTTAG
CGAGCTGTTGATGTAGTCGTACGTCCCGACCAATTCTGCGGGAACTATTGTGCCGTAGTAATCATAGCTTCCGTTGGGAAAGAGCCTATGGCCCGTCAGATTCCTGATTAG
TAGAAATTACAGGGCACATTTGGATCGTCTATGGTGTGGTAGTGGTCTCTCTCGGCCATAACGTAAGTGCCGAAGGGAATCCCCGGAATCAACCGGAACACGACCAAGCACA
GGACGCCCAGCAATGTAACTCCGCAGTATAGGGATCCTCCAGGCTGATGAATTTTCTTCGGCATAATGAAGGTTCTGAAATTCGTAAATCTTTATTAAATATTATTACAAAT
ATTTGTTATTATTCTTTAACGTTTATTCTTTTAACGTTTAAATATTCAGTGGAATATAGTTATTACAGTTAGTCATCAGTCGCAACACGCAGCAATTAAGCCTTAGCAAGTG
AAGTCACTAATTAAGACCTATTTGCCGATTAGTTAGTCGTTTAATGTTTAATCTAAGTGAGTTCACTAATTTGGGCAATAGAGCAACATCTAGGGACCCATTAGCGGGGACGA
GTGGTGAATGATCTATGCGGACAACAGGTTGTCGAAAAGAATTAAGGAGGCGAAACAGGATAGCGTCACAAGCAATTAGCAGCCAACGTGTCCCATGGGGAGGAACCAGGGG
CGGACTACCCACGACCTGAGCGCCATTCTCCGCGGGACATCAATCATAAGGTCAACCACGCAGGGAGTGCAGACTGAGCAAACATTTATGGATTCGTGTTAAATTGATAGTA
ACTGCCATTGTCTGTCAATAGAGGTGACAGTCTCCCCGAACTCCACTCCAAACCAATCCCGATCTGCCCACTTTTCAAGCGCTGCTAACGAGCCCGTCCATAAATTCATTAC
CAGTCGCGAAAAGTTATACCGCTCGCTATCTTATCTTGTATCATTAGCCTTTGGGGACCAACTAATTCATTGATCCGCTGATTGTTTGCCTTTGGGGGAGAAGCAGAAGGGTA
ACCTGCGGCATTGTCAGGAGTGTGGGCCACTAAATTAGTCCGAATTTATGGGATGCGAACGGGTGGAGAAGGACAAACACATTAAACTCCGCACAGTTGGCTAATGGGGAAA
ATGAATACTGGCAGTGGGTGGGGAAGGGAGAGCCAGAGCACTTATCTTGCGGTGGGAAATTAGCATAATTAATCGCTGAGCACATGCACTTGGGAAATTTCAGCGGACCAAA
TTCAATCGTATATATCTGCGCACTTTAAATGTGCGAATGAGTGCTGCGGATGTTTG
(SEQ ID NO: 166)

Exon: 4208..3455
Exon: 3344..2771
Exon: 2695..2501
Exon: 2355..2207
Exon: 1242..1001
Start ATG: 4208 (Reverse strand: CAT)

Transcript No. : CT33415
ATGCCGAAGAAAATTCATCAGCCTGGAGGATCCCTATACTGCGGAGTTACATTGCTGGGCGTCCTGTGCTTGGTCGTGTTCCGGTTGATTCCGGGGATTCCCTTCGGCACTT
ACGTTATGGCCGAGAGAGACCACTACCACACCATAGACGATCCAAATGTGCCCTGTAATTTCTACGATACAGTGAATCTGACGGGCCATAGGCTCTTTCCCAACGGAAGCTA
TGATTACTACGGCACAATAGTTCCCGCAGAATTGGTCGGGACGTACGACTACATACACAGCTCGCTAACGGAGCGCATAGAGGTTCGGGAACACGTTAGGGGATGCGTCTGC
AAGTTCAAGTCCTGCCTGAATATCTGCTGCCCGTGGCGGCAGGTCTTTAACTCTGAAGTTGACGGCATAATGAGACCTCTGCCCCAAGATGTTTTCTCTGCAGCCAGAGAC
TGCTCAATATAACCTTCCGCAACGAGTCTACGATATTGGTCAACATGTTTACGCAGTTTGCTATCCAAAGCTTCAGACCCTGCCCCAAGATGTTTTCTCTGCAGCCAGAGAC
CAACAATTGGGATGATTATCTACTCTTTGAGAACGGATCCATGCTCCGTGTGGACGATAAACTGCTAATCAGGAAGAACGAGTTCTGCATGGTTCCGACATACGTCAACGAA
ACCAGCACGGAAAGAGCTTGGTCTGCTATTTAATAGGGCTCTCCGTGGGTTACTCCTCGCTGTGCTACGTGCAACTCTATCAAGTTGATGCCACTGGTGTTACATGCAAAGT
GTTTGGATACACAGCATATTTCTTTTTTATGGGTGCCTACATGTGGCTAAGTGTCATTAGCTTTGACTTGTGGCACAATTTCCGAGGGACGAGAGGAATTAACCGATTCCAG
GAGAAGAAACGCTTCCTGTTTTATTCGCTGTACTCTTGGGGTATTGCCCTAGTTTTCCTAGCCTTCACCTATTGCGCCCAGCAACTTACCAATTTGCCCGCGAACCTAAAGC
CAGGTATTGGTGATGGTGTATACTGCTGGCTGGATATGAGCAACTGGGCAGCCATGATCTATTTCTACGGTCCCATTCTGGCGATCGTTGTTGCCAACACCATCATGTTCAT
CGCCTCTTTCTCATAATGGGCATCACCTGGCTCACGGAGCTTATCTCGTACTTCGTGGGCAGCGACAAGGGATGGTCTAAGCTCTTTTATATCTCGGATCTGGCCAATGCGA
TGCAGGGCTTTCTCATTTTCATGTTGTTTGTAATGAAGAAGAAGGTCAAGCACTTGATCACAAACAGAACGATACGTGTGCCGAGTCTGCGGCAGACTGAGAGCGTAACGAT
GGGACCGACTTCGTTCTCGATGAAGCAGCGGTTTATGGACGCCTCCAACCAGATCCGCAAGCTGGTGGTGATCCGCAACGCATTTGCCAATGGGTCCACCAGTGATTTACCG
CCATTGTCTATTCCACGCTGCCCACGCAATGGACGTCATAACCACTCCACCACTTCACACAAACACAGATGCTCGAGTGTTCGCGATGGCAGCAACCAACGTCAGAGCCAGT
ACTCCACCAAGACCACGTCGAGCAGCGTGGCCAATCTGTCGCTGCACGAGAAGCCATCGGTGGAGAAGCCGCTAGTGATCAGCTCGAGCGTGGATCCTCAGAAAACCACCAT
CTTCCGCTGA
(SEQ ID NO: 167)

Start ATG: 1 (Reverse strand: CAT)

MPKKIHQPGGSLYCGVTLLGVLCLVVFRLIPGIPFGTYVMAERDHYHTIDDPNVPCNFYDTVNLTGHRLFPNGSYDYYGTIVPAELVGTYDYIHSSLTERIEVREHVRGCVC
KFKSCLNICCPWRQVFNSEVDGCIIDHSDNRTWPDPPMLNITFRNESTILVNMFTQFAIQSFRPCPKMFSLQPETNNWDDYLLFENGSMLRVDDKLLIRKNEFCNVPTYVNE
SDMFYTIHPANCDMQDDHSTVKIINSYAVYLLIPELRNQHGKSLVCYLIGLSVGYSSLCVQLYQVDATGVTCKVFGYTAYFFFMGAYMWLSVISFDLWHNFRGTRGINRFQ
EKKRFLFYSLYSWGIALVFLAFTYCAQQLTNLPANLKPGIGDGVYCWLDMSNWAAMIYFYGPILAIVVANTIMFIMTAIKIHGVQREMARIIASENSTKNLRTEKDKFGLFL
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RLFLIMGITWLTELISYFVGSDKGWSKLFYISDLANAMQGFLIFMLFVMKKKVKHLITNRTIRVRSLRQTESVTMGPTSFSMKQRFMDASNQIRKLVVIRNAFANGSTSDLP
PLSIPRCPRNGRHNHSTTSHKHRCSSVRDGSNQRQSQYSTKTTSSSVANLSLHEKPSVEKPLVISSSVDPQKTTIFR*
(SEQ ID NO: 168)

Name: mth-like 10
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384577
CCAGACATGCTTCCTCGATGGGGCTTAACGTCAGCGGAGCAGCGATGTCAGTGGCAGCCATCATCTGAACCGAATGACAGTGGAGGTCGCTAGAAAAGGGGTTCCATTTCCA
CTAGTTTATACTACCGAACTGATACTTAAATCAAGGCAGTTAAAAATTTAATATGAAACCGGAAATGGCTTCAACATCTCGTTAACGCTCTGCCCAATTCTACAGTCATCCG
ATTTTAATGAAGCAAAATTTACTGCCATGCCATGCCAAGAGATATGAATCACCGCATGGGAATAGCCCACAAAGGACCCTTACCCCATGCACTCTATCATGAACACCGCACAC
ACTTTTAATCTGCGACTAATTGCTGCTCCGTATTGAATTGATTTCGGTTGCCCCAAAGTGCCACATTCCAAATCTCCGTTGATTGGGGAAATCCCCGAAAAACATTCGAACC
ATTCGTCCCTGGCGAGCACAGAAACAGCGTCTCTGATTCTGGCAGGAATTGGAGGGCATAGGGCGGACCTTGTGGCGGTTTGTCGAGTGCACAAAGTGCAAGGTTGCGTGGC
CATTCATTTCGCAGCCGATGGGTGGAAGTGGGCAGCGGTGGGTGGCGCCCGGAAGGAAGAGCATCAGTAATCTCTAAGTGCGCCTTGTTCGCATTCGTACTCGTGCCAGCAT
TGCATAAGTGTCAGTGTCAACGGGGCGGGGATGTGGTTGTGCTTGGTGGTTATGTGGGTGTTTGTGTGGTAGTAGTGTCCTTGTTGGCAGACAAAAAGACTGATGATGATGG
CATTTTGTTACTTTGCTACCTTCCTTTGTCGCCCGTCGCACGGCAGCTCCTTTAGTATGAAATGAGGCGACCAGGCAAGCGCCTCGTCATCGAAGATCACCCAAACAGAGTA
CGGACCAGGACACGGCAACTCGCACAGGCACAGGAACAGGTGCAGGCACAACAACTGGCAGGAGCATCGGTGTCGGCAAGGGATACTGGCGCGGGATCGAAAGCATGAACAG
CAGCTGCCCGCGGACTACGACTATGGCAACTTTAGTCTAGGCAATCCGTATGACGTGGACTCAGAGCACTCCATTTCCCCGCTGACGCTGCTCCTGCTCGCTGTTAGCTATG
GCCTGGTGGTTTTCGGCGGCGTCGTGGGCAACTCCACGCTCGTTCTGACCCTCTGCTCCGCCTCTTCGGTGCGTTTGCGTAACCCGCTGCTGCTGGCCGTCTGCATTGCCGA
TCTCCTGGTCACCGGCATCTCCGCTCCGGTCACGCTCCTCAATCTCGCGATGAACCGGAGGACGCGATCGCTGCCCCTTGTGCTGTGCAAGGTCATACACTACGTACAGGTG
AGTGGGTCAATCAAACAAGCTTAAGTTAGCCAAGTAACTAAGTTAACCCCACGCTATTCAGGTCATGCCCGTTTCGGCCAGCACTATTTCGTTTTTCATGCTCTCCCTTGAC
CGCTACGCCACAGTAAAGCATCGCGATTGGCGCAGCTTCGCCAGCGGCGCTACTTGCACGTCTCCCTGGCGCTGCTATCCTGGCTCGCCTCTGCCGCCATCAGCACTCCCT
TTCTGTTTGCCTACAAAATCATCGCCAAGTCGATGGTGGTCAAGGGCGGTGGGGCGGCGAACACCACGCCCAAACCCGGTCAGCATCAGCTGCACCTCCGACCTGGGCGCCAA
CGCCATGTTCATGTCCTTCATCATCTTCCACACCATCGCCGTGTTCGTGTTGCCTGGCATTGGTGTGCTACTCAACCACTACGGCGTCCGACGCAAGCTCTGCGCCCTGTCG
CTAACGGCTCGAGCTGCCCATGGAGAGCTGCCGCTGCCCATTCCCATCCTGCGACGCCAGACCCACATGGTCATTGTGACGGGCTGCCCCAACGCCCAGCAAGCGGCCTGTG
GTGGGGGCACCACGGCGGACGACACCTCGAACGGGAACGGCACGGGCACCGGTGGCGGTCCCATGGCCGTCAGTCCGGGCGACATACAGCTTCACACACTGCAGCCGCGCCA
GCCAGGCTCTGCCGGATCGGCCCTCGAACCGGGCTCCTACCGCTCTAGCAATCCCATATCACCCAGGTAAGTCATAAATATTGTGAAGTTATCAGCAAAATCGTTGTAAACA
GGATGTATGCTTGATGTAGTCAAAAGCTATTAGTTTATGTTAATCATACGCCCGTTGACTTTGGTCAGAATATATTTCATCGAATGGCAGTACGTCATTTGGTATAAGTTA
ACTAACTTGCAAACCCACTTAGGGCCATGAGGGAGATTCGCGCCCACTCGCAGCGCCAGCGCATCAACCGAGCAGGCAGGGGACCAGCGACACCCGGCATCCCACTGCCCCA
GGCAACAATCAGCAGTGCAGCCAGACCTCTGTTTACTTCAGCCTTCTGCTAGGTAAGTCTGAATTGGCAATCATTCCCAATCCGAATCCGAGTCCGAATTGCAGCTGACTAG
TTGATCGCGTTGCAGGCTACTTCTACTCGGCCATCAGTCCGGTGATCTACTGGGCGCTCAACCACAATTCGCTTCGACAATCTCCCTGCGCGCCCATCATCCGGCCTGCGCTC
CATGCAGAACTTCCTGAGGTCGCGCTTCCGGACGCACACCGCCCCGCCGCCTCCCTCGTCCACCAACGAGGCGGCACTGGGGGCATTCAACCCCAAGCTGATCAAGCTAACA
CCGAAACAGTATAGAGCTCAGGCCTCTTCGCATTATCTCTACTAGTGTGATACTAAGCTAAACTTGATATACATATATACACATTTATATACACGCATATATAGTATATTTT
TTACCTACGACCCCACCCCCCCCCTGACCCGTCGATGCCCTCTTAGTACCCTCTAGTATCGAACTCCGAACCCGAACTTTGACCCAACCGAACGAAACTATCTAGATGTTTT
TCAAAAGCTCTACGCAACAATTGCATAATACGAAAGATACATGCTACATATACACATATATAGAGTACATACTACCTTGCATAGCAGTGTTAGTCGACGCTTATTTACACGA
TGTTGTGCGCCTGAAGCTATGCAATAAGGACACCGGAGTCCTGCCGCAACTCTTGCCTATAACGAGGATAGCACTGGTAACGAAAGCAAGAAAAAAAAAAGGAAAAAAAATA
CAAAAATAACGAAACCCTTCTAGTGACTTGTTCGAATTGTTGTTTAGTCTTTTAAGCTGAAATATTGTACTATGTTCCTTCTCATAGATAAGCAATAAGTGAACGCTTTAAG
CCAAGTTAAACAAACGGAAAACGAATCAAACTAAACTAAAACTCGATCTAAAACTTTTAAACGATTTAAACGTAAACTCGAAAGCATACCTAACGAAACATTAATAATTATA
TACATACGCGACTACATACAAATAACAACTAACAAGTGAAAACTAAAAACAAAAAATGAATGTAAATGTGAGCAAAAAAACAAAAGGATAACATTTAGTATTGTATACATAT
TCTTCGACTTAATTCTTTATACACTTTTTCTAACCATTTTTAATATCGTTCAGTAAACTGAACACGGTGTATAGGGCAATTCAAGCTGCTGGATATATTCGCGTTTCAGATG
CCAGAGCCACCCAAAGGATCGGACTCTGGATCGGGTTTCATTTCACTCCATTCAGTGGCGACCGTTTCCTAATTTGCCAAACTTTTGTACATGCTCCGCTGCGAGCGACTCT
CTCCTTACTCCACCTGGTTTTTCGTTCAATCCTTGGA
(SEQ ID NO: 169)

Exon: 1001..1453
Exon: 1518..2194
Exon: 2375..2628
Exon: 2704..2957
Start ATG: 1001

Transcript No. : CT33551
ATGAACAGGGACAATCTGCAGCAGTGGTGGGAGAACTCGTATCGGCGCCAACATCCAGAGCCCACCGATGACCTCGGCCTGGACTCCGCGGAGCTGCATCTCGCCCTCCAGG
AGCCCAACCAGCTGCCCGCGGACTACGACTATGGCAACTTTAGTCTAGGCAATCCGTATGACGTGGACTCAGAGCACTCCATTTCCCCGCTGACGCTGCTCCTGCTCGCTGT
TAGCTATGGCCTGGTGGTTTTCGGCGGCGTCGTGGGCAACTCCACGCTCGTTCTGACCCTCTGCTCCGCCTCTTCGGTGCGTTTGCGTAACCCGCTGCTGCTGGCCGTCTGC
ATTGCCGATCTCCTGGTCACCGGCATCTCCGCTCCGGTCACGCTCCTCAATCTCGCGATGAACCGGAGGACGCGATCGCTGCCCCTTGTGCTGTGCAAGGTCATACACTACG
TACAGGTCATGCCCGTTTCGGCCAGCACTATTTCGTTTTTCATGCTCTCCCTTGACCGCTACGCCACAGTAAAGCATCCGCGATTGGCGCAGCTTCGCCAGCGGCGCTACTT
GCACGTCTCCCTGGCGCTGCTATCCTGGCTCGCCTCTGCCGCCATCAGCACTCCCTTTCTGTTTGCCTACAAAATCATCGCCAAGTCGATGGTGGTCAAGGGCGGTGGGGCG
GCGAACACCACGCCCAAACCCGGTCAGCATCAGCTGCACCTCCGACCTGGGCGCCAACGCCATGTTCATGTCCTTCATCATCTTCCACACCATCGCCGTGTTCGTGTTGCCTG
GCATTGGTGTGCTACTCAACCACTACGGCGTCCGACGCAAGCTCTGCGCCCTGTCGCTAACGGCTCGAGCTGCCCATGGAGAGCTGCCGCTGCCCATTCCCATCCTGCGACG
CCAGACCCACATGGTCATTGTGACGGGCTGCCCCAACGCCCAGCAAGCGGCCTGTGGTGGGGGCACCACGGCGGACGACACCTCGAACGGGAACGGCACGGGCACCGGTGGC
GGTCCCATGGCCGTCAGTCCGGGCGACATACAGCTTCACACACTGCAGCCGCGCCAGCCAGGCTCTGCCGGATCGGCCCTCGAACGGGCTCCTACCGCTCTAGCAATCCCA
TATCACCCAGGGCCATGAGGGAGATTCGCGCCCACTCGCAGCGCCAGCGCATCAACCGAGCAGGCAGGGGACCAGCGACACCCGGCATCCCACTGCCCCAAACCTCCACGCT
GCGGTCGCGAAGGCACCTGGCTAACATGCTCATCGCCTCGGCCGTGATCTTGCATTGGGCACCGCACGTCTTCTGCATCTTCTACAAGAACATCAG
CAGTGCAGCCAGACCTCTGTTTACTTCAGCCTTCTGCTAGGCTACTTCTACTCGGCCATCAGTCCGGTGATCTACTGGGCGCTCAACCACAATTCGCTTCGACAATCTCCCT
GCGCGCCCATCATCCGGCCTGCGCTCCATGCAGAACTTCCTGAGGTCGCGCTTCCGGACGCACACCGCCCGCCGCCTCCCTCGTCCACCAACGAGGCGGCACTGGGGGCATT
CAACCCCAAGCTGATCAAGCTAACACCGAAACAGTATAGAGCTCAGGCCTCTTCGCATTATCTCTACTAG
(SEQ ID NO: 170)

Start ATG: 1

MNRDNLQQWWENSYRRQHPEPTDDLGLDSAELHLALQEPNQLPADYDYGNFSLGNPYDVDSEHSISPLTLLLLAVSYGLVVFGGVVGNSTLVLTLCSASSVRLRNPLLLAVC
IADLLVTGISAPVTLLNLAMNRRTRSLPLVLCKVIHYVQVMPVSASTISFFMLSLDRYATVKHPRLAQLRQRRYLHVSLALLSWLASAAISTPFLFAYKIIAKSMVVKGGGA
ANTTPNPVSISCTSDLGANAMFMSFIIFHTIAVFVLPGIGVLLNHYGVRRKLCALSLTARAAHGELPLPIPILRRQTHMVIVTGCPNAQQAACGGGTTADDTSNGNGTGTGG

FIGURE SHEET 74

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GPMAVSPGDIQLHTLQPRQPGSAGSALEPGSYRSSNPISPRAMREIRAHSQRQRINRAGRGPATPGIPLPQTSTLRSRRHLANMLIASAVIFIACWAPHVFCIFYKNFGNNQ
QCSQTSVYFSLLLGYFYSAISPVIYWALNHNSLRQSPCAPIIRLRSMQNFLRSRFRTHTAPPPPSSTNEAALGAFNPKLIKLTPKQYRAQASSHYLY*
(SEQ ID NO: 171)

Name: GASTRIN/CHOLECYSTOKININ RECEPTOR like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384577
GAATGATAACTAATTCAATAAAACTACAGATTTCAATAACTAAAGCATACATGTATATGTATCTATGTATCTATGACTATGTATCTCGAATCCTCCGCTGAAACTCTAAACT
ATTCCCATGCAGTTTCTTTTCCTTCGTATCGAGTTTCAGAGCACGGCTTGTAGTGTTGCACGTTTTTCGTATTTTTTGGCAGCTCTGGCTGGTTTTTTTCATTTTCCTTTTT
TTTTTGTACTCCCATTTCCTGTCACCCTGCCCGGTGTAATTAAAAAAGTTTTTCTCGACATTTGCTTGCCATGTGAGGCTCCAGGAACAAATGCGTTACATTGTGGACCATC
CGATTGTAAAATAAATTTTAAGTGCAATACGAAGTGCAAACTCAGCCGTAACAATAAGATTTTTGCAATAATATTTAACTTTTAATTGTAACTTTGGTAAAGTCAATGTTTT
CTTTTTCCAAGTTGGCCAATAAAAAGAGCATAAAGCAAAGCGAAAACTTTAGTGCGTACTTTTATTACAACATTAACTTCATGCTATATATTTTATTTAAATATTTTGGCTT
TTCTATCCATTGTTTTTCAGTTAATATCTTAAACAAACAATTTTTGATGCACTACAAATGCTGTTGATTTTAATAAACGATTTATAGCTTACATGGATTATTAGCTATGTAC
ATATAATTACGAATATTTTTAATAAAGGGCATACTTAATAAATTGAAATTCTGGAAAACACTCATTTATTTAACACTAGCAAATTAGCGCACAAATAATGTGCAAAGTTCGT
TAATCTTTAAAGTGTATTTGTGACCACAGCACAATTAAACGGTGGTCCGAAATTCTATATCTTCTAATTCCGCATTGTTTTTTTTTTTTTTGTGAATTTTTCAGGTAACCTCC
TTGTTATTTTGGTGGTCACATTATCACGACGACTGCGCTCAATAACCAACTTTTTCCTCGCCAACTTGGCGTTTGCCGACTTCTGTGTTGGACTCTTTTGTGTGATGCAGAA
TCTGTCCATCTATCTGATAGAAAGGTGAGTGACAATTGGCAAAAACAACATTATTTCAGTATTAAATTAACGTTTCATCATGCACGAGCGGAGCTGCAAAATTCTCGGAAAG
CATATACGAAGAATACGTGAACTAACTTCACTGTAAAGTTGCCAATAGTTTTTAATGTCCGTTTTCATACGCAAAAAATTTAAGTGAAGCATTTAAGTGAAGCATTTATAGA
AAAGTTTTTAGTTATAGTAGGTTAAAAATTAACACAAAAGTTAAAGTAGCGTTTCAGCTAGTACAGATAGTAGAATGTTATGTGGTCGATTAAATTTATTTATTTATCAGCT
GCAGAATGTGGCTGAAACGGTATCTGAGTGCATACGTATGTATGCATGTGCCTCGAAAACAAAGCCCCAAAAAAAAGTTTCAACTTTCAACCGTGAAACATTTACGCCGGCT
GTCACATAAAGGAAACTAAAACTCCGCAGGCGTCACTTTCACTTCAGGCTTTTCAGGCTTTTATCCCCACGCTCCGCTTTCACTCCAATCATGTTTATTTGCATTGTGTTTC
CTTAACTTTCCCAAAAACACGTCGCAGTGACGTGTTCACTTAAAATAAAGCGTGGGAGTGCTGCTTGAAAATTCAAACAAAAAGAAGCCTTTTCAGATTTGCAGGGCAAATT
AAAAAAGTATTTTGACAAATGAGTTTGGCTTACAGTTTCTATAAGTTATTTAATTTAAAATTTTAGTCGCAGTGTCAGAAATAAATAATGCTTCATTAATTTAAAATTTGTGA
AATGCATGTGTTTAATATGTGTTTAATTAAAAGCTATGTTCTATACATTTAGAAAAAAAGTAATTACCTATCTCATTAGAATTCTTGAAATGACCATTTATTTATTTATGCATT
AATAATAAACAGACATAATGATTTATTTGCATTCCCGATGTTAAATCCTGAAATTGGTTTGCATATTTTCCATTTCATTTTCTAATATGCTTTTTGTGGCCAAAGAACTAAA
TTATTGAGATGACCCATCTGTGTTTGGCATAATTTTAGCTAAATTATGCGCACAACTTGACGCCCACCAGAAATCATATGCAAAATGAGATGAGATTACGAAAAATCATAAT
TTATGCATTTATAATTTATATGTGCGGCATACGGCTGCCAGTGACAATTTAATTTAATGATTATAAACATCAAGTCGTTTTAAGAAAGTTTTTAGTTCATTATGTTAAGGAA
TGATTTGTCCCTTTTAAAGAGAGAAATTGAATCACCAGGCAAATGGGGAATCTTTTTAAGAAACGCCATTATCCAAAATCTTGGCGGACAACCTTCAGGATTATTATGTTTATT
ATAGTATTATTGGGCACATTTAAACGCATGAGTGCGAAATTACGTGGCATTGCTAATAACGAGGCACAAATGCGGTTTTCGAATGTAATTTCAGCCGAAATAGTAATAAAAA
GGAAAAAGCTTTGCGCCTCATAAAATACTAAAGACACCTTAATGTCGCATTAGTTTTGGCGGGCGTGTCATAACATTTTATGTGGCTTGTGTCTAAATTTGGCTCTGCCACCA
ATATTGCCAAGTATATGCTCTTTAAAGAGCGAAACTTTTGCCCATAAATAATTATTTATGTCCTTTCAGCTGGGTCTTTGGCGAGTTCCTCTGCCGCATGTACCAGTTTGTC
CACTCCCTGAGCTACACGGCCTCCATTTTCATCCTGGTTGTCATCTGTATGGAGCGCTACTTTGCCATCGTACACCCCATTACCTGCAAACAGATCCTAACTGCGGCCTCT
TGAGGGTAAGTTCTAACCATAAACCTCATATTCACGGCCAGTAATAGGCAAGTATGCATTTTAAATGAGGTCTATGTGTATGTGCCCTGCTTTTTCAATTCCCATTTTGAT
GGGTCAAAAGCGGAGGAAATCTGTTTATGTATTGTATTTGAGACATTCTCGCAACTTTAATAACTTCATTTGAATACAATTTGCAAGCTAATGAAACTTATTAGACCAAGC
CCGGAGACTCATGCAAATTAACCGGCAGAACAGAACCGACTCGAAAGGCTTAATAAGCCGTGGGCATAACTTTGTGGCCGGGAAAACTTTTCCGCACTCGAAGGGTGAAGTG
GAGGGAGCGCAGCCAAAGGGTTGAACCACATAGCCCGGTTGTTTCATCACAGCCAGACAAAAAATACGTTTCGGTAATGACGATTGCACTAATTAAACTACAAGAGACAATAA
AGACAACGAAATGGGCTATCCATTAACATGCAAATTCAGTGTGTTCATTCGCAATTTAACAAATTGTTTGCGTGTTTGGCAGCCGAGCAGACAAAACAAAACGTCAATGCGT
GTTTTTTTTTTTTGCAGATGGTCATTGTCACAGTTTGGATTACATCGGCAGTTTACTCCACGCCCAAGTTGTTTTCAGCAAGACCATTAAGAACATCCACACGCAGGACGGG
CAGGAGGAGGAGATATGTGTCCTGGACCGTGAGATGTTCAACTCCAAGTTGCTGGACATGATTAACTTTGTGCTTCTCTACGTTATGCCGCTCTTGGTGATGACGGTAAGTG
TAACAAATGATACGTAGCTTGAAGTTAATAATTATGTTTAACCAATCCTTGGATAGGATGTTCATAAATTCATTTTCAATCCAAAAGTGTTTCCTAGTCACGTTACCTAGCA
TTGAGCAGACTATAATTAATAATTAATAATTGTATTTTTTTGAATTGCTTATTAAAGTGATTAATTATATCAATAACAACTATCTCTCTAATGAGATAGAATATAAATAATTTTG
GGTACATAATAAATAAATCTATGAAATGATTTTTCTTCGTCTGTTAAAAAAAGTGATTAATGGAAGTGTAGATTTCCCTTTATTTTTTTAACGACTCCATTTTTCAATTTCTTC
TGAGAAATTTGATAAGAATTGAGAAGCTTTTTGCATAAAATCGCCCCTTGTTCCGCAATGAAATTTGAATAATGAATTTAACGAACCCATTTGCATTGCAGGTGCTGTACAG
CAAAATCGCCATCGCCTTGTGGCGCAGTTCGCGCGGCCTCACGCCGCATGTGGTGCAGCATCAGCATCAGCAGCCGCAGCAGCCATCCTGCCAGGACATTGGCATGGGTATG
CACAACAGCATGTACCATCACCATCCGCCATCATCATCACCACCACCACCAGCATCACGACTGCAATCGGCGGCTTCGTCGGCAGGATGGTGGTGGTGGTGGTTTGGGTGGTG
GTGGTGGGGGCGGTCCTCGGTCCGTCACTCGCTTCCGGCGGCAGCAGCACCACGTCCTTGTCCCGCAAACAGAGCAGTAAATATGAGAAGCGCGGCGTCAGCATCACGGAGAG
CCAGGTGAGCTGCCAGGAGAACACTGCATCAGAAAAATCGCCGGTTGAGCACGGAGGAGTAGCCTTAAAAGCCTAACAATAGCAATAAACCGAAAGTGGAGTCGAACCTTTG
TTCCCTAATTGGCCAGAACGGCTTTAACTTCGATTGAGTCCGCACGTGCTGTGTGGTAAATAATGTTTTTTGAAAATCACATCGCTATCGGAGCACTAATTTATTAGATACA
CCATTTGTCGGCCTGGCCAAGTTGGCAGTCGTAAAAACTTTACCCGTAGCTGTTACTCCCGCACTTTCGCCGGGCCAAGTGGCACGGTGCTCGGAGCAGGTGTCAATTCACA
TTAAGGCCATCGCAGGACCATGCCACAAGCTCGGCCACCGATGTGACACCTGGAGTGGTGGAGCGAAGTGACCACCGGCACAGGGCGAAACTGCAAGTGCGAGGC
CAAAGTTATGGCAAAAGTGTTTTTTTTTTTTCCATTATCGGTGGCCGGACAGCAGGTTCAATTGGTCGGGTGCACCATGGCGTATTTCTTATTTCTTATTTCGAGCTCGACAG
CAGCTTTGCCACACAAACTGGCACACACATCATTGTTCTTGATCAGCATCAGCAGCTCACTTTGTCAATAAAAGCCGGCGGATAAAAATCGAGAATTTGTGACACGATGACA
TTCGGAAAAGTTGTGCAACTGCCGCAGATTGAAAATTGGTAAACACCAAAGGCAAGGCCCTTGAATTTTTTAATATTCCTCGAAGTATCAAATGTCAGGGGAGCACTGGTTC
GATTTCGGTATGTTTTCCGTTTTAAAAGTCACAAAAATGGAAGTTTGGTAGGAAAAACAATGGCGGGAACACCTTTATAAAACTTTTACATAACTTTTAGTTTACGCTGTTCC
TTAACTTATGACCCCGATATACACAGATAACAACCTAACTATCTTTCTGTTGAACTCTTTTCTCTCTCTCTACCTTTCGTTTGATCAATAAAACTCTGTGCTCTCCCCCTCT
ACTAACTCCCCAATTATAACAACAACCACACACAATCCCACACCACAAATTAGCTCGATAATTGCAAGGTAGGTTGTAATCGAATATCAAAATCGATATGATAATGTTCAAC
AACTGTTGCGGCCAGCGACCTAATGCCATTACACCTGTTAATCCGCACAGGTCCTGGAGGCCGATCGTCCCATTGTCAGTGCCTGCCGCAAGACGAGCTTCTACCACCA
CGGCCACGCCCATCACCAGCGGCGGGCAACGCCTCAGTGGGCGGTGGCAGCGGCGGAGCCGGGGCCGGAGCCACCCACATGTCCCACTCGTCCAGCAACGTCCTACGCGCC
CGGCGCGGCGTTGTCCGCATGCTGATAATATTCGTGCTGACATTCGCCCTCTGCAATCGCCGTATCATGCCCGCAAAATGTGGCAGTACTGGTGAGTAGTCCCTTCGTCCA
CCCACCACCCATAATCACAATCCAATGCGAATCGGAATCCCAATCCCTATCCCTATCCCTTACCGCAGGCCATTCATCAGCCCACACGGACTGAGTGTAAACAATATTTTAT
GGTATATTGCACCGGCAATCGGCGGGAATTTGCATAGTCCTCCGTTGGACGGGAAATTAACATCTGCGAGTGGGCAGATAAGCTCTAGATGGCTTCCTGCTGGAATCGAGGC
TAGTAAACAATTAAGTCATCAATGGACAGAGCTGGAGCTGCAGCCAGCTTTGCCGCTGGCCTAAATGATTTGAAAGCGGTCTTCCGTTTTCCAATCCCACTCCCTTCCCAAA
GACGCCAGTTTCGCTTTCTTCTCGCCTTTCAAAAGCCGGTCGCCAAGCAAAAGTCCGTTTTAGCCAGCCCTTTGGCTATCAGTTCCGCTTCCGGTGGAGCACTTTCGAATAGGT
GGACGGACCGCTTAGTTTGCTTTGAATTCGGGCAATTTGGTTTTTTCCGGCTGGCGGGTGTGGTGGGCGTATAACTTGATAAGTGAGTGGGCGGTGGAAGTGTTTTTGTTTGC
TAAATCGAGGAGGAGTTAATTGCTCCCTGGGTAGAATTAAAAACGTGCACTTAAGCTGCTGACTGCTGTAAATTGGAAATAAAATAAAAGTCACAGAAATGTCCTTTAAGCG
AAAGTCGAAAGACAAACGATTGATTGAAGATGGGAAAAGTCATCAAGTGTGAAAATCTGGAGACATTGGCAATTTTGGCACGTAAGAGAAACGTTTTTATTTTGAACTTTTC
ATACAGATTCTACTAAACCAAACGTTTTTGAGTCAATTGTAAATTGTAAAGCATTTTACATGCCGATGTGCAATAAATCCAATTTAATGTTCATAAGTTCATGTTTTTGGTG
AATAACTACTGAAATAAATATCGATCTCTAGTTCTCATTAGTGCAAATATTCAGTGTAATTTTGTAAGAAAATACTTCGCTGCAGATTTGCAACGTTGCACTTTTGGCAAAC
GCAACGAAAACGAAATGTTTTTGAATTTTTGTTCGAGCACTCAATTTGCACAATTGTAAAACGAATGGCGGACAAATAAATATAAATAATATCTGGCCAAATACAAGAGAA
ATGGATTTCCACATCGCCACTTTTCCCGCAGTGCCATAATTGAGATTTATGTCTAGCCCGGAATGGGCAGCGAGACTTGTTTACTTGTTTGAACTTTCAGCTTTTATTTATT
TGAAGAATTGGTTGCCCCCAGGGATATTGGTATTGTTAGGTGGAATTGAAAGTGTT
(SEQ ID NO: 172)

Exon: 1001..1032

FIGURE SHEET 75

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Exon: 2646..2805
Exon: 3377..3577
Exon: 4022..4372
Exon: 4614..4820
Exon: 5539..5804
Exon: 5893..6112
Start ATG: 1001
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Transcript No. : CT33559
ATGCAGAATCTGTCCATCTATCTGATAGAAAGCTGGGTCTTTGGCGAGTTCCTCTGCCGCATGTACCAGTTTGTCCACTCCCTGAGCTACACGGCCTCCATTTTCATCCTGG
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AGTTTACTCCACGCCCAAGTTTGTTTTCAGCAAGACCATTAAGAACATCCACACGCAGGACGGGCAGGAGGAGGAGATATGTGTCCTGGACCGTGAGATGTTCAACTCCAAG
TTGCTGGACATGATTAACTTTGTGCTTCTCTACGTTATGCCGCTCTTGGTGATGACGGTGCTGTACAGCAAAATCGCCATCGCCTTGTGGCGCAGTTCGCGCGGCCTCACGC
CGCATGTGGTGCAGCATCAGCATCAGCAGCCGCAGCAGCCATCCTGCCAGGACATTGGCATGGGTATGCACAACAGCATGTACCATCACCATCCGCATCATCATCACCACCA
CCACCAGCATCACCAGCTGCAATCGGCGGCTTCGTCGGCAGGAGTGGTGGGAGTGGGTTTGGGTGGTGGTGGTGGGGGGCGGTCCTGGTCCGTCACTCGCTTCCGGCGGCAGC
AGCACCACGTCCTTGTCCCGCAAACAGAGCAGTAAATATGAGAAGCGCGGCGTCAGCATCACGGAGAGCCAGTTGGCAGTCGTAAAAACTTTACCCGTAGCTGTTACTCCCG
CACTTTCGCCGGGCCAAGTGGCACGGTGCTCGGGACGCAGGTGTCAATTCACATTAAGGCCATCGCCAGGACCATGCCCACAAGCTCGGCCACCGATGTGACACCTGAGTGTGGA
GTGGTGGAGCGAAGTGACCACCGGCACAGGGCGAAACTGCAAGTGCGAGGCCAAAGTGTCCCTGGAGGCCGATCGTCCCATTGTCAGTGCCTGCCGCAAGACGAGCTTCTAC
CACCACGGCCACGCCCATCACCAGCGGGCGGGCAACGCCTCAGTGGGCGGTGGCAGCGGCGGAGCCGGGGCCGGAGCCACCCACATGTCCCACTCGTCCAGCAACGTCCTAC
GCGCCCGGCGCGGCGTTGTCCGCATGCTGATAATATTCGTGCTGACATTCGCCCTCTGCAATCTGCCGTATCATGCCCGCAAAATGTGGCAGTACTGGCCATTCATCAGCCC
ACACGGACTGAGTGTAAACAATATTTTATGGTATATTGCACCGGCAATCGGCGGGAATTTGCATAGTCCTCCGTTGGACGGGAAATTAACATCTGCGAGTGGGCAGATAAGC
TCTAGATGGCTTCCTGCTGGAATCGAGGCTAGTAAACAATTAAGTCATCAATGGACAGAGCTGGAGCTGCAGCCAGCTTTGCCGCTGGCCTAA
(SEQ ID NO: 173)
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Start ATG: 1

MQNLSIYLIESWVFGEFLCRMYQFVHSLSYTASIFILVVICMERYFAIVHPITCKQILTAARLRMVIVTVWITSAVYSTPKFVFSKTIKNIHTQDGQEEEICVLDREMFNSK
LLDMINFVLLYVMPLLVMTVLYSKIAIALWRSSRGLTPHVVQHQHQQPQQPSCQDIGMGMHNSMYHHHPHHHHHHQHHQLQSAASSAGVVGVGLGGGGGGGPGPSLASGGS
STTSLSRKQSSKYEKRGVSITESQLAVVKTLPVAVTPALSPGQVARCSEQVSIHIKAIAGPCHKLGHRCDTWSVEWWSEVTTGTGRNCKCEAKVSLEADRPIVSACRKTSFY
HHGHAHHQRAGNASVGGGSGGAGAGATHMSHSSSNVLRARRGVVRMLIIFVLTFALCNLPYHARKMWQYWPFISPHGLSVNNILWYIAPAIGGNLHSPPLDGKLTSASGQIS
SRWLPAGIEASKQLSHQWTELELQPALPLA*
(SEQ ID NO: 174)
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Name: Neuropeptide receptor-like
Classification: G_protein_linked_receptor
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Celera Sequence No. : 142000013385217
CCTTCGACTTGAGCGGACAGTTGAGGTTCTCGAACTAATTGCAAAATTGTCAATGATTTATTCAGTTGGCAATTAAGGTGCCAACTAACGGTGTGGCTGGCACGGCTATATC
GATTTGAAAATATTCAATAATCCCGGAGCCTTGATAAGCTCATCAAACATGCACATGGCCATCAGCAGGGGGGGGGGCAAGTTTGTATTTAGAGCCAAGTGTGTTTGGTGAAGG
GGGGTTAGCTGTATATTTCAGGGTTTCCCCTTTTTTTGTCGAGCGGTTTGGGGGGGGGTTTTGCGAGGGGACACAAAAGTACAAGTTGCTATGGATCAAGCTCAAGGCGTGG
CAGTTGGGCATTAGCTCTATGGTGGAGCACGGCAACCAAGCGAACAAAGGTCAACTCGACAAGTGAGTTAAATGACAAGGACCTCACCTTGCCTTCCTTGGGCTTCGGCTTT
GGCTTTGGCCCGTGCGTGTTTGCATGTTTGGCTCGATGAGGCGACGCGACCCCAAAAATGAAACTCAACTTTGGCTTTGACTGCGGCTCGGGATTGTGGCGTGCAAGCATTA
TGGCCTTTCGCTTTCAAAACAATGCCCCCATCCTGTTTCCCGGTTGGCCTAGTGGCACTTGCTCCTTGTTGTTGGTTTTTCGCATTGCCCTTGGCCAATTGCGAGTGAATTT
TGATGTTTTGACTGGCCATTCCTGGGGCCATTTGACAACTCTATAAAACCGGTGTCCTTAAGCCCGCCCTCGTCCTTGCGCCCAACCCCCAATTACCGTCCAACTACCACCC
ACCTACACCCCGCTACACCCACCACAAAGTAAACGTAATTGCCCGGACAGTCTAATTGCGCCAGGCACCTTGCACTTTGCGCGCGACGCAAACTGAAAAAGCGAAACTTCAAAAAACCCGACTTG
ACTTGGCAACTGGAAAAGTGGAAAAGCGGAAGCACGAGCTTTCCCACCGAAAAGCTCTCGTGCTCTAAGCTTTCGTCCTGGCGAGGCGAAACGTAAATGTCAGTCATGGAG
TTCCAGTCGTCGGATACATGTGGAACACAACGAACACAGCAGGAGCCTCTCGCGTCTCATCCCCCGAATACAATGCGAAAAAGTCTGTACAAAAAATAGACAAATAAGGAGC
AGGAGCGAAAACACCACTCTGTGCATAAGATATAAACTCCCGCAGAACTGAATACCTGCAAAAAGAAATACGCGTTAAATGGAATTACGGTGCGGGAATTGATAAAGTGAAGT
GTGTTACAGCTAGAAAGCAAGTGAAATAAAACGAATACATTAAATAATTCATGCCCCTCATGTCAGCTTACTAGTTTGTAAGGAATTCAACGTAAATCTGATATAGTA
ATGTAGAAAAGTTGTACAAAGTAATATACACATAGCATATAGCATATAGCACAGTTACACAGAACACACCGCAAACTCAAACAAAGTTGACAAAAAAAAAAGCTCACGCCCCTCA
CATCTCAGTTTTTTTCTCGAATTATTTGTGAAAGTGCAACAAACATATATAAAAAATAAAAAAGAAAAGGGAGGAGAGAGCACAGCAAAAAAAGGCAGTGACAGCAGGACCTG
CAAAGGAATTGCCATCATTTGGGGATTACGGAATTATCGGGATCCGTTCTCATTAAAATGGATTTAAGGCAATGCCGATGTGCTGAGCTGCATTTGTGCATGGGATTATCGA
TTGTAATGCGCAGTCATCAAATTATGTTTGAACAGCCGCCGCCGACAGCGATAATAGCAACAATAACAACAACAACCAAATCAACAACAAACACTGATTTGCCC
CTGACCCCCTTTGGCAGCACCCCCTCCATCCAACACCCCCTACGACCCTGCCCAAGCAAAAGGAGCAGCGAAAAGAAGAAGCCTCTTATGAAACAATTGAAGCACCGGCCA
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TGTTTTAAGCCAAGTGAAATCAAAATGATTTGAGAAGTACAAATAAAAGAAAGAAAGGAAAGAATGATATATGATATTTATTGGTTGTAGTACAGGAAAATAATAGTTAAAA
TGATATCCCGGATTGATGGTCATTACAATGATCGTACCACAAAACTCTTTCTAACTCAAATTAAATTGTTAAAATTATTTTTCAATACAAATTTGATATATTTTTGTTTTTT
CGCCGACAAGATGCATAGATCTTTCATAGAATCTGAAATCTATATCTTTTTTATATTGCTTTTGAGAAGAGTAAACCGATCATCATCTACGATCACTCCTTTTTGTTCTGTG
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TAACTGGCAAACAAATTTGGAGTGACGCTGCGGCGATGTACATACATACATATGTATGCATGTTTGTGCTAAACCGACAGCATTTCCATTCAATAACACACGCGGCTCGT
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TTCAAAATGTGCCATCTATTTTATATTCACTTACAAGCAGATTTCAATCAAGACCACTCTTTAATATGATATATTATGTCTAGAACAACCGAGAAGGCACTCTTAAATTAAA
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TTGAACAGCAACAACCAACAACAAAAACAAAGAAGAACAAGAGCAAATAAAATACAAACTGCTTATTTATTTATTTGTTTCGACAAATCTCAATTGAAACAAAGCTTAAAAG
CTTCGAAATCAAAACTTAAATAGAAACCACACAGACATCCATCCAGACGAATAAAACGAAAACGATAGAGCGCGAGACAAAGAGACAATTACTATTAAATCCAAGTTCAATT
CGGTCCGCAAACAATTGAATTTGTTGCAGATTTGATTTGGCTTCATGTGGATTGCGATAACTATTTTCCTGGGATTAGTATGGGATTGGATTCATTGGCCCGACCGCAGTTT
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GCTTCCTAATGAGATTTGCTTAATTAAAATGAAATTCAATAACTGGAATTCCAATGAATTTAAATGTTAGAGAAAAACTCTAATTCGGACTTTTGTGGCTAGCCATTATTTG
CAGCAAGGGGGACATAAAAAGCATTTGGCTTTCGTTTGGATTAGTCAGCAAGGTCAAATCTCGAAACTGACCTAAGCTAATGCAAATGACTTTTCCTGTCAATCACAATCT
ATATTTAATTCAAGCGAAATTCTCTGCCACATTTCTTGCGCTATAAATCGCAGTACCCATTATAGCATATCAACAACCAAATTAAGACGAAAGTACAATAAAATGCAACTAA
TTTCAGTTTTAATAATGGATTTGCTGGCGGCTTATTTTTGTTTCAAATTTGGTTATTTTCTTTAGAAATGTGCGCATACATTAAGACGAACACAAAAACCAGCTTTGGCTCA
ATCTCTTAAACCTTTAAAACGTTATATGTACGCACATATTTATGTACGAACAAATGAAGGAAAATCTCAAGCCTAATTCCGCATTAAGCTGCAAGGAAACACATAACCCAAA
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CGTGGCCGGGAGGCCCGATGAACTGCACATCGGCGGCATCTTTCCGATAGCCGGCAAAGGAGGATGGCAGGCGGCCAGGCGTGTATGCCTGCCGCAAGACTGGCGTTGGAT
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TTAATATCACTGCAAATAATATCCTGACCAAAAACCCCTCCTGATGCACTGAGTTCTGTTTAAGCCTTCTGTTCACGAAGCATTTTCGCTCAGTGCACTAGTAAGTTGGAAA
GCGATAAGCCCTACTTATATGCAGCCCCTGCTGCCTCCTCTGCTGCCATGCCACATACCCTTGGGTGCCACTTATTTTGTTTCGTTTTTGTTTCTGCTCACTGATGAGTAGT
CATTAAAGGGTATTGCTGCGCGTGTGTTCACAAATTGAATTCGCCGCACAATCCGCCGCATGTCCAACAATATTTGGCAATGCCTCGGCTTAATGACTGCACATAAATTGC
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GCATTAAGAAAATGTGTGTATATCTCGAACAAGGTCGCCCAATAAATGTCGCCCGGTGTTCATTAAATCATAAATGTATTTACATTTATTCGTGTAGTGCAACGCTGTAAG
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ACGCATTTTATCTTTAATGCCAGCAGCAGCACGAACTGAACTTCTGCACAAAGCTTTTCTTGAATAAATCGGTATAATCAAAGTGAACACAGTATTGATCATATTTTTTTTA
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CATAATAAATGGCCAGTAACCGATGTAGTTTCCGTTTTCCAGTTCCCAACCAAGTTGCGCGCTATCAATGCCCCTTGGCGCGTATCTCTAATACAATACATATAAAACCAAA
ACCAAAACTATCTTTATACAATTTTCATATTTCGCACATATTTTTTGTTTTTTTGTGAATTTCGCATTTTAAGGGTCTGCGGTACAGTTGTTGCGGTTTCCACTACTTCGGCG
GCTGTTTTGGGCCTGCCTATTTTTAAGCGCGAACCTCATTAGTTTTTAAGTGAGCGAAAGCTTAACTACTTGTTTTGAGTTTTGAATGAGGTCACTTTGCCCCGGCCGAGCCG
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CAGATACGGACATATAGATAGGAACAGAGCCGGAGAGGTAAACCAAGTCCTATCCCTGGTCATATCTGTTCCTATCTGGCGTGGTCTGGTCTGGTCTGGTCTGGTTAGTTCA
GTTCAGTTCAGTTCGCTTCGCTTCGCTTCGCTGGACTGAGCCTGAGACGCAGGCGCGTTATGTTTGTGGCTTAGGCAAACAGCTTCCGTTAAATGCTGCATAATTAGTTGCCATCTC
CAGGTCCCACAGCCACCTTCTCCTCCGGCACATCCACATCCCACACTTACTCCCACAACGCAACGCACCCACCCCCATCCCGCCCACATCCACGTCACTTGGCAAGCGACAAGGG
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TCTGCTCTATAATAAACCGCAAAAGCTGATGCTGTTGGCAGGATGCAGCACGGTCTGCACCACTGTAGCCGAGGCTGCCAAAATGTGGAATCTAATTGTGGTAAGTGAAATT
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TGCACTGTTGAACAGATGCGAATAGCTGCCGAAGGACATCTGACAACGGAAGCGCTCATGTGGAATCAGAACAATCAGACAACTATATCCGGAATGACTGCAGAGGAATTTC
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CTTAGTTAGTTACTTATTTTTTTTATTTGCAGGGTGTGGTGGCATTCAGTTCTCAGGGCGTACGTATTTGCTCTTACACAGATCGAACAGATGATAGACGGCAAGTACGAGAAG
TTGGGTTACTACGATACTCAGTTGGATAACCTATCCTGGTTGAATACTGAACAGTGGATTGGTGGCAAGGTAAGCAAATCAGTTAGCGTTGAAAAAACAATCATATAATCAA
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ACACAGTAACCCAAAAAGTCAAAGAAAATGAAGAGCCCAGGATTTTCTAAACAATTTGAAAAAGAATCTATTGGTGTGCGAGCAAATAGAAACAGCAGTGCAACAAAAAGGA
AAATGAAAAGCTATTAGTAAAGACCGTGCCCGGAAAATCTCTTATAAAAGAATCTAACGATGAAAATGTGGAACCATCTAGACGCACAAAAAGTCAGCCAGTTGGAAAAAAA
AAAAAAAACTATCTTGGGAACCCAGACAGTACACTTCGACGTCGTTTTGTCAGCAATAATGAATATCATTCTAGTCTTGAAGGTGAGGAGGAAGAGATCGATTTAGATTCAGT
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CAACGCGAATCAACTAACGTATTTCGTAACAATCGTAGAGATGATAAAAACCATTGATGAAGTGAAGGGTTCCAAGATCACAGGAACACAGGACAGCCAAACAACATGTTGAAGAAGTTA
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CAAAGAAAGTGAAGAAGACGAGAATAAGGACGAGAATAAAGATGTAAAAAAAGATGAAAATAAAGACGATGAACAGAAACTTCCCCCGGAACCAGAGATCGAATTGGAGGCC
AAAAAAGCTTGGACTTTTCCGATCGCAGAGACATCACCTGATATCCCTGGAGAAAATCAGATCCTGCAAGAATACCAAAAAGGTTAAAATTGGCAAAAGAAACAGGAAATACA
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FIGURE SHEET 77

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GATGTATAGGCATCAATACGGATATAAGCAGAAAATCTAAGATTAAAACATTTATCAGCAAGTCTGCAGGTGATGACTTAGTAGTATACCATGATGGTGGAAGATTGCGAGA
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GATGCCAACCAAAGAAGATAGACGAACGTACTACAAAGGTTGTGAATATCATTTTCCTGGCCGAACGGAATGGCGCAGGCTTTTCTTCAACAAAATCCATGGAAAATACAAG
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GAAAGGTACCCATGATAAAGATGGCACAACCCATTTATTAGTTTCACTCCCATCGGACCACGAACTAATCCCAAGGCGGTATCCTTTGATCCTAGAAACAGCACAGAAGTCAT
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CCGTGTGTTTTTCTTAAAGTTAATCGGATTATTGGATTTAAGACCGAACCCTACATCAATTCCGATGAGCTTGTCAAAGCCAAGATCGATGAGGTTGAATTTACGGCCTTAA
AAAGGTTATTGGAAAATACAACAACAGAGGAGGGTCATTTGAATCGCACTTGGATAACATGCCGTTCAGATAAAGATAAGAATGTTTTGATTGAATTCATCCAGAGCCGGC
GATAAGAACGGAATACACCGATATTGAAGAGAAAATCGAGTATATTGCGAACGAGGGTAAAAAGTCATTTTTCGGCCCAAACGATGTGAATCGAATCGTGGCTCTTAAGATC
AAAAATCTCAAAGCAAATGAACGTGTCCATATAAATTGCAAAATGTGGGCTCAGAATATACATCATAGGAAAGAGGGTTATGGCCAAGTTTCGTTTTTTGTGTTATTAGCTA
CAAATGAAAACCGCGAGAGGGTGGAAAAATTACTCCGAACCGACTACTCATTATAAAATACATAAATATAACTTTCTAATAAAATGTGTTATATGATATATGTATGTATTAT
TTATAACATCTATAATCCAGGTTCCTCAAGATCGCACAATTGTCACCCATGTTCTACGCACCGTGTCCTTGCCATTATTTGTGTGCATGTGCACAATATCCAGTTGTGGCAT
ATTCGTTGCCTTCGCCTTGATCATCTTTAATATATGGAATAAGCATAGAAGGTAACTATTTAATTGGTAGTGCTCGTGCAGAACTAACTAAGGGTTATATAATTTCTAGAGT
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CGGTTTTACACTAGCATACGGTGCTATGTTCAGCAAGGTCTGGCGTGTGCATCGTTTTACAACAAAAGCAAAAACTGACCCAAAGGTGGGTTTAAATTAAATTAACTACAAC
TATATATATTAGTTGCTAATCATTTTGTGGAATTGCAGAAAAAAGTGGAACCTTGGAAGCTATACACCATGGTTTCGGGGCTATTATCAATAGATTTAGTGATATTACTCTCAT
GGCAGATCTTTGATCCGCTGCAGCGTTATCTCGAAACATTCCCACTCGAAGATCCAGTATCTTACTACTGATGATATTAAAATACGTCCAGAGCTTGAGCATTGTGAAAGTCA
ACGCAACTCCATGTGGTTGGGTATGTTGTGATAACGATCCATTATATTGTATATAATATATTTATATTATTTTGCAGGTCTTGTATACGGCTTCAAGGGGCTAATCCTGGTG
TTTGGCCTCTTTTTGGCGTACGAGACGCGCTCCATTAAAGTGAAACAGATCAACGATTCGCGTTATGTGGGCATGAGCATCTATAACGTGGTCGTCCTTTGCCTGATAACAG
CAGCCACTACACTGAACTAAAAGAAGTAGCACATTGTAATGATCTCTATTCGCACAGGTCATTGAGGTTATACGTCATCCCAAGGATAAGGCCGAATCGAAATACAATCCC
GATTCAGCCATATCGAAAGAGGACGAAGAACGCTATCAGAAACTTGTTACCGAAAACGAGGAATTGCAACGATTAATAACACAGGTATGCTGAATTATGGTAGATTATCTTA
ATAAAATCGTATTTTATTTAATTTTGTTTAAAGATTAAATTCAACTGTTCGTTGAACGTTAATCTAAAAGTATTTCGGTCTTATCATAATTTGAACAAAAGTTAAGGATTGG
AATTTCCAGCGGCCCCAGTGAATTCCATTCAGCATGCCGGTTTCACCTTCTCTAAAATAAAGTCCATTTAGCGAGCTGCAATATGAAGTATTATCAACCTCTTATAAATCAA
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TGCAGGTAGAGAAGACAAATTGTTGATTTTGTGTTTAGTAAATACTGTTTTTTTAGTTAAACGAATTATCCTTTCGAACCTCATTTGCTCAGCGCTGTCTCCTAGAGCTCTC
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(SEQ ID NO: 175)

Exon: 1001..1090
Exon: 1165..1208
Exon: 1810..2052
Exon: 3783..3856
Exon: 5748..6002
Exon: 10046..10180
Exon: 10271..10441
Exon: 10503..10719
Exon: 10812..11284
Exon: 11344..11493
Exon: 11565..14044
Exon: 14446..14569
Exon: 14902..15028
Exon: 15086..15342
Exon: 15403..15540
Exon: 16659..16847
Start ATG: 1026

Transcript No. : CT35221
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CAACAACCGCAACATCGCATTTTTAAACGGCAATACGCAAAAAAAAAATATTGCTGGCAGGAGTTTAGAACATTGCCAAAGGGGATGCGGACAGATGAAGGGGCGGGGGCGTGG
CGGGATATGACAAGTGATGGTGCTGTTACGTTTTGGATATTTTTGCTTTGTTTAATCGCCTCGCCGCACCTGCCAAGGGGGCGTGGCCGGGAGGCCCCGATGAACTGCACATCG
GCGGCATCTTTCCGATAGCCGGCAAAGGAGGATGGCAGGGCGGCCAGGCGTGTATGCCTGCCGCAAGACTGGCGTTGGATGATGTCAACAAGCAGCCAAATCTGCTGCCGGG
CTTCAAGCTCATCCTGCACAGCAACGACAGTGAGTGTGAGCCCGGTTTGGGCGCCAGCGTGATGTACAATCTGCTCTATAATAAACCGCAAAAGCTGATGCTGTTGGCAGGA
TGCAGCACGGTCTGCACCACTGTAGCCGAGGCTGCCAAAATGTGGAATCTAATTGTGCTCTGCTACGGGGCCTCGAGTCCGGCTCTTTCGGATCGCAAACGATTCCCCACTC
TATTCCGCACCCCATCCATCGGCCACGGTGCACAATCCAACGCGCATCAAGCTGATGAAGAAATTCGGCTGGTCCCGGGTGGCCATTCTGCAGCAGGCGGAGGAGGTCTTTAT

FIGURE SHEET 78

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ATCGACCGTAGAGGATCTCGAGAATCGATGCATGGAGGCTGGCGTTGAAATCGTAACTAGACAATCATTTCTATCCGATCCAACAGACGCCGTGCGCAATTTGCGACGCCAG
GATGCACGCATCATTGTGGGACTCTTCTATGTGGTGGCCGCCAGGAGGGTGCTCTGCGAAATGTACAAACAGCAGCTATATGGCCGAGCTCATGTGTGGTTCTTTATTGGCT
GGTACGAGGACAACTGGTACGAGGTGAATCTGAAAGCAGAGGGCATCACCTGCACTGTTGAACAGATGCGAATAGCTGCCGAAGGACATCTGACAACGGAAGCGCTCATGTG
AGACATCGACTGAATCAGGCGCTAATCGAGGAGGGTTACGACATTAACCACGATCGCTATCCGGAGGGATATCAGGAGGCGCCACTCGCCTACGATGCAGTGTGGAGTGTGG
CTTTGGCTTTCAACAAGACCATGGAACGATTGACAACCGGGAAGAAATCTCTGAGGGATTTTACCTATACGGACAAGGAGATTGCCGATGAAATCTACGTGCCATGAACTC
CACACAATTTCTGGGTGTATCGGGTGTGGTGGCATTCAGTTCTCAGGGCGATCGTATTGCTCTTACACAGATCGAACAGATGATAGACGGCAAGTACGAGAAGTTGGGTTAC
TACGATACTCAGTTGGATAACCTATCCTGGTTGAATACTGAACAGTGGATTGGTGGCAAGAAGACAAAGCATGTAACGACTGAACCGAATAAGAACGGAAATCCGTCCAAAG
ACGACGTTAATACAAGAGGATCATTAACAAGCTTAAGTGAGAAAAATGATGAATCCAAAAATCCATCATCATCTGCAAGTCTTCAGCAAGCTCCTAAGGTAGCACCAAAACC
GAAAAAGTTATCAATTTCGGATGCTGGTAAAGACACAGTAACCCAAAAAGTCAAAGAAAATGAAGAGCCAGGATTTTCTAAACAATTTGAAAAAGAATCTATTGGTGTGCGA
GACGCACAAAAAGTCAGCCAGTTGGAAAAAAAGTTTACGAGGAATCTTCAACGAGGCGAGTTCGTGAGCCATTTGATTCTTTTGATAGGGAAAAGTACCTGTCTGCTATGAT
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TCAATATGGGAAAGTTGAAGGAGCTCAAGGAGCAACGCGAATCAACTAACGTATTTCGTAACAATCGTAGAGATGATAAAACCATTGATGAAGTGAAGGGTTCCAAGATCAC
AGGAACCAGCAAACAACATGTTGAAGAAGTTAAATATAATGAAACAGCAAGTAATGAAGATGATGACAATGCACAGGTAAAACATATAGGTACAATCACAAAAATCTTTAGC
ATTGCGCAAAGAATGAAAGAGAAGAAAGCTCCAAAGAAAGGTACCCATGAAGAGGAAGACGAGAATAAAGATGTAAAAAAAGATGAAAAACGACGATGAACAGAAAC
TTCCCCCCGGAACCAGAGATCGAATTGGAGGCCAAAAAAGCTTGGACTTTTCCGATCGCAGAGACATCACCTGATATCCCTGGAGAAAATCAGATCCTGCAAGAATACCAAA
GGTTAAAATTGGCAAAAGAAACAGGAAATACAGATGTATAGGCATCAATACGGATATAAGCAGAAAATCTAAGATTAAAACATTTATCAGCAAGTCTGCAGGTGATGACTTA
GTAGTATACCATGATGGTGGAAGATTGCGAGATATAGGACAAACCACTGAAAATCTTAAGAATCAACGAAAGAATCATAAACACAAAACCGAACCAGATGATATACCCGTTG
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AAGGGACATTGGAACCAGCACAGATAAGCCATTTTGGCCAATCGATGACGGAACTGATGTAATCTACATGCATCCCATTAAGACTGATAGGAAGAAATTAAACAAACTGATT
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CTGGTTCGATTTCATCAAAGATGACGCTTCCAGAAAGGTACCCATGATAAAGATGGCACAACCATTTATTAGTTTCACTCCCATCGGACCCACGAACTAATCCCAAGGCGGTA
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CGAATGAAAAGTTTGGCTATCCAAGCGGCGAACCGTGTGTTTTTCTTAAAGTTAATCGGATTATTGGATTTAAGACCGAACCCTACATCAATTCCGATGAGCTTGTCAAAGC
CAAGATCGGATGAGGTTGAATTTACGGCCTTAAAAAGGTTATTGGAAAATACAACAACAGAGGAGGGTCATTTGAATCGCACTTGGATAACATGCCGTTCAGATAAAGATAAG
AATGTTTTGATTGAATTTCATCCAGAGCCGGCGATAAGAACGGAATACACCGATATTGAAGAGAAAATCGAGTATATTGCGAACGAGGGTAAAAAGTCATTTTTGCGGCCCAA
ACGATGTGAATCGAATCGTGGCTCTTAAGATCAAAAAATCTCAAAGCAAATGAACGTGTCCATATAAATTGCAAAATAGTAATACAATCCTCGCATCCCGTTTGCAATACGAT
CATGTTATTTGGTGTCATCATCTGTCTAATATCTGTCATCTTACTGGGCATCGACGGACGCTTTGTCAGCCCCGAGGAATATCCAAAGATCTTTGATCCGCTGCAGCGTTAT
CTCGAAACATTCCCACTCGAAGATCCAGTATCTACTACTGATGATATTAAAATACGTCCAGAGCTTGAGCATTGTGAAAGTCAACGCAACTCCATGTGGTTGGGTCTTGTAT
CGTGGTCGTCCTTTGCCTGATAACAGCTCCGGTGGGCATGGTCATTGCATCGCAACAGGACGCGTCCTTTGCCTTCGTTGCTCTAGCTGTGATATTCTGTTGTTTCCTAAGC
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ATCAGAAACTTGTTACCGAAACGAGGAATTGCAACGATTAATAACACAGAAGGAGGAAAAGATTCGAGTCCTGCGACAGCGTCTGGTGGAGCGGGGCGACGCCAAGGGCAC
AGAACTGAATGGTGCAACAGGTGTCGCCTCCGCCGCCGTTGCAACAACTTCGCAGCCCGCTTCCCTCATCAACTCATCAGCACATGCCACGCCCGCAGCCACACTCGCAATC
ACACAAGGTGAGTAG
(SEQ ID NO: 176)
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Start ATG: 26

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DSECEPGLGASVMYNLLYNKPQKLMLLAGCSTVCTTVAEAAKMWNLIVLCYGASSPALSDRKRFPTLFRTHPSATVHNPTRIKLMKKFGWSRVAILQQAEEVFISTVEDLEN
RCMEAGVEIVTRQSFLSDPTDAVRNLRRQDARIIVGLFYVVAARRVLCEMYKQQLYGRAHVWFFIGWYEDNWYEVNLKAEGITCTVEQMRIAAEGHLTTEALMWNQNNQTTI
SGMTAEEFRLVLLLYPLLKFLLQCAFFLRRHRLNQALIEEGYDINHDRYPEGYQEAPLAYDAVWSVALAFNKTMERLTTGKKSLRDFTYTDKEIADEIYAAMNSTQFLGVSG
VVAFSSQGDRIALTQIEQMIDGKYEKLGYYDTQLDNLSWLNTEQWIGGKKTKHVTTEPNKNGNPSKDDVNTRGSLTSLSEKNDESKNPSSSASLQQAPKVAPKPKKLSISDA
GKDTVTQKVKENEEPGFSKQFEKESIGVRANRNSSATKKENEKLLVKTVPGKSLIKESNDENVEPSRRTKSQPVGKKVYEESSTRRVREPFDSFDREKYLSDMIDYDRSSED
VPEKKLSWEPDSTLRRRFVSNNEYHSSLEGEEEEIDLDSVGSSTMRGSYRMPQNAEDERPVILAEIINMGKLKELKEQRESTNVFRNNRRDDKTIDEVKGSKITGTSKQHVE
EVKYNETASNEDDDNAQVKHIGTITKIFSIAQRMKEKKSSKESEEDENKDENKDVKKDENKDDEQKLPPEPEIELEAKKAWTFPIAETSPDIPGENQILQEYQKVKIGKRNR
KYRCIGINTDISRKSKIKTFISKSAGDDLVVYHDGGRLRDIGQTTENLKNQRKNHKHKTEPDDIPVDIGHSDDRVREIGVNTKKLPKIIPPIAEMHVHKNGKLRDIGTSTD
KPFWPIDDGTDVIYMHPIKTDRKKLNKLIVDPPPDNGPYKMPTKEDRRTYYKGCEYHFPGRTEWRRLFFNKIHGKYKLRRPSHWLYTLVFSVLYILFVIIFSMAWFDFIKDD
ASRKVPMIKMAQPFISFTPIGPRTNPKAVSFDPRNSTEVMEKYAGIMALLEKYGDYDNPRFGTCTANEKFGYPSGEPCVFLKVNRIIGFKTEPYINSDELVKAKIDEVEFT
ALKRLLENTTTEEGHLNRTWITCRSDKDKNVLIEFHPEPAIRTEYTDIEEKIEYIANEGKKSFFGPNDVNRIVALKIKNLKANERVHINCKIVIQSSHPVCNTIMLFGVIIC
LISVILLGIDGRFVSPEEYPKIFDPLQRYLETFPLEDPVSTTDDIKIRPELEHCESQRNSMWLGLVYGFKGLILVFGLFLAYETRSIKVKQINDSRYVGMSIYNVVVLCLIT
APVGMVIASQQDASFAFVALAVIFCCFLSMLLIFVPKVIEVIRHPKDKAESKYNPDSAISKEDEERYQKLVTENEELQRLITQKEEKIRVLRQRLVERGDAKGTELNGATGV
ASAAVATTSQPASLINSSAHATPAATLAITQGE*
(SEQ ID NO: 177)
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Name: GABA B receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384569
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AAGCTTTTATTTGCCGAAACTAAAGCTCGGAGGTATTTATTTATTCACAAGTAAAATGACAAAACTTGGAAGTTCTTTGGTAATGTAATGAACGCCAATATTTACATTCGGG
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TAGAGCTTGCAGACTTTATAATCATCCAACAAACATTATGGTGCATTGTATACCATTTATGTTATGAATGAAAGTGGTTCAGATAAGTTACATTTTTATTTTATCTCACACAT
CTAAGTTTTTGTATTGCTGCACAGGAAAATAAATCAAGATTATCCACAATAGTTTAAAAGTCAATTTATAGGTACTATGTAGAATTTATTTACATTTTGTTGTACTAATGGT
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```

FIGURE SHEET 79

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ATCCTTCCGAAATCGAAGTATGTACACAATCCAAAAATCCATGTTATTCCCAAAAGAAAGAAGAGCAACACAAACAGGCCGAGTTGCTTGAAGATAAGGTCACGTTTGAACA
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GAATCGAATATCTCCGAAATACTGAAGACATCGGCGGCGGCCGACCCAGTTTCTCCTGAGTTTGAGTCAGGAGGTTACTCAGTTGGCTAATCATGTCCGGAGGGCTCTTCACAGCGA
GAAGGTTTATACTCGAGCTGAGTTCCGGTGCCGACCTACAGGTCACGTGATCCAAGCTCTGCCAAACTCTATTCCCATTGCGAATTTGGCACCTCCGTCGGATGGGAATTCC
CCGTTCGTTCAGGCATAGATCCCTTAGATTCGCCTTTTGCCCAACTCTCGTTTTCTCCACGCGATTGATTCGCTTTTCCTTGCCTTCATCCGTTTCGTATTCCAGTTCAAAG
TCCTCGGCCTTGCAGAATCCTCGGTTGCAGTCCTTGTAGGGATTGTGCGACAGCTGACCATCTGCATCCACGCAGAGGAGGAAGCGCAAGTTCTTCAGGTGGCAGTAGTCCA
GACACCGGGCCACATTCGGCTGATCCAGGGCGTACAGGGGGGGATTTGTACCTCCAGATACGAGTATTATATAGCCAGCAATCCACCAGAGAAACAGCAGCATACTGCTATC
TATTTTTAACTAATTTAAGCGCAGGCTGCGATGTCGCACTCCCGAAGCTCCGCGATCGACTGACGAGGCGGAGATAAAATGCGAGTGGCGATAAAACGAGTTTTCCTCTCCT
CATCCCTGTAAATAGGGCCTGCAAGAATTGCCACTTTCCTCACTGTTCTAGCTGGGTATTTGAATTGCTGGTCTACTTCGAGCAGAGCTCAAGGTCAACTGGTTATCTGGCC
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GCATGTATCGATAAAACTAATAGGAATTACAAATAAATTAAAAAATCTGAATTTTCTTTTTTGCTCTGGGTAACAATGGCTGCCATTTCTGAATGTTTCTGTTATTCTCTCTG
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AGCAGCCACCTTTAGATACTTTCCTTACTAACACCTAGAAGGTAGAGATAGAGGTATTCAAATATTTGCATTCAGATATAAAATAATGTTCTCTTGTTCAAGCTGTGAAATC
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(SEQ ID NO: 178)

Exon: 3463..2341
Exon: 2281..1491
Exon: 1024..1001
Start ATG: 3463 (Reverse strand: CAT)

Transcript No. : CT35672
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ATCCGACGGAGGTGCCAAATTCGCAATGGGAATAGAGTTTGGCAGAGTTGGACTCACGTGACCTGTAGGTCGGCACCGGAACTCAGCTCGAGTATAAACCTTCTCGCTGTGA
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TGGAATATCCACCAGCGGTGGTGGCAGCTTGGAAGCCTCATCGCACCCAGTGATCCTCTGCCATGCGGATCATCTGACCCAGTTTACATTTCTACTGGGAGTGAGCAAAATG
CAGGCAGGTCTGGACACCAATGAAGATGATCACTCACTTTAGATGTAATCACCAATGTCGGCTTGACCCTTTCTCTGTTGGGCCTCCTAATGATTTTTATAACTGCAGCCGTGT
TTAAGAGCTTCCGGACATTAGCCTCCACGAAGATATTGCTGAATCTGTGTGCTGCCCTGGGTCTTCAGTTGCTCTTCTTCCTGATCCTGAGTCAAAGCCATTGCTGGAGCA
GCTGGAACAATCTGAGTCGGAACGATGTACTCTGGTTGGAGCCGTGATGCAATATCTACTCTTGGTTGTCTTCAGCTGGATGTTTATCATTGGATTTCTGCAGTATCAAAGA
TATGTGAGAGTCATTGGAGTTAATCACCCACGACATTATATACTAATGTCGGCTGTGGCGGCCTGGACATTGCCACTTATACCCACCTTGTTGGTGGTTTTTCTGGAGCCCG
GTTCCTACAGACCCAATAATTCCTCAATGGACTATCCCATCCTCTGCTATCCTTCTGGATATGGTTTAAGTCTGGGCGTCATACTCCCTATTGGCCTTATCACGGTGGCCAA
TGCAATATTGCAATACAAAAACTTAGATGTGTGA
(SEQ ID NO: 179)

Start ATG: 1 (Reverse strand: CAT)

MLLFLWWIAGYIILVSGGTNPPLYALDQPNVARCLDYCHLKNLRFLLCVDADGQLSHNPYKDCNRGFCKAEDFELEYETDEGKEKRINRVEKTRVGQKANLRDLCLNERGIP
IRRRCQIRNGNRVWQSLDHVTCRSAPELSSSINLLAVKSPPDMISQLSNLLTQTQEKLAAADVFSISEIFDSLVKKPERNAAVVGDLMKICQKVMSTDNETLRVSADANATN
ALLSNFEDYLDELSPTILKLNTTIFANSTEFTFHPLFDMGVIVLKTSELRVFFVDPEVRNVSGIVNFSGGNMSHFEMLHLSDNEEDIRAMKNLESAVFIPEKLWTQLKRKGA
SYLVFKVYTRDSLFVETEEEIKRRPTSNVISITIPGLNDTKLPGKLPFFLRNAKANETQFEGGCGYWNYETWLSDGISTSGGGSLEASSHPVILCHADHLTQFTFLLGVSKM
QAGLDTNEDDHSLDVITNVGLTLSLLGLLMIFITAAVFKSFRTLASTKILLNLCAALGLQLLFFLILSQSHLLEQLEQSESERCTLVGAVMQYLLLVVFSWMFIIGFLQYQR
YVRVIGVNHPRHYILMSAVAAWTLPLIPTLLVVFLEPGSYRPNNSSMDYPILCYPSGYGLSLGVILPIGLITVANAILQYKNLDV*
(SEQ ID NO: 180)

Name: HE6 Receptor-like 2
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384028
CAGCTAGTAGTGAATAATACTTGAGTTTTTGAGTTTGTTGGGCTGGGTTGAAAAAAAAAAAATATGCACTTTAGCCTCTATTAAGCATTTTCCTATGGTTTTCACTCTCGTTC
GGGAACTGTGTGTTTTGAAAATGTAACAATTTGCGCTTTCGTCCTCGTACATTGTGTGTATTTACAGAAAGTCTAGCCCATTTTTAGATTTGTATGGGAATGAGTGGAAAT
TACAAGTGTATAATATATAACAAATACACTTTAGTTGGTAAGATTAGCAAGACGTAAGACGTACGATAGTTAATGAGGGGGGAATTGCTAGTTTTATGTTAATGCCTATA
AGCTCAAATTTACAACTGATTATTCGCTGATCGAAAATGATCTCAAGATCTCTATCATTTGTTTAGCTTTAGTGTGGATAGTGTTGAAAGGTTGACTTGAAAGCAAATGGTT

FIGURE SHEET 80

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AGTAACTAACTGTCGAGGAACTTAGAGGTAAACGAAAACGCGTGTTTTAGGAATGGGTTTGTTTTTCTTAGTGTATGTGGCCTTGTTTTTACAGTTATATCGTTACCTACAC
AGGTGGGCTCTGTTTTACCGATCTAAACGTTTGAACAACTTTGATCTATCAGTGATCCTAATCAATCGAAATCAATCGAACTCAAGACTGACAGAAATCAACGTAAACTAAA
GTAAAATCGTCTAAAAATTTATCAAAACTTTATAAAACTTCTTGGCTGCTTTCAAGGTTCCTCACTTTACGTTTCATTGAAAAATAAAGTAATATTTGTTATTGTTTGTGTT
TGGTGAGTGTTTGTTGCATCTCCATTTGCATCAATCATTTTCCTGCTGGTTTTTTTTTTTCTTCTTTGCGAAATTAAAGTAATTCTTTTATTGTTTGTTGTTGCGCTATA
TAATAACTATTTCTCACATATTATCTACACATACCAACGTGTATCGTACCGTTTAATACCTATATACAATTCTCAAATATCCGCCATGAACCAGCAAGGACTCCCTACTTCG
AATGCGAGACCACGGAGTGGGAGACCATCGAGTGAGAGAGCATTGAGTGGGACACGCCGGAGATTTCCGCATAGGTATCCGTGGGTCCTTCGGCACTGCACACCGAATCCTC
GGGCGTCCTGGAAGGTTCCGCCTCGGTGATCTCGATGTCCTGATGATGCTTGTTGCTGCGGTGTTTGGCACTTAGAGCCTGCGAATTTGAGATATTTTAGTGGGTCACATGG
ACAACTGGTGGATATGTGTTTTCTCGTTGTAGTTTCGTGTGCAATCTGTTTTCGATAAGACTTATGTGGTGCTATCTATGGGACGGACACATGCACACACACACACACAC
GCACAAGCTGGTGGTTTCGGGTTCATTGGGGAACTTTGGGTCTAAGTTTATAGACAAACGTGCGAGAAATTCTTTTGATTTAGTCGTTTTGTTTTGTTTTGTTTTACATT
CACAACACAGATATTTTAGCAGGTTAGGTTTAGAGGTTTATGCTAAAAGCAACCGAAAATTCTTACCTTATCCTTGCTGCCCTTTTTCTACATTGAACATTGGTGGTTATTG
TTTTGTTTGGTTTGGTTGTGGTGGGTTTCGAATATATTGTACATAGTCATGACAAGAACAATGATATTTATAGATGTATTAATATAAGTGGCAAACAGTACTGCGAGTTCAC
ATTGGAGGATCAAGAGAAGTACAGATTCATAGACGGTTAGAGAGACGGGGGAGAGAGAAAGATCTAGGGAGCGTGGGGATGGGCAGCAAAAGGTTTGGTTTCGGATTGAAGA
ATAACAGCAATATCGATCTGAGGCCTACAGCCCGGTTCCCCATTCTGGCCACGTCAATGTCATGTACAGTGAGCACTATGGCTGGTGGTGGACTACGCTGCCGTTGTGGTGA
CCCCGACTCACCTGCAGGGAGAAGCGACGGTGACCCGCCTTGCGTCCGCCACGTCGCTTACTGATGTGCGGATTGTCCTGCCGCAGAGTCTTGTTCTTCATTATCTCCAATT
GGGTATACAGTCTGGAATCGAAAATGTATAGAAAATAGAGATAATAGAACATATAGATATGCTTCGTACCTTTTGAGTTCGGCGCGTATGTCCTCGGGACTCATTTCGGATA
TGGTCAGCTCACCAATGTCCGGATCGCCCAGACAGAGCCCGGCATATCCTCCGCCCAGCCGCTGGCCGGCGTCGTGTGACGTACCCTTGAAAGCATCCACAGGTAAACGTAT
TGATAGATCATACGCTAGCGAACGAACCTGCAAGCTATGAAGATGCAACAAACACCGCAAACCACACTCAGGAAGTCAAACGGAAAATGGAGAACGGAACGGAAACGGAAAT
GGAAACGGAACTCAAAGGTAAGAGAGAGCAAAATCGCATGGTATAGATCTGTGCTGAAGAGTTATGTATAGTTATATGTATATAGTATGTGTATGGGTGGTCTGTGCTTATT
GGTCGTGATTGTATCTTTGGGGGTGCTGGAAATGAACGAAAAGAAACAAATCAAATTAAAAAAGTAACTCAAAAGGTAAACAAGATGGACGATAGCTATAAGAAGACTACTT
AGACAGAGAACTTCAGTTTAAGATTATTCAGTTGAGGCACAGAAAGACAGAGAAAGTTACAGTGAGGCAGAGTCTTGGATACACTAGTTTGGAATTTTTTTTTCTGGTATGC
TGGCGTGCTTATTGAGTTCAAGTTAAAGTGCAATACATTCAGGCATAAATAATAAGAGCTAAAAACAGTCGAACATTCTCTGTTTAAACGAGACACACTTGCAGCAACTTCA
TAGCTTGACTAAAGTTTCAATTCAATGTTAGCTTATTACTAAAATTATGTTAATTTTCTCGGTGAAAACCAGAACAAGAACTCAAAATATAACCATAAACAAATGAAATATT
CAAATTGTATTTTAATTAGCAAAAGCAACCAAGCTTTTGAGTGGATGTCCACATTTTAATACTTCTTGTGTTTTGGCTAGTTATTTAACAAAAATCGTTTCCTCAACCAATG
TCAATACCAAGTACGCATTTCGATGACTATAATGACGACCACGCCCACGACAGACGAAAGGCACAAAATGAACGGGTGTGAATACTCTAAGCATATGAATTATATTCGTTTG
GTGCCCGACTAGGACAAAACACTTCCTAATTACATCATATATCTCAATGTGTAGAACACAAAAGCGTACTCAAACCAAAAAAAAAAAAAAAAAAACCAAAGCAAAGTAAGTA
AATCATATCGTTTCGAACTCAAATCGGTTACCTGCTTGTGCTGGTACCACAACTTTGGCACAAATATCAGACCCAAGGCGAAACTATTCGTCAGCTGGGAGCGGATGAACAG
TCCTTCAATGGGACAAAAGGAAATTACCGATTAATTCATTTGACTTGACTTAAATTCCCCTTCTACTTAGTTAATCATCTAAGCCAATCTCTTGCGCTTAATTGATAAAGAA
AGATCTGCAATCGATTTGACTGTACATCTTACCCGGAACTGGGTGTTGGCATTCCGACTGGCGATGGACAGGTGCAGTCCAAAGCACAGGATGAGCATCTCGCTGGTCTGCG
TGACCAGTTCCCACTTGAGCGGATGGCAGGTGTTCGTGTCCGCCTCCCTGAGGCTCTCCAGCTGCGCACTTTCGAGAAGATCCAACGACGAGGCCGTAAAGGCGGCCATGTA
GCAGATGACGGCAAAGACCATGGTGCCCAGATACTTGAGCAGGTCCACGTCGCGCAGCACCCAGCGATGCGCTTTCCGGGTGCGAAAGTCCACCAGGTGGCGGTACAACTTC
AGTATGATGGCGCCGTAGCAGGTGATGAAGCCCAGCTCCCGAAGCCAGGGCTCCAGAAGGCAGCGCTCGGTGGATGCGGGAAAGAAATGGACGGCAACCTAAAGATGAATAT
GTAAATACACACGAAGTTGAAGGTGACCATCGCCAGGAGCACTCACAGATGCATAAAGTAAAACAATGCCCAGCGTATCGTCTCCAGCACAGTCCACATACCAGACGCAA
TGGCCTGAAAATGATGAAAGGATTACTCAAAGTTTCCCAACTTTAGGATATGTAAACTAAATACCTTGCACTTTCGCTGCCGGAAGCAATCACCCCGAGGACAATGCAGCA
CAGGATGCAGGCGCCCAGTACGATGGCCACCAGGAGGCGCAGACAGGCGTCCACATTGAGCACCTCCTCCTCCTGAAAGGTCAGACAGACGCCGTTGCTATCGCAGTTAGTG
CATCCGCCGGGACACGGAATGCACGAGTAGTTGTCGTAGCCCTCGGACAGTTCCACTCGATCGCCACGGAATCCCTGGAGCGTGGAATTGGGCAGGTAGTAGGATTCCCGGC
ACAGACAGGTGTACACATCCCGGGTGGCGGCGGGTTTGTTCTCGGTGAGCAGGCAGAGAAGGTCGTATTCCGATCGCAACTACAGAGATATGGTATTATATATATTATCCAGAA
CTAATGTCACGAATTATCGTATAAAGTTTGGCCACAACTCACCCATGACGGCGGACCGAAAACTTCCTCCAGGCCATCGTTCGCACACATCCTCGTCGGCGGCAATGAAGGCAG
CCGCCACAACTCTGAAAGCATTTAGCATAAATTACAAAGTTGTGCCAACCAGCTGCACATCGATGCGACTCACTTGATCCTGTGCTCGCTGAAGGATATGCGAAATGGCCAG
AGCCAGCGACGCGTCAACAGGTTGCAGTCGCGAAATGGAGCGCCCCACTCCTGGGTGCCGTCCGTGCTGTTCCAGGCCGCACTGTAGTCGGGTAAAATAATACATTTATGGG
CAACTTTCCAAGATTATACGGCTTATGGTCTATTCAAATTAAGCGATGCACATTATTTCGGCAAGCTACGGTGCATATTGAATTTAATTGTATTTATCTTTTAGAGTTAACATT
GTATTTGCATTTCAAAGCCATAAGATAATTGATTTTAATTTGTTGCTAATTAATGTCGCACACTTTTTTGGGACACAACCAGTCTTCGAAACTTACCCCAACTCCCGCCAAT
AGGAACCCAAATATGCCTTATTGTGCACCTGATCCGGTGGTATCTGCAATAAGTTAAATCGATTAGCCCATGGCCCCATTATCGCTGATTAGCGAGTGCATACCGTAACGTT
ATCCCTGAATTTAACGACCACCGTGTGAATGCTGGGCGCGGCAATGGCGAATGCCAGCAGATTGTCGTCCTCGTTGAGGGCGTAGCTGGCGATTCCATTGGCCCGGCGACTC
CGTAAAACTGTTGAATTCATAAAACCAGATCACAATTAATTGCGTTGTGTCATAAATAATCATTTCAATGTATATGAAATGGGCATATAAATATCATTTAAATCGAATTCGA
TTTAAATACACAAAGAAAAAGTTCAATAAAATTAACACAGCATAAATTTACGCTTTGCTAAACTCAATTTATTTATACCACACTATATAGGAAACGGAAAACGTGTGCTTTC
ATTAATTATTCACCTGGCGCACAGGACACGTTTCACAGCAACACCTTGCGGCAAGAGTGCGAAAAGTTTTGCTTCGTTTCGACTGTGAAATAATAGGATTTAATTACCCTCGC
CGTGCTGTGGGACTGCGGGAAGGGTTTTTAATCCAAGTTCGTTCAGCTCCTAACCGACCAAATGTTTATACATAATTTACACGTTACAAGAAACTCTCGAGATCTACGCACC
AAAGTGTAGGAAATGGTAGGGCCACTTTGATGACATCATTATGGCTTTGGGAAACAAAAGTAACCACAGAAGGGAGCAGGGAGGGGGGTTGCTGGTAGCGGGGAAAAAAGGACA
CGTTGTTTGGGCGTGAGTCATGTAGTTGGGCTGGCGGCACCTTTTGGCTTTTAAAACAAATATTTCCCATTAGCTGGGCTTTCGGTGATGAGCGACCACATTGCGTATACGC
ACGTGAGCCAAAATTTACACATCGAGGCAAAAGCAATCAGTATAAGGCAGCTGGAGAAATGGCACGAGACCTGCTCCCAGATAAAGTCATTATGTAGTGCTCCTAGCACTCG
CGCGCAGCCATAATCATAAACATTTGGTATACTCTTGCATGCTAGAGAAATATTGTAGTTGGGTAAGTGTTTTCAGATATTTAAACTAAGTAAGGAAATATTTCTATTTTTAC
ACCATTATTCATTGTTTTTTTCTTCAGGAGTTATCTGAACTTTTAAGTAATCCCACCACAGTTCTTGGAAGCAGTAGAATGTCTTCATTACCGCCAAATCCTTTTGATATCCTT
TTTCCCAAATGTCCGCAATTACACACATACCCTCGCACTAGCGCCCCTCGTTTTTTCAGGGTATAAATGTATGGGGAAAACACTTGTAAATAGCGGCAGCAGCCAC
(SEQ ID NO: 181)
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Exon: 5938..5903
Exon: 5607..5368
Exon: 5307..5249
Exon: 5009..4890
Exon: 4827..4747
Exon: 4669..4321
Exon: 4260..4192
Exon: 4130..3729
Exon: 3586..3392
Exon: 2213..2086
Exon: 2027..1916
Exon: 1543..1523
Exon: 1198..1001
Start ATG: 5938 (Reverse strand: CAT)

Transcript No. : CT35779

FIGURE SHEET 81

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ATGGTCCCAAGTCGGGGGAAGTGGCCGTGCCGCATGTTTTACGACTACACCGACATCGCCGAGGATGCCGCACGCCAGTTTATTGAATTTTTATCGGGCAAATTCCCAAATG
CCAACACACCGATTGCCATCGATGAGCCGACACGTGCGGAGGTGAGTCGCCGGGCCAATGGAATCGCCAGCTACGCCCTCAACGAGGACGACAATCTGCTGGCATTCGCCAT
TGCCGCGCCCAGCATTCACACGGTGGTCGTTAAATTCAGGGATAACGTTACGATACCACCGGATCAGGTGCACAATAAGGCATATTTGGGTTCCTATTGGCGGGAGTTGGGT
GCGGCCTGGAACAGCACGGACGGCACCCAGGAGTGGGGCGCTCCATTTCGCGACTGCAACCTGTTGACGCGTCGCTGGCTCTGGCCATTTCGCATATCCTTCAGCGAGCACA
GGATCAAAGTTGTGGCGGCTGCCTTCATTGCCGCCGACGAGGATGTGTGCAACGATGGCCTGGAGGAAGTTTCGGTCGCCGTCATGGTTGCGATCGGAATACGACCTTCTG
CCTGCTCACCGAGAACAAACCCGCCGCCACCCGGGATGTGTACACCTGTCTGTGCCGGGAATCCTACTACCTGCCCAATTCCACGCTCCAGGGATTCCGTGGCGATCGAGTG
GAACTGTCCGAGGGCTACGACAACTACTCGTGCATTCCGTGTCCCGGCGGATGCACTAACTGCGATAGCAACGGCGTCTGTCTGACCTTTCAGGAGGAGGAGGTGCTCAATG
TGGTACGCCTGTCTGCGCCTCCTGGTGGCCATCGTACTGGGCGCCTGCATCCTGTGCTGCATTGTCCTCGGGGTGATTGTCTTCCGGCAGCGCGAAAGTGCAAGGCCATTGCGTC
TGGTATGTGGACTGTGCTGGAGACGATACTGCTGGGCATTGTTTTACTTTATGCATCTGTTGCCGTCCATTTCTTTCCCGCATCCACCGAGCGCTGCCTTCTGGAGCCCTGG
CTTCGGGAGCTGGGCTTCATCACCTGCTACGGCGGCCATCATACTGAAGTTGTACCGCCACCTGGTGGACTTTCGCACCCGGAAAGCGCATCGCTGGGTGCTGCGCGACGTGG
ACCTGCTCAAGTATCTGGGCACCATGGTCTTTGCCGTCATCTGCTACATGGCCGCCTTTACGGCCTCGTCGTTGGATCTTCTCGAAAGTGCGCAGCTGGAGAGCCTCAGGGA
GGCGGACACGAACACCTGCCATCCGCTCAAGTGGGAACTGGTCACGCAGACCAGCGAGATGCTCATCCTGTGCTTTGGACTGCACCTGTCCATCGCCAGTCGGAATGCCAAC
ACCCAGTTCCGGGAACGACAATTTCTGGTCACCGCACTGACGCTGGAGTTCCTGGTCTCGTCCTCCTTCTACTTTCTGCGCTTTGTCTACCTGCCCGGAAATGAGTCCCAGCG
CCATCTTGCTGGCCCTGTTCATCCGCTCCCAGCTGACGAATAGTTTCGCCTTGGGTCTGATATTTGTGCCAAAGTTGTGGTACCAGCACAAGCAGGGTACGTCACACGACGC
CGGCCAGCGGCTGGGCCGGAGGATATGCCGGGCTCTGTCTGGGCGATCCGGACATTGGTGAGCTGACCATATCCGAAATGAGTCCCGAGGACATACGCGCCGAACTCAAAGA
CTGTATACCCAATTGGGAGATAATGAAGAACAAGACTCTGCGGCAGGACAATCCGCACATCAGTAAGCGACGTGGCGGACGCAAGGCGGGTCACCGTCGCTTCTCCCTGCAGA
AAAAGGGCAGCAAGGATAAGGCTCTAAGTGCCAAACACCGCAGCAACAAGCATCATCAGGACATCGAGATCACCGAGGCGGAACCTTCCAGGACGCCCGAGGATTCGGTGTG
CAGTGCCGAAGGACCCCACGGATACCTATGCGGAAATCTCCGGCGTGTCCCACTCAATGCTCTCTCACTCGATGGTCTCCCACTCCGTGGTCTCGCATTCGAAGTAG
(SEQ ID NO: 182)

Start ATG: 1 (Reverse strand: CAT)

MVPSRGKWPCRMFYDYTDIAEDAARQFIEFLSGKFPNANTPIAIDEPTRAEVSRRANGIASYALNEDDNLLAFAIAAPSIHTVVVKFRDNVTIPPDQVHNKAYLGSYWRELG
AAWNSTDGTQEWGAPFRDCNLLTRRWLWPFRISFSEHRIKVVAAAFIAADEDVCNDGLEEVFGRRHGCDRNTTFCLLTENKPAATRDVYTCLCRESYYLPNSTLQGFRGDRV
ELSEGYDNYSCIPCPGGCTNCDSNGVCLTFQEEEVLNVDACLRLLVAIVLGACILCCIVLGVIVFRQRKCKAIASGMWTVLETILLGIVLLYASVAVHFFPASTERCLLEPW
LRELGFITCYGAIILKLYRHLVDFRTRKAHRWVLRDVDLLKYLGTMVFAVICYMAAFTASSLDLLESAQLESLREADTNTCHPLKWELVTQTSEMLILCFGLHLSIASRNAN
TQFRERQFLVTALTLEFLVSSSFYFLRFVYLPEMSPSAILLALFIRSQLTNSFALGLIFVPKLWYQHKQGTSHDAGQRLGGGYAGLCLGDPDIGELTISEMSPEDIRAELKR
LYTQLEIMKNKTLRQDNPHISKRRGGRKAGHRRFSLQKKGSKDKALSAKHRSNKHHQDIEITEAEPSRTPEDSVCSAEGPTDTYAEISGVSHSMLSHSMVSHSVVSHSK*
(SEQ ID NO: 183)

Name: Metabotropic Glutamate-like RECEPTOR
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384249
CTCGTGACCTTTGAACCCGACGCTGGCACTTTGAAACGGAAACGGAAACACACACTCACACACACGTAATTTGGTTAGTCTGATATCGATGCACTATATGTTGGCTAATTTA
GACGGACTTTGGTTTTGACCAATCGCCAGGGTCCTACATATATGGTTTTGACTATATATTCTCGCTATGTTTAGTTGATTATACGATTTAGGGGTTTACTTTAGGTATTTTG
AGCATTTTCAATTCATGCGATTGTCGTTGAAATAACAATTGGGTTTTAGCTTTGCTTTAGCTGCCGTGACTTTTGTTTGTTTGTATCTCTATAAATTTATCAATATTCTCCGATTC
TAATTGCGTTGGGGGTGTGGTTGTTGTTATTCGCAGGACTTCTCACGTAGTTGTCTATAATTTGCGGTCTCTTAATTGGCACAGTTTTAGTTTTAGCTTTAGCTCGTCGATTTT
GCGAATCCCTATGTACACGCATAGCTCAGTGAGTTGCAGTGATTGCCATTTTGAATAATTTATTTGTGGTTATTTCTTTTCGTGAGCAAAATGCTTTACGGCTTACAGATTT
TAAACGACATAAAATCATAAATAAATAAGTTATCCTATACAAAGTCCCGATCTGTGCTCCAAGGAACCCGGCAAACTCGAATTGAGATTAAATGTTTTAAAAACGAAAACAA
AAATGAAAAAATGTGAAGAAAATGAAATGGCACGCTCCACAGATTGAATAATGTCAACATTACGAGTAAATCAGCCGACGCATTTGCCGGCATATTAATTTTACAAATTAAT
GGAACACTTTAATTGCATTAAATTGATTCCACCCATCCGGCTGGCATCGATTGATTCGATTCGCATCCTTACACCAGTCGCACCATTTGCACCATTTGCACCATTTACACAT
GACTCGAGGCCGTCGAGGCGGCGGCATTGTTGTTCTTGTTCCATTTGTTGATGTACTCCATGGGTATTTCAATCTGGATCTCCTGCACATCGTCGCCCGCCAAGCAATCGAC
ATTGCATTTCAATTCCTTGCCCGCTATCCTTTGCATCCTTGCGACTCCGTTCCGGCAGCTGCCAATTGTCCGCCCAGGCGGGTACCGCCCGCGCC
AGCCGCTGCTGCTGCTGGCGATGGGGGTCAGCAGCGCCTCATCCCTGTATTATAAGTTGTCCACCATCTGAGACTGGCGGCGATGCGAGGGCGTTGTCGAGTTAAGGTAGC
TCTCCGAGTAGAGCGCTCTTCGCCCGCTGGTCGTAGCGCAGGCTGGAGCGCCGGATGTCGATGTCCAGAGGCAGGTGGCGATCCTTCCACCAATTGCAGAACAGGCAGAGCAG
CGTGTTGCGGAACGCCTCCCGGAAGTCGCGGTTGAAGTACGCGTAGATCAGCGGGTTTAGCGTTGAGTTGAAGTACCCGATCCAGAAGAGGATTGAGACGACTATGTCCGGC
ACTTGGCACTCCTCGCAGGTCATGGAGAGTGTGTACCTAAAATTAAAACAATATAATTATTAGCTTACACTCATTATCTTTAACTTAATTTAAGTCAATTTTAAATTAGTTG
CACAGGTAATGCAATTTTATGTACTTTTTTTTTCCCGGCATTGCATAATATCTATTTTTTAATAATACAAAAGCAAATATAAAAGATCAAATGAATATTTTGTTTCATAAA
AGTTAAACCTCATAAACGATCTATATTTGAATACTTTGATCACCATTTGAAATCTTTCTGCATCACTTTTTGTCTGTGTAGCACATAAAGATGAGATATATATACCCATAAA
TTCCAGATGCATGAGTGGGCCAGGGCTTTGCATAAATGAGATTATACTCTGGGTGGTGTGAAAAACAACAACCGCCGAAACAATGGCGCACGGGCCGTATGAGTAATATTTA
ATTATGCATGCTTGACATTAGATAAATTATGCCTGGAATCCCATGTCAGCGGGATTGGCCTCCAACTCTCAACCAAACGTTCAACCTTCGACGGCTGGTTGGTACTCACCAC
AGGAAGAAAGGCAGCCAGCAGAGGATGAAGGTGCCCATGATGATGCCCAGCGTGCGTGCGGCCTTGTGCTCCCGCTTCATTTTGATTAAGTGCTTGTCCTTAGTGGGGGTGT
GCTCCTGCTCGACCTCGTGCAGCGTCAATGTTTTCGACGACCCGGATCCGCTCAGCGCCTCGCCTGCCGTAGGAGATAAGATGGAGATTTGATAAAAGTCCAGGCTGGAGAT
TTCTGTCCTGGTAAATTTATATTTTTGAAGTATTATTTCCACTTAAAACCCATTATATATTCAAACAAACATTTCTTTACAGCCAAACTAGGTAAGCCTTGTTGTTTACA
ACCCAACTTTGACTCCAAACTCACCTGATGGCTGCATGGATGGTCGGTGCATCAGCATGGCATTGCCGTGCCGCATCATCAGCTGCTTCTCCTGCCGATTGGCTTCCCGGAA
GATGGCCAGGTAGGTGAATATCATAATGGTGCAGGGTATCCAGAACGATATGGAGCTCGAGATGACGGCGTAGTACTTGTTCACCACGAACGAGCACTGCGTCGGATTCTGG
ATGACGAACTGCTGGTGCTGCGGCGTGGTGTACCAGCCGATGAAGATGGGCAAGAAGGAGAGCAGTGCCGGCGATATCCATGTGTTTAGCAGCATAATGCCGACCACGCGTT
TCGTCATGCTAATCGGATACTTGAGGGGCTTAACAATAGCATAGTATCTGTGAAGTGGGCAAAACGCCAGGTTATTGGGCCCTCATATAGCTATAGTTCTGGCTGTGGCATG
CAACTTACCTATCCACAGATATGCAGCATAAATGCAAAATACTCGCTGTTGAGAAGTAGACATCGAGGCTGTTCCACAAATCGCACAGGAAGGGGCTGAAGTTCACCACTGAA
AGGGTCCAATGAATGGAGGCATTAGTATCGCGATGCTTACCCAATAACGAGGCAATAAACTTTGGCCTTTACTTTCTAACGTCATTGTATCTGATTATCGAGTCCATGAATT
TGCAGTATATATTTTTGTTGACTCATTTCTGGTTTTTTGCCTCACCTAAAATGCCACGCGAAATACTTTTATGAAGTCATCGCTTTAAAACTGATTTCCTGGTTTTTAGCTG
TGCAAAAAATTTAGTTTTTCACGATTAATTCCCTTTGTGACAACACAGTTATTTACGTACTCTGATTAAAATCATTTGATTGTGGGTAAAATTGCGCTAGTTCTAATATTTA
CTACCATTTAAAATACAGATATATAGGCCATAAAACTCACTAGATATGCGCATAAGGTTGCTCTAAATTTAAACGGCCATTTTACTGCCAATTCCTGAATGTAGGTCTATA
AAAAACTCAAACTGACTAGACACACTCTCTTTTTCGCCTATTTTCGTTATCAGGCCGCCTGATTTATGTGTTTATCGATTTCATCTTAGTTTCGGTTGCCAGGTGACATTGC
CCCTGAACTGCCATTCTGGAGGGCAAATTAAAAGCTTAGATGCACTGTGAGACCAGAAAATAGGCCATAAGGCCCGAGGTGAAAAGTGGCAAGGAAAGCGGAGCGACTCT
GTTCGCTGCATGAAAAACTCATTAAAACTTGCGTCGTCGCTGTTCGCCTGTCGCTTCTGCCGTCGCCCTTGGTTGCCACTCCGCATTTTGGCCATTTCGGTGAAGGCGGATA
CCCGGCCTTTTTGGGGCCCAGGAGCCAGTGGAATTTATTATCGGGCGCCCCGTTTGGCATCAGTTTCAAAAACTTTTCGACTATCCAACGAGGCTGTTTTTGCTCGCTGGTTT
TTGCTGCTTTACACTACATTGCCATTTGGGGCGGGCGCGCCATCGGTTTTGACACTTAAGCCATGAAATGGCAGTTCCTCGTGCTGCAATTATGCAACTGGCAACTGTGAAG
GTAAAATGTCTCCAAGTGGCGGCGAGTTGGCTGTTGCCAGAACCAAACCGATGCCAATTTATATGCAACTCGCGCTTGGCCAAAGTTTTC
(SEQ ID NO: 184)

Exon: 3243..3209

FIGURE SHEET 82

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Exon: 3131..3033
Exon: 2959..2601
Exon: 2303..2126
Exon: 1604..1298
Exon: 1246..1001
Start ATG: 3243 (Reverse strand: CAT)


Transcript No. : CT21650
ATGGACTCGATAATCAGATACAGATGACGTTAGAAAGTGGAACTTCAGCCCCTTCCTGTGCGATTTGTGGAACAGCCTCGATGTCTACTTCTCAACAGCGAGTATTTTGCATT
TATGCTGCATATCTGTGGATAGATACTATGCTATTGTTAAGCCCCTCAAGTATCCGATTAGCATGACGAAACGCGTGGTCGGCATTATGCTGCTAAACACATGGATATCGCC
GGCACTGCTCTCCTTCTTGCCCATCTTCATCGGCTGGTACACCACGCCGCAGCACCAGCAGTTCGTCATCCAGAATCCGACGCAGTGCTCGTTCGTGGTGAACAAGTACTAC
ACGGCAATGCCATGCTGATGCACCGACCATCCATGCAGCCATCAGGCGAGCGCGCTGAGCGGATCCGGGTCGTCGAAAACATTGACGGTGCACGAGGTCGAGCAGGAGCACAC
CCCCACTAAGGACAAGCACTTAATCAAAATGAAGCGGGAGCACAAGGCCGCACGCACGCTGGGCATCATCATGGGCACCTTCATCCTCTGCTGGCTGCCTTTCTTCCTGTGG
TACACACTCTCCATGACCTGCGAGGAGTGCCAAGTGCCGGACATAGTCGTCTCAATCCTCTTCTGGATCGGGTACTTCAACTCAACGCTAAACCCGCTGATCTACGCGTACT
CTAACCGCGACTTCCGGGAGGCGTTCCGCAACACGCTGCTCTGCCTGTTCTGCAATTGGTGGAAGGATCGCCACCTGCCTCTGGACATCGACATCCGGCGCTCCAGCCTGCG
CGCCTGGGCGGACAATTGGCAGCTGCCGCCAAGGATGGCAGGGAGTCGAAGGATGCAAAGGATACGGGCAAGGATGCGGGCAAGGGCAAATCCAATGTCGATTGCTTGGCGG
GCGACGATGTGCAGGAGATCCAGATTGAAATACCCATGGAGTACATCAACAAATGGAACAAGAACAACAATGCCGCCGCCTCGACGGCCTCGAGTCATGTGTAA
(SEQ ID NO: 185)


Start ATG: 1 (Reverse strand: CAT)

MDSIIRYNDVRKWNFSPFLCDLWNSLDVYFSTASILHLCCISVDRYYAIVKPLKYPISMTKRVVGIMLLNTWISPALLSFLPIFIGWYTTPQHQQFVIQNPTQCSFVVNKYY
AVISSSISFWIPCTIMIFTYLAIFREANRQEKQLMMRHGNAMLMHRPSMQPSGEALSGSGSSKTLTLHEVEQEHTPTKDKHLIKMKREHKAARTLGIIMGTFILCWLPFFLW
YTLSMTCEECQVPDIVVSILFWIGYFNSTLNPLIYAYFNRDFREAFRNTLLCLFCNWWKDRHLPLDIDIRRSSLRYDQRAKSVYSESYLNSTTPSHRRQSQMQQQRLAAGGS
RLGGQLAAAAKDGRESKDAKDTGKDAGKGKSNVDCLAGDDVQEIQIEIPMEYINKWNKNNNAAASTASSHV*
(SEQ ID NO: 186)


Name: Beta 2 Adrenergic Receptor-like
Classification: G_protein_linked_receptor


Celera Sequence No. : 142000013384249
GTGAATCGTTTTTGCAGCGAATGGCGAAATTTCCTACAGCTTGCCAATTGTTTTGGTTGTTCGCAGTTCATTCTTTTTACTCATTGGTAAGATTGTCTTTCTGCATGAAAAT
TCATAACGTCAGCTACACAATTCTCTTCCATTCAATATTTGTCCATACATAATTTCGATTGCGTAAATTGTAATTTTCAATAACTCTGTTATGTAGATTTGGTTTGCTAGT
TATGAAATAAAAGCAGGGAGTTCATTCCGCTCAGGATTTGCAATCCTAATATACGATGATGACACATGTGAATAATCCAATTTTGGATCGTATTAATACTCCAAAAATCGAT
GGAAAAAGTGTTTCGCCTTCGACAAGCCGAAGTGGTGTACATAATTCTTAGATGATTCATTTGACAACATTTCACTTGAAGTTGGAACTTTTCTACGCAAAGAGTCGCTCGA
TTTCTAATTGGCTTTCGCTCTGCCATATATGTATAGTTATTACGTATATCTTCTGTTTAGTTGGACAAACAACACTTATATATGGATAGTATAGTTCCGGGGCAGCATTGTC
TCAAGGATTATGCTAGCTATATCCTGGCACAAATGCCACTGGTATGGCCGTTGCTCTTGTTACTTCTCTTCACTTCAGCTGGTGTTTTCCCTCCTTGGGCACATATACATGT
GCGACGATTCACTCAAGTATTAAATATCACTTATAGGGGCATTGTTCCGCATCCACGAGGGTGGACGAAGCAGGAATGTGGCCGGGATGCAGACGCTATCCGGTCTAGACGT
AGTAGGCGTTGTACGGATTTCGTTTCTCCAGACAGGGCAGCACCACTCCAGCGTATTGCGGAATGCCTCGCGAAATCGCGATTAAAGTAGGCGTATATAAGCGGATTTAG
CAATGAATATGAGTCACCAGAAAAAGAAGAATAAGAAGGCCAACAATGGATTACGGGATTAGGTGTTTGCTTAAGCTTACCACCACCACGAAAAGGGG
CAGCCAGCAGAGCAGAAAGACGCCCATGATGATGCCCAGGGTGCGGGCGGCCTTGTGTTCGGCCTTCCATCCTTTGGCCGGTCGCACGGAACCGCCTGTGGGGCAGATAGAG
AGTTTAGAAGGGATATGAAAGCTGGCAATTGGCTGATTAAGTTCAATTCGAATCGATTCGTTTCGATCCGCCAGTCTGTTTTTTTTCTTTTGTTGGGTCATAGCAATCGACA
GTTTTCTGGTTCATTTCTGTCTGTCTGCGAAAGCACTCGAAAAATGGGTTTCTTTTTAAGTAGTCTATAATATGCTTAATGTGGTATTTGTTGTCTACCTGTTGGATGTGTT
GTAAATTAATTGAACTTCAATCAATTAAAATACAGAAAATTTCAAACAAACAAATTTTAAAGAGGTAACTAAACTAATCTTAAAAATTATTAAATATTTTCTCTGTGTGTAA
ATTGCCAAGAAATGCGGTTTATGTTCGTTTTATTGTGAGAGAAAGATTATGCCGGCATGTTGCGTATACGCCATGTGTGTGGTATCCTTGTTTAACTTTGACATTAGTAATA
CTTTTTGCTGTTATATGTTGTTGGCATCGATGGCATTTCAAACCCCACACCGCCCCGCTCCCTGCGTCCACCTTGCAAGTGACTGTCATTAAAGTGCTGGAAAGGCCAACAT
GTGTGCAGTATCTTGGTGCTCGGGCGTGTGGGTGTGCGGGAAAAGCAATAAAAACGAGGCAAACAATTGAAAATATTTACACAGGACACTTGTTATCACAAAGACATACAAT
CCCCGCATCCATCCAGTCCAGTGCCGCCCGCCCCCAAACATAAACATAAACATCACTGGCGGCCAGGAGGGAAAAACAAATCAGACAGACAACAGTGAGCAACAGGAAGCAACG
GACCATCGCCCTTGTTCACCCATTGCCCATCGCCCATTGCCCATGTTCCCCCATCCAGTTTGCCACCTGGATCCCTTGATGGACGCCACTCGGTGATGGCCACAGCCAGGTG
AAATCATAATGCAAAGGCTGTGTGGAGGGAGGCGTAATAAAGCAAAGCAAACGCACGTGCAAACGGAAGCAATTATGTACAGCATGAGAGCAGCGAAAGGTGAAGGATTCGG
TGCCAAAAAACTGGCACTTCTGTGGGTATTTGCCACTAAAGCTGGGGGCTACAAAAATTTGAGGTAGTTCTTTTCGGTTTCATTTCACGGTTGATTTAATGATACTTAGGTT
AACCACCGTTGAAATGATTGGGATTGCAGAAATTCAGGGATATCTATTCTAGTATGATTTTTGGTAAGAACGTTAACTAGTTTCAGGTGTATTCAAAAGCTTTCAATTTTAA
ACATAATAGGTTTAAACATATACGGAACAGTAATATTGATTGTTTTTTGACTGACAGGATATTTCATATGAAATAAATAGATTTTTGATATGTTTGGTCTAATGCAGTGGCA
TAAAATACGAAGTGAATGGGACTTGATTTGATTAAGATTTTCTGATGATTATATATGTATTGATATAGAGAAACTATAACTATTGGTGTTGTGAAATTAGTGAATTCTGAGT
GTGAAATGTATTATAATATAATGCACAAGTTCTGGACTGTGGGAAATCGAATGTCATTATCGTTGGCTCCCTGTCTCTGGAAGTAGGTCGTCCCTTTCTGTCTTCGTTTGCAGGTGC
CAGAGATAGAGAGAGGAAGCGGGAGAGAAAGAGCGAAACGTAGAGAGCTGGGGGAGGAGAGGAGGGGGAGATACGACAAGACTCACCGGTTGCACCACAGTGACTGCGCATCCGGTT
TTGAAGCGGCGCTTCCGGTTCTTGCTCTGCTGCCAACATGCTGTGACCGCCGCCGTTCGCTTGTGCCAGAATCGAGTGGAACTGGACGAGGAGGCGGGCCTCTGGCCAAGAT
CTGGAGTTTGCTCGTGAATACTACGTTTACTACTAGTGGTTACTGTGGTGTCGATTGTGCTGTCGGCGTTGGCGGTTGCGGTTGCGTTTGCGGTGGTGCCGGTGGTGCTGCT
CAGATGCCGCCGCGTCGGATCAGCGAGGATTTATTGGAAAATTCGTGCTCTGCTTGCAGTTGATTGTTGCATTTTCGTACGATTTCGATTGTCAATTTGGCCATGGCATTTT
TGGGGTTTTATTGGTTGGATTTGGTTTTGGAGTAGAAGTAGTTTGTTTGTTTGGTTGGACATAATTTGGTGATTTCGATTTACATATATACACATACAACACACAACGAAAT
GGCGTGGAAGAGAGATAGATATAAAGAGATAGAGACAAGTAGTAAACAATGTACACAGGGTATTTCACAGGATACGAAAGGACTTCAACTTCTGAGATCACATGCAGCCATG
AACTAACTAAATGCTATACATTATATTTATATATATATAGATAGTAAGCTAGTTAACTAAAGTTTCATTCGAAGCATTTGAAGTTACTTTTCCAATGAGGGTTTATAGGTTCTATA
CATTTTAAAACACTGTATGATTTTTCAGAAATTCGCACCGCTTTTGAAAGGAACTTAAATACACAATTCACAGTTTTCTTCAACGTAAGAACTATATTTAAATATGGTAAAA
GTTCGTATCTTTATTTTAAGATCAAAATTCTAGTAAGACCAGATTCCTTATGTTAAACCCGAATTCAGGCCAATTACTCCTCAAAAAAACAAGGACAAAAGAATGTGCGAAA
AAGTTAAGTCAAACATTGAAACACTTGAACTTTTCGTGGAAAACTGACAAAAACAGAACGAATTCTCTGGGGCAGATATAAATTGTCTTAAAAGAGCTACTTAAATCAAGC
ACGAGCTATACAGTCTACACAATGACCAAATGGATGACTACTCACTTGCGGAACTGGTGGAAACGCGGCCCATCGGGATGTAGCTGCGACTGTCGCTGTTCTCCTGCGAGAA
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FIGURE SHEET 83

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GTTGATGACATTCACGTCGTAGGTCACCACGGACGCCTGTCTCTTCCGCACAGTTTGGATGCCATCGTAGCCTGCCAGGATGCTGCAGCGGCCTTGGCGGCCACCCACTCCT
CCAACGCCACCAGCCCCTCCATTGCCGGAAACGCTCACGTCCGCATCGCCGGCGCTATCTTTGCGCTTGAACAGTGGCGACGTGACATCCCGGTGCTCATCGCCGCATCCCT
CAACCGGCGACAGCGTGGAATCGAGTATGATCTCCGGCTTGGGCGGATATGTTGGACTGTGAGGCCATTTGGGGATTTGGCTGCGGCACTGGAACGGGCATAGGCAGGCTGGT
CACCACATCCAAGGACACAGTGGATGTGTCACTGGGCGTATAACCAGGTGCGGCGGCGGCGGCGATAGGAGTACACATTGATGGACGCCGACTGCGCGTTGGAA
GAGGCGGAAGAGTCCATGGCACCTCCGTTCGGCACGGAAATGGCCGGCGGAGCCGGTCGTGTTCGGTGGGGGACATCAGATAGTTGGCGCACACCTGGTCACTGAGCGTGCTCA
GGCGCTGTGGAGCACCAGCCGGTCGGCCCAGCGGAAAGCTCAGCGAGCGAAAGATCTCGGCCAGTTCCGAGCTGCTGGCAATGAGCAGGCCACTCGGTTCTGGCAATTCTGG
CGGCGATAACGATGGTGGCGGCGTGGCCGGCTGCTGGGGCGACTCCCCAAAGCAATCGGCCAGCTGCGCCAACTCGTCGTCGCTCCGAATCCTCTCGGGCGGTGTTTTCAGC
TCACTGAAGTCAATCAGCTGTACCCCGTCGCTGAACTGCTGGATCACACTGGCTCCACTCTGCTCGCTGAGCACCATTGATGTCCAGCAGGATGTCCGGCTTGTTGGGCGTGG
AGTCCGTATCGCTGTGCTGCCGCTGGCGTCTCTCAAGTTTGCGTTCCTTGCCGCCACCGCATCCGTTGTAGCGTGCGACAATTTCCGGTTCCGGGAGCGCCGGAAGAAGCT
GGATCCCTCGGAGTTGGCCTGATGTCGCTTCTTTTCCAGCGTAAAGCACTCGGTGCTCGAGCGTTTCGTCTTCGACAGCAGGGACAGAATGTTGAAGCCCTTCTCCTTCCCG
GGCACTGGCTGCTCCGGCAACGCCCGCGATTCACTAATGGTGCGCAGGAACTCCGAATCGCTGGAGGCGAATGCCTTACGCCCACAGGCCGCTGCGCCCGCCTTCAGCCTGA
TGAAGTCCGTTTCACTGAGGGCAGCGTACTTTCCTCCGCCTGGGCCACTGATAATGCGTGCCGCCCGTCTGGCGCTTAAAGTACAGATAGTTGTCCTCTATCAGGCGCTTCAG
CTCCTTGTTGTCCTCGGCCAGCGGCAGGTGGGTGTCGTACAGGTCGTTGCCCTCGCTCTCGCTGTTGAGACCACCAAAGACCCGGTACGCAGTGGACTCCGGTTCCGGT
TCGCTGTTCCCACTGCCGCTGGTCAGGCTGAGCTGCTGTTGCGGGCCATTGGGATGAGAATGCTCCTTATCGAGCTCCTTCGAAGGGATCATCTTGCCCTCCGTCCATATCT
GCGGATTGAACACTGGCGCCGGTGGCTGCAACTGATTGTGGGAGGCTGCTGTTGCTGCAGTGCCATCATCGAGGGAGCACTGTCCGTGTGGGTGACCTTCTCGTACCGCTC
CTGCTCCAAGTCCCTCAGATCGATGCTGCTGCGGCTGAGGCGGCGTGGCGGCGGCGATGGCACTCTCAGTTCATCGCACTGTCCCTATCGTCGTCCTCGTCGGTGGCCGGC
TGCAGCATGTCCTGTGGGCAAAGGACAATCACTCAAAGGGAAGTCATGGTGGCGCATCAATTACGCACAGCCACAAGGGAAAAGGAAAAACTCTCAAGCCGGAGTGCTTCCCT
CTAGCACCTAATCTAATCGCTCCACATCCGTTCATTGAGGATGGGCAAAAAGCTTTAGAGCAGGATGTCAATGTTGCCCGTTTGTATACATGAACTGCATTGCTTTAAAGTC
TTTGTATATTTATTTAGGATACTATCTGGATGTATCAGCAACTTTACCAAATTTTACTCAATAAAAAATAAATAATGTTTTATTCAACTACTAAGAGATCTTCAGAATGGCA
AGCAAATGCGAGTACTAAAGCATTTATCGGTTTAATAAAAATAAAACATTTTTAAGTATCTCTAGGTATTTTAGGCATCTTTGGATTAATGTGTATTTTTTCATTTTGAACA
TCTTTGAAATGTTTATTGTTTATTGAATGATTTTATATCAATAAAATGCAGCAAAATACTCTTTTGGCTTTCAATAAATGACATCTGTATCTTTTCGGTTCAGT
AACATTTAGTAACCTTCCAAACTCACCTCCAAGTTACTAAGCGCACTGTGCGTCTCCTCCCGGGCGGATGTGGCATTCAGATCACAGTCACTGGGATGCAGATAGCTCAGGC
TGGTGGGCTGCTGGGTGTGGCCCATGTGGACGCTGTTAAGGAGGATGTTGGAGCTGGTGCGGCTGAGGGCCTTGCGTTGACGAATCGCCTCCCTGGAAAACCACAGAGCACA
GATCAGCAATTAAGCAAACTCATCCACTACGACCAGCGACCATCGACCATCGACCATCCGGGTAAGAACTCACTTAAAGATGCGCCAGTACATCACCAGCATCACAATGCCG
GGTATCCAGAAGCTCACCGAACTGGAGATGAGGCGTAGGCCTTGTTGACCAAACGAGCACTGGTCCGGATGCAGGGAAATCTCCCGCCAGGTGCTCCTCCGTCGTGATGGCC
AGCCCAGAAAGATGGGCGTGAAGGATATGAGGGCGGGCAGGATCCACACATTGGCGAGCATGAAGCAGACCGTTTGTGTGTCATATTCAATGGATACTCCAGTGGACGCAC
AATGGCGTAGTATCTGTTAAAAAGAAGAGGGGGTCATCTTTATTAATGGAAATGAATTGCGGACAGGTCCTCCGCACAAAGGTGCCAGGTGGCTTTCAGCCATTTCCTCCTT
CTCCTCCTCCTCCTTTTGGCTTACTAATTGATTATCGCTCTTTGGTTGGCTGAATAATTGTGTTTCGGTACTCAGGTTGCCATGCACAGAAATCGATTTATTAACCTTTTAA
AGATCATGTTGCATTTAAATGAAGGATAAATGCTCTTAACCGAATTCATTATCGGAATCCGTGAAAATAAGGTGGTGTATTCTTTTTAATTATCAATATATTAATAAATGCA
ATTGAAATGAAATAATTATTAATCCACGTATATTGTACCTCATTATTTTTATCGAAACTTAATGCTCCTTTTAAAGAGTAATGATTATGTTTGGAACATTACAGATTTATTAG
TTTAGCCAAATTTCCGTTAGTGGCCATCATTAATTCTCTAATTTTGATAGGTTCTGGTTGAATTTCCCTTTGTTTCTTGGTATGTTTTGTGGCCCGTCGAAAGGTGAGTGAA
GAATGGCGCCAATTAACGGCTTGACAGGATGGAGAAGGTTGTGGGAGTTGGGTGGAATATGGGCAACGCCCACGTTTCGGCCAGCTGCAAATCATTTGGGC
CGCATTCATCATACGGGCGGGCCTAATGTTTGCTTTTGATGTGCGCGCCTTTCATAGTAATTAATTGTTTCTTCTTGGCAATTCGCCGGGCTTTGGTATTGAAAGTGATTTG
GTTGCCAGGCATCTGGGCAAGATTAATGGTATTTGGCCAAACTAAACGGCTTTCTTCAGTACCATAGCCCAGCACAATTGACTTTAAACCGCTTAATATATAGATAGAGAGC
GACATAAATGGGCACTCACCTGTCCACTGATATGCAGCACAGGTGCAATATGCTGGCCGTGGAAAAGTAAACATCCAGGCTGTTGTACACGTTGCACATGAACGGTCCGAAC
ATCCACTTTCCGCCGGACAGTTCCACGGAGGCGTTGAATGTCATCGCACAGAGGGCCACCAGCATGTCGGCCATCGCCAGCGACACAACAAAGTAATTGGTTATCACCCTGC
GAACGAAACAAAAGCCCAGGAATTTGTGAATATGGCGTGGTTCTGGGCGGGATTTGACCAGCTTCTCCCCACATCTAACCACTTGTCACAGCGCAAAACCACGCCAAACGTA
ATGGCATATGGCATGCATCATATGTGCACATGCCGCTGTACTAAGCGCTTTGGTTGGCTCCTTCCGTTGGCCAAGCAGTGCACCACTGCTTTCCATTTCCTGTTCCGGTGTT
CAGGAGTTTGGAGGCAATAGGTCACCGGTATGCAGCAATTTCCTTGGCTGTCATAAGTCACTCGACTCACCAGGCAGCTGCCACCTTCAGCTGCAAGCTACTGGCTTGTGAA
GTTATCATCTTGTCTTCGGGGCGTATGTGGTTAAGGAGCTGTTTATGCGAAGATGAAAGCACTTTTGTGCTTCCAAGTCATTTATTACATATTGCGACATCTATTACGTTG
GAAAGTGTAGTTTTACAGGGGCTGACAACATTGTCTAAAACATGTTATTAACGTATATTGTAGTAATGAAGCTCAATTAAATCAAGATTATTAATCTGTGCATT
TAGAAGGGCTGTTAATTTCGAAAGATCCTTTTATGTCAAGCCGTTTTTTCTTTTATGCACTGCTTTATTTTGTAATATCTCAACGCAATTCTATATGGCGAACGTTCTATCG
TAAGGTAGTAAATGATAATCTGAGCACTTTAAGCTCCTTTAGCGGTATAATAAAGACTTTAATCAACATCTACCCTTGCTGCAGAAGGCATAAACGTTGCGCAACATTAAAC
GGATGTCGTGGGTGTACGTGTGGGGGCGTGGCCGGGGGCGCTGGCGGTGGCAGAGCGCTCAATGGTATGCTACACTTATTTGCACTGCACTCTGGGGCGTCCTGTCATCGCG
ACGCTGACATGGCAGCGATGGGCTTGGGATCGGCTTGTGTGCCGCATTTAACTTCGTTTTGTTCTTTATTATTCCACTTGTCGCTCATTTAAATTACATTTATCGCGATGGC
GAAAAGGATTCGCCCTGCCGCGTCACTGTTTGTTTGCCATTTCCATTGTCCTGCGACCCTTGCGGCAATGACCCTCAATTAAACTCAGTTACAGGTGGTGAAAACAAAAGTA
ATTGGATATAGACTTACCGCAGCTTTCGATTGCGCTCACTGAAATGATGACCAATGCATTGCCGAGGACAGCGGCCAGGATAATTGACGAGAAGATGAATCCTTTGAGCAG
CAGCAGCGATAGATCCAGCCAGCTCTCCTCCAGCTCCGCCTGGTTATCCACCGCAATGTCACTGCCATTGGCCGTTATATTTGGGCCGACTGTCGAGAGGAGCTCAAACGTG
GAATCCGACGACAAGTAGGATGAAAAGGGCGAGGATAGGGAGGCATCTGACGATGTGGTTAATGATAGCGAAGTCAACGAGGCATCCACAAATTGCCGATGTTATAGGCA
AACTGCTCGTCGGCGTCGTCGTAGTTTTGGCTGGCTGCTGTCGTGGAAATGTGGCCTGTTAATGTTGCAGGTTGCAGGTGGCTGGCGTTGGTGGCTGATGTTGCTGCTGCTTG
TGATGTTGCTGCTCCTGCTGCGGCTGTTATGGGTAATGTCATTGTCGTGGCCAGAAGGTCAGCCACGTTAACCCCTGACATCTCGTCGATTTCGCAGCCCAATTGAGTCGCA
GCTCATTCAAGTTGCTCCGCCAATGCTTTTTCGCTGTACTTGTCGTTTATCTTTTTCCCGGCTGCTGTGCGTAATTTAAAACTCGAGTAATTGCAATCTGCAATGCAAACAA
GGCTGCCGAAGTTTGCCGTCATCCTGGTTGCCAATGTTGCTCCTCTGCGATTTCCATGTATCTGCTCACAGCTCCGACTGAAGGTCTCTGCTCCATTTCCCAATCCTCCATAGG
ACGCTTTTCCCGTTTGAGTTGCTGGAAATTGGCAAAAAGTCGAGACTCGCGCTTCGATTTGGCACTCAAGCGCGCAACAGTCGGCGACACGGGAACTGCAAATGAATAAATA
AATAATTTATGAAATAATCGGCGAGTGTGAGGCTGTGAAACTGCATGGCAAAATTGGTAAAATGGGAATTCGAACGGTTGCGCCGCCCGGGGTGTTTTTATGTACATACGCA
GCCACTTCAACTTTGCTACACTAGATTAAAATAACAGAAATATATTGCGTATACGCAGTGTGTGCACTCGGCATGCATCTGCATTTCTATATCCCCAGCGAGACAGCCGGTGC
TGTCAAGTGCTGACACTTGTGCAGAGTGGAATGTGGAATATGGACAAGTTGTTGCTTTAAAAGTGAGATTAAAGCAAGATTATCAGTGGGAAAGTTGTTTCAGTAGTGCCTC
ACGCCTGGGCGCAGTGAAAACTGCAAATCCTTTTTGTCCCGGTACTTGTAAGTAAAACAAAAGACTCTTCATAATCTGTGGTAATCTCGAATTTTTTCTTTTTTATTATTTTT
AAACTTTTTGCGACTCAATTTGGCCGTAAAAATGCTAACACATCATCAGGGAAAAGCTGAAAGCGTGCTTACACTTTACTTTCTCCCCCGCAACATTGAATTGAAGCTGAAT
CCGTCCTTGGCACTCAGACAAATCGCTGGCTACACGTTTTCATTGCACTTATTCTGTGCACTCTAGATGCCCTGCCCTCATTCCAATCTTCAGAGTTTTGAATCTAATATTT
TTAAGGATTTATGTACTTATACAGATAACCTTGCCGAATTGATTGCATTGCGTTGTCCTTGAGCTGTCGATTCGACTTGTTTACTCAGACCATCCGGTCACATCCTCCTGCT
AGATTGGCAACTTAATGTTTTAATGCTCGGACTTAAACCACATCAGTGCGCTCTATCATCCTTGGCTTATACATTTCACAAGCCATT
(SEQ ID NO: 187)

Exon: 10847..10568
Exon: 10497..9986
Exon: 8844..8644
Exon: 7629..7354
Exon: 7260..7083
Exon: 3656..3332
Exon: 1439..1331
Exon: 1211..1001
Start ATG: 10497 (Reverse strand: CAT)
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FIGURE SHEET 84

Transcript No. : CT21843
TTCCCGTGTCGCCGACTGTTGCGCGCTTGAGTGCCAAATCGAAGCGCGAGTCTCGACTTTTTGCCAATTTCCAGCAACTCAAACGGGAAAAGCGTCCTATGGAGGATTGGGA
AATGGAGCAGAGACCTTCAGTCGGAGCTGTGAGCAAATACTGGAATCGCAGAGGAGCAACATTGGCAACCAGGATGACGGCAAACTTCGGCAGCCTTGTTTGCATTGCAGAT
TGCAATTACTCGAGTTTTAAATTACGCACAGCAGCCGGGAAAAAGATAAACGACAAATGTCAGGGGTTAACGTGGCTGACCTTCTGGCCACGACAATGACATTACCCATAAC
AGCCGCAGCAGGAGCAGCAACATCACAAGCAGCAGCAACATCAGCCACCAACGCCAGCCACCTGCAACCTGCAACATTAACAGGCCACATTTCCACGACAGCAGCAGCCAAA
ACTACGACGACGCCGACGAGCAGTTTGCCTATAACATCGCCAATTTGTGGATGCCTCGTTGACTTCGCTATCATTAACAGCCACATCGTCAGATGCCTCCTACTCCTCGCCCT
TTTCATCCTACTTGTCGTCGGATTCCACGTTTGAGCTCCTCTCGACAGTCGGCCCAAATATAACGGCCAATGGCAGTGACATTGCGGTGGATAACCAGGCGGGAGCTGGAGGA
GAGCTGGCTGGATCTATCGCTGCTGCTGCTCAAAGGATTCATCTTCTCGTCAATTATCCTGGCCGCTGTCCTCGGCAATGCATTGGTCATCATTTCAGTGCAGCGCAATCGA
AAGCTGCGGGTGATAACCAATTACTTTGTTGTGTCGCTGGCGATGGCCGACATGCTGGTGGCCCTCTGTGCGATGACATTCAACGCCTCCGTGGAACTGTCCGGCGGAAAGT
GGATGTTCGGACCGGTTCATGTGCAACGTGTACAACAGCCTGGATGTTTACTTTTCCACGGCCAGCATATTGCACCTGTGCTGCATATCAGTGGACAGATACTACGCCATTGT
GCGTCCACTGGAGTATCCATTGAATATGACACACAAAACGGTCTGCTTCATGCTCGCCAATGTGTGGATCCTGCCCGCCCTCATATCCTTCACGCCCATCTTTCTGGGCTGG
TACACGACGGAGGAGCACCTGCGGGAGATTTCCCTGCATCCGGACCAGTGCTCGTTTGTGGTCAACAAGGCCTACGCCCTCATCTCCAGTTCGGTGAGCTTCTGGATACCCG
CACCCAGCAGCCCACCAGCCTGAGCTATCTGCATCCCAGTGACTGTGATCTGAATGCCACATCCGCCCGGGAGGAGACGCACAGTGCGCTTAGTAACTTGGAGCGGCCCCGC
GGCATCACCTTCGCCGCCGGTGCCCAGTCCGCTGCCCAAGTGTCCGCTCTGCGGCGCCGACATCAGCAGCACCACCGGCACCACCGCAAACGCAACCGCAACCGCCAACGCCG
ACAGCACAATCGACACCACAGTAACCACTAGTAGTAAACGTAGTATTCACGAGCAAACTCCAGATCTTGGCCAGAGGCCCGCCTCCTCGTCCAGTTCCACTCGATTCTGGCA
AAAGGATGGAAGGCCGAACACAAGGCCGCCCGCACCCTGGGCATCATCATGGGCGTCTTTCTGCTCTGCTGGCTGCCCTTCTTTCTGTGGTATGTCATCACATCGCTCTGCG
GTCCGGCCTGCCCATGTCCCGATGCTGCGTGGTGGTGTTATTCTGGATCGGTTACTTCAACTCCACGCTAAATCCGCTTATATACGCCTACTTTAATCGCGATTTTCGCGA
GGCATTCCGCAATACGCTGGAGTGTGTGCTGCCCTGTCTGGAGAAACGAAATCCGTACAACGCCTACTACGTCTAG
(SEQ ID NO: 188)

Start ATG: 201 (Reverse strand: CAT)

MSGVNVADLLATTMTLPITAAAGAATSQAAATSATNASHLQPATLTGHISTTAAAKTTTTPTSSLPITSQFVDASLTSLSLTATSSDASYSSPFSSYLSSDSTFELLSTVGP
NITANGSDIAVDNQAELEESWLDLSLLLLKGFIFSSIILAAVLGNALVIISVQRNRKLRVITNYFVVSLAMADMLVALCAMTFNASVELSGGKWMFGPFMCNVYNSLDVYFS
TASILHLCCISVDRYYAIVRPLEYPLNMTHKTVCFMLANVWILPALISFTPIFLGWYTTEEHLREISLHPDQCSFVVNKAYALISSSVSFWIPGIVMLVMYWRIFKEAIRQR
KALSRTSSNILLNSVHMGHTQQPTSLSYLHPSDCDLNATSAREETHSALSNLERPRGITFAAVPSPLPKCPLCGADISSTTGTTANATATANADSTIDTTVTTSSKRSIHEQ
TPDLGQRPASSSSSTRFWHKRTAAVTACWQQSKNRKRRFKTGCSHCGATGGSVRPAKGWKAEHKAARTLGIIMGVFLLCWLPFFLWYVITSLCGPACPCPDVLVVVLFWIGY
FNSTLNPLIYAYFNRDFREAFRNTLECVLPCLEKRNPYNAYYV*
(SEQ ID NO: 189)

Name: Beta Adrenergic/ Octopamine Receptor-like
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384518
GTTCCGTTACTTGGTCTTTGACTTCTTACCCCAGAATATGATTCTTGGCAGCAGGAGAAACCAGTACGACTTGTTTTGGTCGTATTATGAGTGAAATATTACCACTCATGTC
ATTTTGAACGTCTTTAAAGCTCACACCCTTATGGACCCATTATAAGAATATGGCGTGGCAAAATTTCCCATTTTTTATCGAGGCTGGAAAAACTTTTCCACACATGCAATCAT
GTTTCGTTTCACTTATCATGGCTAAAACCTAGCAAATAGAAAAAGTTTTTTTTTATCCACAAACATATCTGTATTGAGTGCCAGCAATCTGTATTGCTTTAGCTTAAGATGT
TTACTATTAATAGAGCCAAGTGGCAAATGACATACGGCTTACAGAGAAAATAATTTCCAATTCAATTACATTTACGTACATATATTCCTTCCTACAAGCAGACAGGATTATT
GATCTAAATATAAATAAATATATAATAATTATTTTAATAATATAATATTAAAATGTAGATTAACAGAATATATTTTTTTTGTAGTGAAAGCCTCTAGGGTATTTGTGTGACTT
TTTTCTCTCTGCATAAGTGAAGATGTTTACTATTAATAGAGCCAAGAGGCAAGAGAAAAGTGGCAGCAATCAAGTGCTTTTATTTCGGGACTGCATGTTAAAGGCGATTTCC
TGATCGAAGACTTTGGATACCTGATGCCATCCGTCTGAATGTGACGTCAGCCTGGCTGGGGATTCAATTTAAATTCATCCTTGAGTCTAATGACTTTTAATGTTGTTGCTT
CACAGGCGAGTGCGCAATTTTTGGGCCTGTCGTCGACTGCTTATCGGCTATGTGCCACCGCAGCCGCAAAGGATACGACAGACAATATTAATAACGCATTGATACGAGTGGG
AGGCGTCGCCATCACCTAGCCAACGACAGCCAACGATGGCATCAATCAATCATTCATGGCTCATGTGTCGCCCAGTCCCAATCAGAGTCCCTCCATTGGAGTGGGCATC
GGTATCGGCCTCATCCACAATGGCGAATCCCAGCGAGAGCCCCGAGATGTTGCTGCTGAAGAACGACAAATTCCTAACACATGTCGCCCATCTGCTGAACATAACGACCGAGA
ATCTTTCAAATCTCCTGGGTTCCACGAACGGCACAAATGCGAGCACAATGGCAGCGGATTCGCCGGTCGACGAGTCCCTGACCCTGCGAACAGCCCTCACCGTTTGTTATGC
ACTCATTTTTGTGGCCGGCGTGCTGGGTAATCTTATCACCTGCATTGTTATATCGCGAAATAACTTTATGCACACGGCCCACCAATTTCTATTTGTTCAACCTGGCGGTTTCC
GACTTAATACTGTTGGTCTCAGGTGAGATGGCATTTTTGAGGGACACCATTGCGTATGCGTAATGCGGCAAATATCCTGCAGGCATCCCCCAGGAGCTGTACAACCTTTGGT
ATCCGGATATGTATCCCTTCACGGACGCCATGTGCATCATGGGCAGTGTGCTCTCGGAAATGGCCGCCAATGCAACGGTTCTCACCATCACAGCATTCACTGTGGAGCGATA
TATAGCAATCTGTCATCCATTCCGGTGAGTTTTTAACATTTAAACGTTATATATATTTTAAATATTTATTTACATTATTAAACAAATGTATAATTTCTTCAGTGTTATTGCC
TCGCTCTCATTAACAAAGTGGATCATGCATAATTAGGACAGAGAATATGAATAGATAAATTAAACTTGATAAGCGTCAGTCGGAAACATTATGATATGAAACAACAAAAGTA
CCTCACAAATTATGGGCACAATAATTATTCATAACTAAACAGTCTGGCTGTGGAATGATAAAACAAGTTAGGCTTGACAACCAAATTCCCATCGTTTTTAAATATACCAAAT
TCATTAGCTTTCATTTATAGACACTAATTAAAGTCAGGTCCATAAATGAACCAAGTTCATTACAGACTATGTAATTAAGTTCCAATAAATGCGGTTGTAAAGATAGAAAGTTA
GTTAGTCAATTAATTGCTTAGTACCAACATATTTGCATTTTTGGAATGGTACAACAAAACTTTTCCTTATACAGGTATCACCAGTTCCTTCCAAATGTTCTGACCATTTTGC
ACCTTACATTGTTGTTTCAAACACAATTTCCGTTTCTTAGCATTTTTCACAAATTAATTGTTACGAATACAATCACTTGGAGTATGTCCTTAAGAATATGCAGACACAAAA
GGGTGGTTTTCTATAAGAAGGGATTCCAAGTCCGATTACAAAGTTAAGGCAAAAAACTTTCATGTCTCTGAAGTTGGGATTAAATATTGTTGTCGAAAAGAGTAAAAGGTTT
CTATGTTTGCCATTTAATAGTATTATAGTTATTTTGAAACGAAAGGATATTCGGACATGTGCTTAGCATGAAAAAGGTCTGAAACCCATTGCAGTCACTTTACCAAAAGAAG
TTAAAAGTGATGTCTATTAAATTTGGTATGAAACTGTTTGAATTCCTTCCCATTTACACCCACATTCAAAGTAAATATTTATGTTGCACTCAATATCCCAAACCTTAAAGAG
AAAGTTAAAAAGCGTAAAAAGTGTAGGTGGTCACTGCGTGTACTTTACAACCGTAATATTTTCCATCTTATATCTGCCCACGTTTATCCGAAACATCGACATCATCTTGTCC
TTAATACTTAACATATAATGTAGCCTAATCTTTCCGTCATTTGTAGGCAGCACACCATGTCAAAATTGTCGCGAGCCATTAAATTTATATTTGCCATTTGGCTGGCGGCCTT
CCTTTTGGCCCTTCCGCAGGCCATGCAATTTTCGGTGGTCTACCAGAACGAAGGATACTCGTGCACGGTGGGTGGGACTGAAATGTGAAAACCAACTGACGCATCATCGAGT
GTCCTTTTCGCTGTTTATTCCCTTAGATGGAAAACGACTTTTACGCCCATGTGTTCGCCGTTTCGGGATTTATTTTCTTCGGTGGACCCATGACGGCGATTTGTGTACTGTA
CGTGCTGATCGGAGTGAAACTGAAGAGGAGTCGACTGCTGCAAATCGCTGCCGCGAAGGACTTTCGATGCGAATCGCGGCCTAAATGCCCAGGGACGAGTCATCAGAATGTTG
GGTAGGTGAGTTAAGTTGGCGGCTTGATTGATTAAAGACAGCAATATGCCCCACCGCCAACCAGAAACAACAAGAACATCCACGGCTGTCAAAACTTTTCCGCCGAAAGTC
TTAAATTGAAAATTACTGTCAACGTATTTGCGTTGGCGAACATCAAACAGGGAATTCGTCATAGCCCCGCCCTCATTGCCTTCCGCCCACTTCATTTGCACTTGCGTCATGT
GGGCTGAACGTGCTTCTGTTTTTTTCCCTCTTTTCCCTCAACGGTGTCGTTAATTTTTCGCAAACATCGGTGCGTATGTGTAAAGCTCTTAAATGGCCATCTAGCCTATGAA
GCAAAGGTGAAGCCAGGTGTCACCTCAAAAGTAATCAAGCCGGGGCACTTAAATGAACTCAAGCTGCTGGGTGCACACAGCAAGCTTAAATATTTGTAAAAAGTGTTTCTT
GAATCTATAGACATATGTCCGTTAACGTGCCACGTTATAAGCTTATTTTTTTTTTAAAGAAAAGCTTTTTTTAAAGGAATTCAGCACACATCTCGTGTATTATTCACATATTTTATTTATATAATTAGAAA
TTCTTATCAAACCATACAGTGAATAAATTTAAGTGTAAATCCAGGCCCAATTTTTAGATCCCAATAAGCCGTTTTTTCTTACAGCCTACGAAACAACGTTTAATTTACTGTTG
CTTTTTAACTGAAACACCGACCATTGATTTCGAAATTTACCATTGGCCCTGGCCTGCCAAATGGAAATTGATGGACCAATTCAGATTAAGCCCAGAGCCTTAACCATAAATTA
ATTTGGCCAGCAAGAGTGGAAAAAAAACACACCCGTTCTCAGGGCTTAGTTATTCATAGATAGTGGGATATTATTTATCGTTTGCTAAGAGGTAATACCTTGGCTTTTATCA
AAATGTGATATTTTACCAAAGGCCCGTTTGCGCAAACTATTCGATTTCGGGGGATATAAAAGATTAAGACCACTTTCAGTGTGAGAGAGCCCCTTTTCCGGTGACCTAGTTG

FIGURE SHEET 85

TTCAGGGGTCTTAATACGTTGCTTATCCTTACTTGACCGTATTTGCAGTAGCTGTAGCCGTCGCCTTCTTCCTCTGCTGGGCTCCATTCCACGCCCAGCGACTGATGGCAGT
TTACGGACTGAATCTGATTAATATAGGCATCAGTCGGGACGCCTTCAACGATTACTTCCGGATACTTGATTACACGTCCGGGGTGCTCTACTTTCTCTCCACCTGCATCAAT
CCGCTACTGTACAACATCATGAGCCACAAGTTCCGCGAGGCCTTCAAGGTAAGCCCATGGGATCAACCCTTCTCAGTTAACCACTTCATAATAGTAATCTATTATTAATTGG
GTCCTTCGCATGTTTGTGAGGACGGTCACAAATGCAGATGCTTTTAAAGTTAAATTTAAGCTTTAATTATTCAAAATTGTTTTTCGTAAATTAATGAATTGGTAATCTATGT
ATTTTTTACACTTTTAAGATCACTCTGACGCGACAGTTTGGTCTGGCCAGGAACCACCACCACCAGCAGAGTCAGCACCACCAGCACAACTACAGTGCCCTTCTCCGCCAGA
ATGGATCAATGCGTCTGCAGCCGGCCAGTTGCAGTGTAAACAACAACGCGCTGGAGCCATATGGATCCTACCGAGTGGTTCAGTTTCGTTGCCGGGATGCGAACCACCAATT
GTCCCTGCAGGACAGCATTCGCACCACCACCACAACCACGACGATAAACAGCAACAGCATGCGGCCGGAAATGGAGTTGGTGGTGGTGCTGGTGGCCGGTGGCGGTGGGCGG
CGTCTGCGGAAACAGGAGCTCTATGGGCCAGGTCCGGGTACAGCAGTTCCCCATCGAATGCTGCAGGCCCAGGTGTCTCAACTCTCGTCGCTGGGCGATGCCAATTCACTGC
TGGAGGCGGAGGTGGTGGACAGACACTACGCATCCGGGCGAGCCAAAAGAGCTCTCTTGGCCACCAAAAGTGGTGCCCTGCTGGTGACACCACCTCAAAGTGGTGACCCATC
GGAAGTCAGTCAGCCCGCCACTCGTCTCAAGCTGACTAGGGTGATAAGTAGAAGGGATGAGGTGGCCAACACAAGCACTCCGCCCTTTTGTGGGAGCCACAGTTTGCCGGAT
CCGGAGACTTGTCAATCGGCATCGGTGGCTGGTCGAAGCTCCCGTAAGTTTCCGTGGCGAAAACGAAGGCAAAAAACGGAGGATCCCAGCAGCGAGGGCTTGACCTATGGCT
CACCCAAATCCCAGTGATTTCAGCTGGCTGGTAGCTAGAGTTATACTTAGTTAGGCATTGTTTAGTTAGCGCAATAAACTTTTCTATCTGTAAATAAGCCAGAAAAAGTCCT
GCGATTTGAATGCAAATTTCGGGTGACCATAAAAAAATTTAACGAATGGGCATGGTCCAGACAATTTATGAGAGTCATAAAGCCGGGATAATGAGGCTACGGCGTATCGTGAC
GAATACACGCCCCACATCATTTTGCAATGGCAACCGCATAGCACTCATAAATTAAGTGTTAAGCTACCAGCTAAATAATGTGAATAAATAAAAATTGTTCTCAATATTACAG
TCTCAAGTTTTGCAGGTGCAGCGTTTCCAAGCAATCTGTTCCTACCTTTTGCGACATTTTTCCTGCAGATTGCCTGGCATTCTGTTGATTTCCCACACAAAAACTAAAAGCG
CTGAAAAAAATAAAAGAAGCATAAAATAAAATAAAGTGCCAATAAATTAGCAGTCTTAATATTTTCAGAGCCCCTCAGAAGCAAATCTAGGAAGGAAAACATGACATAAATT
TTAAATGGATTGCTCATCAGGATATCGTGTTGCAGTAGATATATATATTTTCGCAGTGTAAGTCACGACTCCACTTGCACCTGGCAACAAAGTTTCAGTTTGCACCTGGCCC
ATTGCCGGAGGTCCATTAGTCAAGAGGGCTTTGTAGGCTAGGAAGTCCGGATTGAAACGAATGTGCAGAGAGTGGCACGAATGGGCTTATCCTGCGGTGAATTGGCACGTGG
AGTGCATGGAGAGTGGTGTCGGTGCCACAAAATAAATCAACTTAAAAGTAGCATACAAATTTAAGGACCCGACTGATGTTATGTCCAAAGGGAATTATTAATGGTTCTTTAA
AGGCAGGCA
(SEQ ID NO: 190)

Exon: 1001..1478
Exon: 1539..1704
Exon: 2959..3091
Exon: 3163..3361
Exon: 4417..4640
Exon: 4835..5617
Start ATG: 1001

Transcript No. : CT25324
ATGTTGCAAGGCGTCGCCATCACCATAGCCAACGACAGCAACGATGATGGCATCAATCAATCATTCATGGCTCATGTGTCGCCCAGTCCCAATCAGAGTCCCTCCATTGGAG
TGGGCATCGGTATCGCCTCATCCAACAATGGCGAATCCCAGCGAGAGCCCCGAGATGTTGCTGCTGAAGAACGACAAATTCCTAACACATGTCGCCCATCTGCTGAACATAAC
GACCGAGAATCTTTCAAATCTCCTGGGTTCCACGAACGGCACAAATGCGAGCACAATGGCAGCGGATTCGCCGGTCGACGAGTCCCTGACCCTGCGAACAGCCCTCACCGTT
TGTTATGCACTCATTTTTGTGGCCGGCGTGCTGGGTAATCTTATCACCTGCATTGTTATATCGCGAAATAACTTTATGCACACGGCCACCAATTTCTATTTGTTCAACCTGG
CGGTTTCCGACTTAATACTGTTGGTCTCAGGCATCCCCCAGGAGCTGTACAACCTTTGGTATCCGGATATGTATCCCTTCACGGACGCCATGTGCATCATGGGCGTGTCCCT
CTCGGAAATGGCCGCCAATGCAACGGTTCTCACCATCACAGCATTCACTGTGGAGCGATATATGCAATCTGTCATCCATTCCGGCAGCACACCATGTCAAAATTGTCGCGA
GCCATTAAATTTATATTTGCCATTTGGCTGGCGGCCTTCCTTTTGGCCCTTCCGCAGGCCATGCAATTTTCGGTGGTCTACCAGAACGAAGGATACTCGTGCACGATGGAAA
ACTGACTTTTACGCCCATGTGTTCGCCGTTTCGGGATTTATTTTCTTCGGTGGACCCATGACGGCGATTTGTGTACTGTACGTGCTGATCGGAGTGAAACTGAAGAGGAGTCG
ACTGCTGCAATCGCTGCCGCGAAGGACTTTCGATGCGAATCGCGGCCTAAATGCCCAGGGACGAGTCATCAGAATGTTGGTAGCTGTAGCCGTCGCCTTCTTCCTCTGCTGG
GCTCCATTCCACGCCCAGCGACTGATGGCAGTTTACGGACTGAATCTGATTAATATAGGCATCAGTCGGGACGCCTTCAACGATTACTTCCGGATACTTGATTACACGTCCG
GGGTGCTCTACTTTCTCTCCACCTGCATCAATCCGCTACTGTACAACATCATGAGCCACAAGTTCCGCGAGGCCTTCAAGATCACTCTGACGCGACAGTTTGGTCTGGCCAG
GAACCACCACCACCAGCAGAGTCAGCACCACCAGCACAACTACAGTGCCCTTCTCCGCCAGAATGGATCAATGCGTCTGCAGCCGGCCAGTTGCAGTGTAAACAACAACGCG
GCAACAGCATGGCAGCCGGAAATGGAGTTGGTGGTGGTGCTGGTGGCCGGTGGCGGTGGGCGGCGTCTGCGGAAACAGGAGCTCTATGGGCCAGGTCCGGGTACAGCAGTTCC
CCATCGAATGCTGCAGGCCCAGGTGTCTCAACTCTCGTCGCTGGGCGATGCCAATTCACTGCTGGAGGCGGAGGTGGTGGACAGACACTACGCATCCGGGCGAGCCAAAAGA
GCTCTCTTGGCCACCAAAAGTGGTGCCCTGCTGGTGACACCACCTCAAAGTGGTGACCCATCGGAAGTCAGTCAGCCCGCCACTCGTCTCAAGCTGACTAGGGTGATAAGTA
TCCGTGGCGAAAACGAAGGCAAAAAACGGAGGATCCCAGCAGCGAGGGCTTGACCTATGGCTCACCCAAATCCCAGTGA
(SEQ ID NO: 191)

Start ATG: 1

MLQGVAITIANDSNDDGINQSFMAHVSPSPNQSPSIGVGIGIASSTMANPSESPEMLLLKNDKFLTHVAHLLNITTENLSNLLGSTNGTNASTMAADSPVDESLTLRTALTV
CYALIFVAGVLGNLITCIVISRNNFMHTATNFYLFNLAVSDLILLVSGIPQELYNLWYPDMYPFTDAMCIMGSVLSEMAANATVLTITAFTVERYIAICHPFRQHTMSKLSR
AIKFIFAIWLAAFLLALPQAMQFSVVYQNEGYSCTMENDFYAHVFAVSGFIFFGGPMTAICVLYVLIGVKLKRSRLLQSLPRRTFDANRGLNAQGRVIRMLVAVAVAFFLCW
APFHAQRLMAVYGLNLINIGISRDAFNDYFRILDYTSGVLYFLSTCINPLLYNIMSHKFREAFKITLTRQFGLARNHHHQQSQHHQHNYSALLRQNGSMRLQPASCSVNNNA
LEPYGSYRVVQFRCRDANHQLSLQDSIRTTTTTTTINSNSMAAGNGVGGGAGGGGGGRRLRKQELYGPGPGTAVPHRMLQAQVSQLSSLGDANSLLEAEVVDRHYASGRAKR
ALLATKSGALLVTPPQSGDPSEVSQPATRLKLTRVISRRDEVANTSTPPFCGSHSLPDPETCQSASVAGRSSRKFPWRKRRQKTEDPSSEGLTYGSPKSQ*
(SEQ ID NO: 192)

Name: GROWTH HORMONE SECRETAGOGUE RECEPTOR-like 2
Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384518
TTGGGCAAATTAAGGAAACTTTTTGTGGTTTCAGTTACTCGTTTAAGCCACATTTTCCCAACATATGCTGCACTTTATGAATTAAAAGTCATTTATTTTTAGGCTGCACACAC
GTTATGTTTGCCTGACAAATTGCATTTGCTGAAATTAAAACAAAATGCACTGGGACACTGCGTTATGGCATGCTGCTAATTAGTCACCAACAGCGGCTTTCAGCGAATGTTG
GCCCATCCGAGAATGGCTTTCATCCACTGTCTAGACTCCAGACCCAAAAAGCGAATTTGTGCGCCAGATAAACATCTTAATGGCCAGGGATTATGATGCAGTGCCCGCTTTT
TACTGACAGTAATTAGCCAGACGCCCATTGAACCCTCTTCTTGATAATCCCCACTTGATCCACACTCTTTCAAAAAAAAAAAAATGTATTCATTAAATGGGAAAAAAATATTT
ATTTAAATTGTATAATAAAACCATTAGGGTATCAACCTTAATATGTATTTATATATCACTGTACTCCAAATACTATTTACGCTTAACTATGTAGATTCATTTTATTTTTATC
AAAAGTCCATTCTTTTTTTTATTAAACTCCACTTTATAAATGAAACAACGGTCGAATTTTTGAACTGAGTACATAACTACATAGTTTATTCGATTACGTGCACTATAACTATA
ATTCGAACTATAGCTTTGGGCTATATTACGGTTATTGGTAAGGACAACCATATAATTGACCCCAAACGCGGAATATTTGTCTAAATTAAAACACAAACAAGCTGGAGTGGCG
CTTGCTGCTCGTATCACAGTTGTGTGTGTGTGTAATGTACGTAGGTGGCACTGGAATGGACTACCTCGCTTATCGAGTACAGATAGAGGATATGCTGACCCCCTTTAAAAGG

FIGURE SHEET 86

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CGGCCCGCTCTTCAGTGTCGCCTCCATTCACCGTCGCCCCCTTTTCGTGCGGTTTGTGGCTGCCTTTGCGTCTGGCACGCCAATTGAATTTGGTCCTGAGACCCTTGAACGG
GCTTGAGCTCTTGAGCACTTTCACTTTCGCCTTGCGCACTTTGCCACTCGACTCGTCACCGCTCACGCCCCCGACCCCGCGGCCCCTGTTGTGCTGCCTCCTGCCACGCCC
CCCGTCACACCTCCTGGTGGGCGGGTGATGCGCGTAAGTTTAAGGCGTGACCGCGAGATGGCCAAGTCATCTGTGAGCTCGTCAATGGAGCACATCGTGGGCTGGCGCTGCA
GTGGCTCCCCGGGAAACTGCAAATCCTCCTCCAAGAGGGAATGGGCATCGCCCACCGATGACAGCTGCGATATTTGCGTCTGGAGCATGCGACGCGGATTATCGAAGAGGTC
TTGCCGGCTGCGATTCTGACCCTGCATCTGGACACTGTCCAAGGACACGCGGTTCAGGCGGCACCGACTGACCCGTTGTCGTTCCATTGCCACTGCCATTGGCAGAGCCATTT
AGCCCAGTGGTGGTCGTCGCCATGGAAGTCATTGTGGTGCGAACGCTGTCCTGCAGGAGGAAATCAAGGAATGGAGGGATAATCAGAAAGGGAAAGTGCAGTCGCCAGACAC
GAAAATAAGTAACGCAATAAACATCTTATAGTGGTTTTAAAAAAGTCTCGTGATTCAAATTTCATTTTGAGAAACAGGACATACACTATATTAATCCTTTTCATTTTCCTCTT
AAATAATGCCACATAATAGAATTTAAGTGCATATATCGAATGATAATTATGTAATTTTTCTCAGTGCACTCACCGTTGTGTGCAGCCGCAGTGAACCCGTTTGATTACGTCG
AAGAGCGCTGTAAGTATGAGGAAGCCCCCTTCCCTGATTTTTGCCACCAAGTCCAAAGTGTCTAGCCAAAGTTACCTAAAATGGGATTAAATACGTTTTTTAATTCTAGCTT
GAAGTTTAAAATCACTAAATTGACCGTTAAAGAATCGATTAATAAACTTGTAACCTGAAGCTTATTTTCAATTTCCTAACGCAAGCTATAGAAATGAATATCCGGCAGCGAA
ACTCACCTTAAAAGCCTCACGAAACTTGTGGCTCATGATGTTGTAGAGCAGCGGGTTGATGCAAGTTGAGAGGAAGTAGAGAACACCGGACGTATAGTCGAGGATGCTGAAC
GGAAAGTTGGATAAGGGCGCCTGATGCAACCATGAGTTATTTCGGATATTTCATATCCTGCTTACCCAGCATCCGGATGACTCGCGTTTGGGCGCTTATCCCCCGGTTTACA
TCGTAACATCGCCTGGGAAGCGCCTGCAGGAGTCGGCTCCGTTTCAACTTCACCCCGATGAGGACATAGAGCACGCAGATGGCCGTCATGGGTCCGCCAAAGAACAGGAAGC
CCGACACAGCAAACACATGGGCAAAAAAGTCGTTTTTCATCTACAGCAGGCATTTCACAAAAATAATATATATGTGTATTCGCATGCGATACGATATGGTTTTGGCTTACAG
TCTCTATTCGAACTTTCTATACGGAAAACACATAATGAATCAAAGGATCAAAGGACCGGTTCTCTACGAATCAATTAACCAGGTAACTCATAACTGGGGGACATACGATTAAGG
GTCTCGCATCAATCATACGCACCGTGCACGATGTTCCCATGCCCTGCATCACCACGGAGAACTGAATGGCTTGGGGCAGGGCCAGCAAAAGGGCAGCTATCCAGATGGCAAA
TATGAACTTTACGGCCCGTGACAACTTGGACATCGTGTGCTGCCTGTATCGAAAGCAGAACCAATTAAGCAAGTTTGGGGCAAAATGGAAATGGGCAGTGGAAGGAATGAAG
CAGATGCTGTCACTGAAAGGATAATTATCCGGGTGCCAGAGGTTATAGAGGTCCTGCGGCATTCCTAAGAACATAAATAGCAAAATAGCAAAATATATAGTGTGATTATAAA
TATTTAATAATAGCTGAAATTATAGCCTATAGCCTCAAAATGCAAATCGATTTGAGCATCTGCCGAATATCTCACTCTACATTTTCTTGTTTATTTACAAATTTTAATTTAA
TATGCCTCAGTTCCATTTATTGTTTGCACTACTGAACTGAATTAAATTATAATTCAAAAACCATGAACATTTTAGTTTTGCACTCACCTGAGCATAACAAAATCATGTCGGA
TATAGCGAGGTTAAACAGATAAAAGTTGGTGGCCGTGTGCATAAAGTTGTTCCGCGAAATGACAATGCATGTGATGAGGTTGCCCAAAACGCCGGCGATAAATATGAGGGCG
TAGCCCACGCTTAGGGTGGCCAGCAGTGAAAGTGGTGTCATCGGGGTCACCGTGGGCAAAAGCTCCTCCGGCTCCAGGCCCTGGAGAAGGCTGGTCAGGTTGTCCGCGGAGA
TGTTCAGCACTTGTGTCAGATTTAAGAGAAATTTCTCATTGTGAAACAGTTGTAGATCGGTTGCCAGGACACCGGAACTGTTAGTGGGCAGCATTTTGACTGCCATAGGGTG
TGTGTCTTTGTGTGTGTGTATACGCACTATTATTTTCGAATTTCTTTGGAAATTTCAGACTTCTGCGTATGTATTCTCAATCGAAGCTTTCGCTTGCAAATAATGTTTTCAT
GGACCCTATGTGCTATTTAAATAAAACTATGTTTTTCAAAATTTGTTAAAATTTAAATAAAATAATACAAGACAAATAACGCATTTTAACGAATTTAGTAATAAAACAAATT
CAAACATTAAGGCTTTTTACTCCAGATTTCTAAATTACCATAAATTATACATATACACAATTTGGTTGGTAAGCTGTGCGCTTTGTTTAGCTTGCTAAGGTCCACCTTAGAG
AGCCCGTCTTAAAGCGTGTTTGTGTCCTGTGTGTTTACCTGGCATCCTGGGAAACTGGCAGGCGGCAGTCAGGCGTGTCCTAGGCGAAAGACCAGGATCAGGGCGAGTGGAA
GCTGAAAATTAATTTGAATTGCTAAGTGGCATTTAGTCAAAATATTTGTGTACACTGGATGAATTTAAGGATGTTGCTACAAGGCTGAGAAGGACAGGCCTGCCGATCCGTC
TAACATTAACATAGTTTCATTCCATTCAGATGATGAGTGTTTTCGGCTGCTGCTGTTCTGCTCTGTTCTGTTCACATTCTGGCTATACTTTTCGTTATTGTTGCTGCTGACC
GCTGTTGACCGTTTTGGACGTTTTCATTATCATTATCATAAAAAAAGTTTCTACAATATATGCACAACCAAAAGAATGCTGTCGAA
(SEQ ID NO: 193)
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Exon:  3902..3560
Exon:  3312..3147
Exon:  3067..2935
Exon:  2616..2418
Exon:  2349..2135
Exon:  1979..1866
Exon:  1618..1001
Start ATG: 3902 (Reverse strand: CAT)
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Transcript No. : CT25350
ATGCTGCCCACTAACAGTTCCGGTGTCCTGGCAACCGATCTACAACTGTTTCACAATGAGAAATTTCTCTTAAATCTGACACAAGTGCTGAACATCTCCGCGGACAACCTGA
CCAGCCTTCTCCAGGGCCTGGAGCCGGAGGAGCTTTTGCCCACGGTGACCCCGATGACACCACTTTCACTGCTGGCCACCCTAAGCGTGGGCTACGCCCTCATATTTATCGC
CGGCGTTTTGGGCAACCTCATCACCATGCATTGTCATTTCGCGGAACAACTTTATGCACACGGCCACCGTTCCTGTCTATATCTCGCTATATCCGACATGATTTTGTTA
TGCTCAGGAATGCCGCAGGACCTCTATAACCTCTGGCACCCGGATAATTATCCTTTCAGTGACAGCATCTGCATATTGGAGAGCGTTCTCTCGGAAACGGCGGCCAATGCGA
CAGTTCTAACCATTACCGCGTTCACAGTCGAACGATATATTGCCATTTGTCATCCGTTCAGGCAGCACACGATGTCCAAGTTGTCACGGGCCGTAAAGTTCATATTTGCCAT
CTGGATAGCTGCCCTTTTGCTGGCCCTGCCCCAAGCCATTCAGTTCTCCGTGGTGATGCAGGGCATGGGAACATCGTGCACGATGAAAAACGACTTTTTTGCCCATGTGTTT
GCTGTGTCGGGCTTCCTGTTCTTTGGCGGACCCATGACGGCCATCTGCGTGCTCTATGTCCATCGGGGTGAAGTTGAAACGGAGCGACTCCTGCAGGCGGCTTCCCAGGGC
GATGTTACGATGTAAACCGGGGGATAAGCGCCCAAACGCGAGTCATCCGGATGCTGGTGGCGGTGGCCGTGGCCTTCTTCATCTGCTGGGCCCCCTTTCACGCCCAGCGGCT
GATGGCGGTCTATGGATCCACCTCGGGCATTGAGTCCCAGTGGTTCAACGACGTGTTCAGCATCCTCGACTATACGTCCGGTGTTCTCTACTTCCTCTCAACTTGCATCAAC
ACAGCGCTCTTCGACGTAATCAAACGGGTTCACTGCGGCTGCACACAACGGACAGCGTTCGCACCACAATGACTTCCATGGCGACGACCACCACTGGGCTAAATGGCTCTGC
CAATGGCAGTGGCAATGGAACGACAACGGGTCAGTCGGTGCGCCTGAACCGCGTGTCCTTGGACAGTGTCCAGATGCAGGGTCAGAATCGCAGCCGGCAAGACCTCTTCGAT
AATCCGCGTCGCATGCTCCAGACGCAAATATCGCAGCTGTCATCGGTGGGCGATGCCCATTCCCTCTTGGAGGAGGATTGCAGTTTCCCGGGGAGCCACTGCAGCGCCAGC
CCACGATGTGCTCCATTGACGAGCTCACAGATGACTTGGCCATCTCGCGGTCACGCCTTAAACTTACGCGCATCACCCGCCCACCAGGAGGTGTGACGGGGGGCGTGGCAGG
AGGCAGCACAACAGGGGCCGCGGGTCGGGGGGCGTGAGCGGTGACGAGTCGAGTGGCAAAGTGCGCAAGGCGAAAGTGAAAGTGCTCAAGAGCTCAAGCCCGTTCAAGGGT
CTCAGGACCAAATTCAATTGGCGTGCCAGACGCAAAGGCAGCCACAAACCGCACGAAAAGGGGGCGACGGTGAATGGAGGCGACACTGAAGAGCGGGCCGCCTTTTAA
(SEQ ID NO: 194)
```

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Start ATG: 1 (Reverse strand: CAT)
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```
MLPTNSSGVLATDLQLFHNEKFLLNLTQVLNISADNLTSLLQGLEPEELLPTVTPMTPLSLLATLSVGYALIFIAGVLGNLITCIVISRNNFMHTATNFYLFNLAISDMILL
CSGMPQDLYNLWHPDNYPFSDSICILESVLSETAANATVLTITAFTVERYIAICHPFRQHTMSKLSRAVKFIFAIWIAALLLALPQAIQFSVVMQGMGTSCTMKNDFFAHVF
AVSGFLFFGGPMTAICVLYVLIGVKLKRSRLLQALPRRCYDVNRGISAQTRVIRMLVAVAVAFFICWAPFHAQRLMAVYGSTSGIESQWFNDVFSILDYTSGVLYFLSTCIN
PLLYNIMSHKFREAFKVTLARHFGLGGKNQGRGLPHTYSALRRNQTGSLRLHTTDSVRTTMTSMATTTTGLNGSANGSGNGTTTGQSVRLNRVSLDSVQMQGQNRSRQDLFD
NPRRMLQTQISQLSSVGDAHSLLEEDLQFPGEPLQRQPTMCSIDELTDDLAISRSRLKLTRITRPPGGVTGGVAGGSTTGAAGSGGVSGDESSGKVRKAKVKVLKSSSPFKG
LRTKFNWRARRKGSHKPHEKGATVNGGDTEERAAF*
(SEQ ID NO: 195)
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Name: GROWTH HORMONE SECRETAGOGUE RECEPTOR TYPE 1/like
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FIGURE SHEET 87

88/89

Classification: G_protein_linked_receptor

Celera Sequence No. : 142000013384638

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TAATTGCTGCCGGGTAATTGCAACTGAGCTCAGGTCAGCGAGTTTGCTAACCATGGCGTCATTATACTGTTGCACTATAAAATCATTCGACCCAAGTCCGATTAACTTAAGT
GGGTCTTAGACCAAAAGATGTGTATTTCGAATACTTCTCAAACGTTATTTCCTTAAGTCAAATCATTTCAAGAACTGGGAGAGCAAATAAATATGCGATTTCCTCGACTTAT
AGTTACTTGTGTGAAATTTGCGCGCTTGTGCAAATTCGAATGTTTGCAACTTAATTGGACTGCATAATAGATTGGGCAAAAGGATTTTATAACAATTCCAGTGTCCAGCCCA
TCGTACTGATGTGGCTAATTGTTTTGCTGACTTGCACCTAGGCAAAGCAATTTCCCTTGAAAACAATCAAATTCAAAACAATCAAGTAAACAAGACAGCTGAGTGAAAGACT
TTGGCTTCATGGGTGAACATATTTGTCGGTGAAGGTTGAGTTTTTGTTTAAGATGATTGCACATGGCACACAGGTTGATTTTAATCTAAATTTAATTTGAGCATTTGAGCA
TTTTTCTGCTGAACCGGGAAAACCCACATTTGCTTACCTAGAAAAACCGGTTTTCAGAGAAAGTTGCGAGTAATACATATTTAATACGATTTCAAGTCCTGTGTGTACAACG
TTTTATCTAAGAAAACCAGAAAACCAGAAGCTTTTTAGCTTAGACAGCTTTAATATTTAATTACAGTGTTCACAAAAAAAAAAAACGAAATTCCCCTTTTCTTTGCTTCAAA
TTTAATTAGACATGTATCTATTGTTTTTTTTTTCCACTTGCAGCTTATTTATCCAACCTAAGCCAACTAAATGATGCAATTGTGGTGACATATAAAACGAAAGTGGAAACG
GAGTTCATTCCTTAAGTAACCAATTTAAGATGTTGTGCTCCCAAGATCCCTAAACCACCGTCCAAACCCTTCGAATAACTTATTTAAGCCAAGATATAGACAAAATGGAGGA
CGAGTGGGGCTCCTTTGATCGTCTGCCCAGTGTTCCGAGTGCCTCGATGGATTTGGAGACGGAAAACGAGGTGGTCAGCAATTGGTCCACACTGGCCAACTTCACGCGACTT
GTGGCTGGTGCCGCTCCTGAAATCGTCAACTATACGCTCAACATGATCGACGTGGGTGTGGGCATGGCCACGGATATATCCAATTTGAGCGTGAGCACCACGCCCCTGCCCG
CCTACGCAATCTCCAATAGCTCCTCACTGGCGCACACCAATAGTCGCCATGAACGCACCACCGATGGCGGAACAGGTTCCGGAGCACGTGATGGATCACGCACCTCAACTATC
CCGATCCGGGTTGCTGAAAGTGTATGTCCTGGCGGTAATGGCACTGTTCTCTCTGCTGGGCAACCTGCTGACCATCTGGAATATCTACAAAACCCGCATCTCAAGAAGAAAC
TCACGGCACACGTGGAGTGCTATCTACTCACTGATGTTCCATCTGTCCATCGCCGATGTCCTGGTCACCTGGTTCTGCATTATCGGGGAGGCCGCGTGGTGCTACACCGTCC
AGTGGCTGGCCAATGAGCTCACCTGCAAGCTGGTGAAGCTCTTCCAGATGTTTAGCCTCTACCTGAGCACCTATGTCCTGGTCCTCATCGGAGTGGACCGCTGGATAGCGGT
CAAGTATCCGATGAAGTCGCTCAACATGGCCAAGAGGTGTCATAGGCTACTTGGCGGTACTTACATCCTGTCGCTGGTGCTCAGCTTGCCACAGGTAAGTTTTGATACACTG
AAAATAAGACCTTTAAAGTTCTTATAAAATCATTTGCCTAGAACAAACAGATAAGATAGTTACACAAATAAGCAAGATTGTAATAATATAAAAGTCATTTTTGGCCTATAAA
TGGTCTAAAAATATTTGTGGGATATGTTAGATTCAATCTTTAGATAATTTAAATGAAAAAAAGTTAAAGGTGCCCTTTGATTAGGAAATCAGTAAAAGCTTTAAGATCTCCT
CTTAATTTATGTACCCTTTCGGAAAATTTCTGTTCGACGTAAATGCAAAAAGCCTTGAGGGTACCCGTAAAAACATTATTCTATTTAAAAAGATTTAGCCAAAGGGCAAATT
TAAAGCGTCTGCATCTGAAAAAATGGCCCTTCCAGTGAAGTGCGAAGAAGACACGCTTATGAAAATAATCCAGTCACTTTTGGTGGGGCGTTCCATTACGCTAAGTTAAAGC
TGCGACTTAGCCGTGGTAATATTCACCTGCCACTGCCCCTGCCTGTGCCCCTACTCCTGGCACTCCATTTGATCCTTACGCTCGCGCTGATGAAGTTGAAATAATATGTTT
ACTTTTATAACACGTATACGCCCCGTGGCACAGTGCAAATAGTCTTGAGTAGGCGCCAGAATGTGTGCAGACATTAAAAATGATTGCCTTTCGCACAATAAGTGTACACTAAA
TGTGGCTTTAGGCCGCTGCCACGCCCACACACACGCGTGCTGATGGGCGTAGGAATGGGCATAGGGTTGGGCGTATGGGGACACCCAATCGAATTCCGGTCGTCCGACCGAC
AAAGGGTTTTTTCTTCTGGTTTTTCCTCTCGGCTTTTCGCTTGGGGACGGGCGACCAAATAAAAAAAAAAAAAAAGGTCCGAACAAGTGTGTCTTCTGCCTGACGACAGACAT
TATTCATATTCCCGATTTCGGTTCTTTGTGCGCAGATAGGCACACTGGGTGATATATTCCTTTGCCCTGGCAGTCAGCTGGCGGATAAGCCTGAATGGGACTGCATTAATGG
GCGTCACTCGCTTTGTTCTACAACTCTAGAACGACTCGGCTTCAGATTTCCGGCACCCTGATTGTATAATATATGCCGCGTGTCTCCACATCCCGATTTCATACTCGATTCG
CCTGGCCTTTCCTTGATTTATGGCCCCGGGTGAGGCACTTCACTTCTCGAATTCAGTTAATCTTTAGCTGGAGTGCTACGAGCTCCTGCTCGTGTTTTTCCTTAAAGTGGAA
ATTCGTGGACACTTCAGTTTAGGGTGTCACTAAGGTAGGTAATTAGCACGAAATCTCACTTCAAAGTTGCCAAGGGTTAGTAATATAGTTAGATTGAAAAGTGACTGCAAAC
TTTCCACTGCTCTTTATGTGACCCGGGTCATAAATATCGTTCGCAGAATTTGGTTAGCCATAAGTGGGGACAAGTGGGTAGAAAGGTCAAACCTTCTGTATAAAAAGATTTG
TCACCTGAGAGATGCCAAAAATAGATGAAAAAGAACCAAAGGGAAATTTCCTCCTAAGTGGATGGTAAGTGGATTTCCCGCACGCAAGTTATGCAACTAGCACACTTTCCCC
ACTGCTCGCCCGCAAATGTATGCTAAAATGTAGCTCATTTAATTAGGGAGCCCAGCAACCCGACGCCATTTCCTTTTATCTGAATAATGTATTGCGTGGAACAATAATTACA
GACGTACCGTACAAAAATCGAGGCGAGATTATATTTGCTCACTTTGGGGCAAAATGTGTGTGTGGTTTTTCTGGGTGCGAAGGCATGCGCGAGTCAGTTTGTTAAATCATCT
GACTTGTTTAAATGCCGCAAAAAATCTACTGAGCTTAATAACATTTTGATGTTTTTTCCAATCGATGTCAAGCGGAAAATTTGGCCGTTTTGTTGCTGGGAATTTGGGCCG
ACTTTTGGTCCAGCCGACCCATAATGGAAAGGACATAATGTATTGGTTTTGGATTTTTAAAATAGAACCAGACTTTGATGAACTGTCCAGCTTGGGTGTAAATATTTGATGA
CGAACGTCACAAATTACGATGATATGACAGAAGTCATTTATGGATGGCCACTGACACCCAATTAAAAGAAACTTTGCAATCATTAAGCCAATTTTTATGGTCCACTTTTCGA
CATCTCGCTGAGATCCCGGGAAACTTTCTTCATTTCGCTTCTACTCGAATATGCGACATAAAATTTATGCCGCTTACAGACGTGACGGTCGAAACGTTCCCGCCGGAAACGT
AGGAATCATCTCAAACAATTTTCCGGATAACTTTTTCCATGGTCACACGTTCATGGTGCAGGCAACCAAACAGCCAACCAACCAAGTGGCACATGTATTGGTAAGGAGC
CACATCGAATCCAATATGAGACGCGCCGCTGAACTCGTCGGTTTCAAATAAAGGAGCGAAATGAAAATTCACTTCGACTGCCAATAAACAACAAATGTTTCAACAGCAGCA
TTTATTTGGCTCCACTTCTATCGACCCCAACTCCTCCGCGTCCTTCGAACCCAAGGAAAAAAGAAAAAAAGTTTAGTACCACACGCACACAACCACACAGAAGAATCCTGCC
ACAATAACTCGAAGTGTGAGCCCAAAAATGTGGCACAATGAAAACAGGCCGCCATAATACAGTCAAACACAAAGTTATCCACAGGTCCTCCGCAGAGTATTATTGCGAATTG
AATTTCACCCACATATCATCAAATTCAGCAGCCTTAGGTGGCATAATTAAAATTTCGTAGAAGTTTTACAAATTGGAGGGAACTAGTCAATATTACAAGAGTCCCTTGGCG
ATTTCACCTTCAGTGTGCGCGGGCTTTTGATAATCGATAGGGGTCCTTAAATGCTTAGCTTTAAGTGAATTAAAATTTGAATTTAGTTTCAGAATATTTACAGCAGAATTTG
AATCAATAATTGCAATTTATATGTGCAAGCATTGGCGAATAAAGTAAATAACCGGATTTAATTATTAGGTGACAAAATCGTAACATTTAAATATATTTACCTGAATAACAAT
TGGAAATAAGTGCAAAAACAGCAAAAAGTATAATAAAGTTTAGATAAAAAATGAAATCCATTTAATATTTTAATTTGGGCTCATCTGGATTCATATTTTAGGTGACAAAATT
AATTATTATAATTATTAAAACAAATGAGCAGGTAACAAGTCAGTAAGCTCTAACAATCCTTGTTAAATCCTTCGTTAAATCTAGCTGAGTGTCCAATTTAAATGGTCAATTTA
ATCGTGCCTTTAAGCCAAACAAATATGTATATTTTAACAATCTGATAGTTTTACAAACGTCTTAAACGATTGCCAAGCACCTGACCGATGTGTGAAAACTACGAACTTGAGC
AATACAATTTGGTTAGAACGGAAGTTCTTGAAGTTGTTCCCTCACAATGAATCAATCTTGTTTTATTTTACTGTCGCAAGTTTTTGTCTAAAGTTTTTCGTTGCAACTTGTC
TAACTTTGCCGCAAATAGTGCTGAAGGCTTGCTTGTGTGTGGCATGGTTTTAGCGTGGAGCGCCCTTTAAACTTTTCGAGCATTTTTAATGAATGGCAACATGGAAATAATG
AACAAACACTTGAAAAGTTGAAATAATTTAAGAAAGAATATTGAAAGCCACAATTATCCTTGCTTTCTTTTACTAGTCATGACCTATAAAAATATATTTTTACTATATAAAA
AGCCACTGGCACTTTACTTCGGTTTCGGCGGAAGGCAATGGCTTGGAAGTTATAGGCGAAATTAATAAAAAATCAACCATTAGACGATTATCCGCTTCTCGTTATTTCTGCGC
GGGGGGTTTTTGTGTAGTTTTTACTACGCCACTCGGCGGAGCGCGGAAAGTTTTCCCATTTCCTCCATTTGGGTCAGCTGTTGACACAGCGGCCGCCAGAAAACCCATAAAA
AGCGCAAATAAAAATACTTTTAGCGTATTAGTTATGCGTAGACACATCCATCGTTGGTGTATTTAAGATGCTACACTTCCTTTATCAGTTATGGCCACACATTTTCCTGCTC
GAAAAGCTTTTTCATGGTACGAGAATTTCCACCTTTCTACGTGGCACTCTGCTAAACTCGGTAAGACTTGAACAATGGAGCAGTAGCAACTGCAGAATGTATACATTTCCA
AAAATGTTCCATCAATTTGGAAATGATTTCAGCCAAACAAGAAAATCAAGCAAAAGCACTTTTCACCCATAACCAAGCCGCTTGCCACCCACAATGGAAAGTAGATCAAAGC
CACAACGTTTTGAGTCAGCAGTTTGTTACCATGGACCGCATGTGGGTATTTCCATGTAAACATGCCTGTACTTAGTCCTTGGTGCAATCAGGACATGGTAGGTTTGCTAATA
AAAATCTTATTACGGCACCATCTTATTTACACAACACGGTAGAGATATATGGTTTTAAAAATTTCCATTTTCCTGCTTAAAACAGGCAATAAATTGATAGGAAGGTAAATAT
CCTTAAGAAACACTTGTATAAAGTTCAAGTTCAATCCATGTGTCTTAACCTTTAATTGTTTACTATGTTGCATGTTCGTTCCAGTTCTTCATCTTCCATGTAGCGCGTGGCC
CATTCGTGGAGGAGTTTTACCAGTGCGTCACCCACGGATTCTACAGGCGGATTGGCAGGAGCAGATGTACGCCACCTTCACGCTGGTCTTCACCTTCCTGCTGCCGCTGTG
CATCCTGTTTGGCACCTACATGTCCACCTTCCGCACCATTTCCAGTGAGTTTTCAGCGAGAAGGAGTTTACATTCCCGTACTAACCTGATAACCTGATAATCGTCAGGCAG
CGAAAAGATGTTCCAGGGATCAAAGTTGGCCAACTACTCAACGGCCAAATTGCCCACACAGACGAATCGCCAGAGGCTGATACACAAGGCCAAGATGAAGTCGCTTCGCATA
TCCGTGGTGATCATCATAGCGTTTCTCATCTGCTGGACGCCCTACTACGTCATGATGATTATGTTCATGTTCCTCAATCCGGACAAAAGGGTGAGTTTCCGCCCGTTCCCCT
GCCGAATTTGAAGCTGAATGACAAGCAGATATCGATTCCTGATACCAAAAGGCTCATCAATCAGCAGTCGATTTGTCAGTTTGTAGCGCACAGGTTTGGGCGAATCCTTTGTC
CTGTTCCCTACCATATTTACGACTTGGGGTCATGGTTGTACGAGTAAAATAAAAACGAGAATACGACACGACCTAGTCGCAGCTGGCAAATCCGTTTGGAGCTATACCCACT
GCCATAAAAATGATTTCTTATGCTCAATTTTTAATTAATCGTTACGCCACCCGACCGACCACACGGTCGCAATTTTTCCTTAACGGCGTACCCAACTTTGATGACTTGCCAG
AGATGGTCCGTAAAAGCTGGCCCAAGTTGCAAGATTACGGCGAGGCAATCCGGGCAGAAGGAACACAAGGTCGAATTGCTACAAACCGAGCATTCTGTACAGTAGGGGAAA
TGAATGAGTAGCAAAATATTTCCAAAGTTTATTTGTTTCGATTTAAATTTTAAAAATGCTATAATTGACAAAATAGAATCATTTTTGCTGTCACTATTTTTAAGTGAATGGG
ATATTTGTCCGCCGATTAACCTGAATTTCATATCCTAATGAATTGGATTGCACATTCATAATGGCATTTCCGCTGAAACTCTTTCTCGCTGTGGAAATCCCAGCGATGGCAG
TGTGCAAAATAATTAATTTGGAAGCCAAATTTTTAGCGCAGTGTATCCATAAGCGACCTGAGCCCCAATTCGACCGCAGGAACGCCCACAATGCGCCCACGCGAATGTAGAG
GGGAAAAGGTGAAAGGTGTGCGACAAGGGCAAGGAAATTAATTTGAATTTCACGGATTGCTTGCAGCTGGGCGACGATCTGCAGGACGCCATCTTCTTCTTCGGCATGTCAA
ACAGCCTGGTCAACCCACTCATCTACGGTGCCTTCCACCTGTGTCCTGGCAAAGGGGCAAGTCGAGCGGCGGGGGCGGCAACAACAACGCCTACAGCTTGAACAGGTGAGT
GGTGAGCCAACAGAATAAGTAATTCTATTAACCACCACATTTCGTACTTGTTTTTGCGCTTTTATCGTGTCAAAAAATAGTTACTTTTCACTCAAGCAATACACTTTTAAG
ACAGCCAAGCAAGCTTTTGAAGTCTGAATTGCTGCTTTTCTGATCAAAGAGTTTTTATTCTTGGTAATATTTCACATTTAAGAGTATAAATGATAGTGTAAATTTAAATAAA
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FIGURE SHEET 88

ATAGTAGAAAGTTTTCCCTAAAGATCGATGTATAACTATTAATACATATTTTACTTAATCTAGTGTTGCTTTTTAATGACAGTTTTTGCTGTGCTTAAATTTTTACAAAATA
AATCTTAAATCCTTGCAAAGAGTTTTCTTTTATGCAAATGGAAAACATTGTTTCATCGCTTGTTAATATCATTTACTTTATTTATTTATTATTCTAAACAGCTGCCAAAGCA
GCGAACTATCTCAGGATCAGATATGATTTGCTATGATTTTGTCACACTTCCTATGTTTGTTTTGATAACGCAAAAAGCACACACACCGTGATTGGCAATAAACTGATAAATT
CTTTTCCGTCTGGTTTTTATCACCTCACCGCATCGTCCATTCCCCCGTCCACTTTCCATCCGCAGGGGCGACTCGCAGCGCACTCCATCCATGCTAACGGCGGTGACGCAGG
TGGACGGCACAGGTGGCAGTTCCCGCCAGATGCGGGCCTTCCGCCAGCAGAGCTACTACCGCAGCTCCTCCAACGGCACAGCCGGACCGGGTGCAGCTCCCTTTAAGGAGCA
GGTTGGCCTGCTGCACGTGGGTCCCGGCAATGGGACGCCCGGTGGCTCCGTCTCTAGCGGCGCCACGCCGCAGTTGATCCGTAAGGGATCGGCTCTGTTGGCCCGACAACCC
AGCTGTCTGAGGGAGCAGGAGCACCAGCAGCGTTTGCTGCTGCACGAGAAGCCCTCGACCCTGGTGCTCAGCTACGACAGCCAGCGGGGCGGAGTGGGCGTGGGCGTGGCCA
GCGGTCTGCTGGACAACAACGAGCGAGTGTCGAGCGTGTGAGAGCAGCTGGCGATGGCGGTAGCGGCGGCGGCGGTGGCGGTGGATGCACCGGACACAGTAGAAGCAGCAGC
AGCAACAGCATCAGCCGATGCGGATGCGAATGTGGCGATGGAGGACGCCTGCTCCTGCTGCCATTGCCTGAGCAGGGAGCTGGTGCGGCGGCAGTTGGAGCTCCAAGTGCTT
CCAGTGCAGTGAGGCGACTGCCAGTGGATTTGATCCGGCTGGCTGAGTGGCCGGAGCTGGGGATTCCAGCGATTCCCTCGGTCAACGTGGGGAGTGGCGTCGATGATTAGAT
CACCGGGGCGTGCAACATGTGCTTAGATAGTGCTAATCGAGAGTTAAGTCTTCAAACACAATGGGTGTGCTTAGAAGTAGCGTAGGATTAGAGCTAGTCCGTACGAAGTGGT
TGCCCTACACTGGGAGAAACTCGTGGTCACTTTGCATGTTCTCTGAATGTTCTACTAATACTTGACTTCAACAAGGATACAAATATAAGAGATAATATCTATGTACATCCCA
TAAAACCATAAAAAATTGCAATTAAATCTGGTTGTGAAAAAAATAGATTTAACTTCTGAATGTTTCAAATGTTGCCAATTCGCCAGCGTGTAATCCGATATAAGCAACAATA
ATTACAATTATAATCAATGTGCAATCAGAGTCAGTTACAATTTACAATTATATGACTGAATAATTGGACTATGAATATATACGACTTCAAATGAGTTTCTCTCATTAGCAGG
GCAACTTTGTAATGTTAATTAACAGCGTTTTTCAGTTTTTCATTTTGTTCCCCCAGCCGAGTAACTCAAAAATCGATTCTATAATTGTGTAAAATAGAAATCATCTAAAAAC
AGGGTAAATCTAACTATTGTAAATACATTTACTCATTATTTTGAGAAGAATATTGTAAAAAAAAAAGATTGTAAAGTTTAAAATAAATATGAGTTCATGTTCAACGACACAA
GGAATTATTTTGATTAATTTAAAGTACTAAAAA
(SEQ ID NO: 196)

Exon: 1001..1210
Exon: 1307..1774
Exon: 6357..6540
Exon: 6605..6810
Exon: 7683..7834
Exon: 8466..8889
Start ATG: 1001

Transcript No. : CT29989
ATGGAGGACGAGTGGGGCTCCTTTGATCGTCTGCCCAGTGTTCCGAGTGCCTCGATGGATTTGGAGACGGAAAACGAGGTGGTCAGCAATTGGTCCACACTGGCCAACTTCA
CGCGACTTGTGGCTGGTGCCGCTCCTGAAATCGTCAACTATACGCTCAACATGATCGACGTGGGTGTGGGCATGGCCACGGATATATCCAATTTGAGCGTTCCGGAGCACGT
GATGGATCACGCACCTCAACTATCCCGATCCGGGTTGCTGAAAGTGTATGTCCTGGCGGTAATGGCACTGTTCTCTCTGCTGGGCAACCTGCTGACCATCTGGAATATCTAC
AAAACCCGCATCTCAAGAAGAAACTCACGGCACACGTGGAGTGCTATCTACTCACTGATGTTCCATCTGTCCATCGCCGATGTCCTGGTCACCTGGTTCTGCATTATCGGGG
AGGCCGCGTGGTGCTACACCGTCCAGTGGCTGGCCAATGAGCTCACCTGCAAGCTGGTGAAGCTCTTCCAGATGTTTAGCCTCTACCTGAGCACCTATGTCCTGGTCCTCAT
CGGAGTGGACCGCTGGATAGCGGTCAAGTATCCGATGAAGTCGCTCAACATGGCCAAGAGGTGTCATAGGCTACTTGGCGGTACTTACATCCTGTCGCTGGTGCTCAGCTTG
CCACAGTTCTTCATCTTCCATGTAGCGCGTGGCCCATTCGTGGAGGAGTTTTACCAGTGCGTCACCCACGGATTCTACACGGCGGATTGGCAGGAGCAGATGTACGCCACCT
TCACGCTGGTCTTCACCTTCCTGCTGCCGCTGTGCATCCTGTTTGGCACCTACATGTCCACCTTCCGCACCATTTCCAGCAGCGAAAAGATGTTCCAGGGATCAAAGTTGGC
TGCTGGACGCCCTACTACGTCATGATGATTATGTTCATGTTCCTCAATCCGGACAAAAGGCTGGGCGACGATCTGCAGGACGCCATCTTCTTCTTCGGCATGTCAAACAGCC
TGGTCAACCCACTCATCTACGGTGCCTTCCACCTGTGTCCTGGCAAAGGGGGCAAGTCGAGCGGCGGGGGCGGCAACAACAACGCCTACAGCTTGAACAGGGGCGACTCGCA
GCGCACTCCATCCATGCTAACGGCGGTGACGCAGGTGGACGGCACAGGTGGCAGTTCCCGCCAGATGCGGGCCTTCCGCCAGCAGAGCTACTACCGCAGCTCCTCCAACGGC
ACAGCCGGACCGGGTGCAGCTCCCTTTAAGGAGCAGGTTGGCCTGCTGCACGTGGGTCCCGGCAATGGGACGCCCGGTGGCTCCGTCTCTAGCGGCGCCACGCCGCAGTTGA
TCCGTAAGGGATCGGCTCTGTTGGCCCGACAACCCAGCTGTCTGAGGGAGCAGGAGCACCAGCAGCGTTTGCTGCTGCACGAGAAGCCCTCGACCCTGGTGCTCAGCTACGA
CAGCCAGCGGGGCGGAGTGGGCGTGGGCGTGGCCAGCGGTCTGCTGGACAACAACGAGCGAGTGTCGAGCGTGTGA
(SEQ ID NO: 197)

Start ATG: 1

MEDEWGSFDRLPSVPSASMDLETENEVVSNWSTLANFTRLVAGAAPEIVNYTLNMIDVGVGMATDISNLSVPEHVMDHAPQLSRSGLLKVYVLAVMALFSLLGNLLTIWNIY
KTRISRRNSRHTWSAIYSLMFHLSIADVLVTWFCIIGEAAWCYTVQWLANELTCKLVKLFQMFSLYLSTYVLVLIGVDRWIAVKYPMKSLNMAKRCHRLLGGTYILSLVLSL
PQFFIFHVARGPFVEEFYQCVTHGFYTADWQEQMYATFTLVFTFLLPLCILFGTYMSTFRTISSSEKMFQGSKLANYSTAKLPTQTNRQRLIHKARMKSLRISVVIIIAFLI
CWTPYYVMMIMFMFLNPDKRLGDDLQDAIFFFGMSNSLVNPLIYGAFHLCPGKGGKSSGGGGNNNAYSLNRGDSQRTPSMLTAVTQVDGTGGSSRQMRAFRQQSYYRSSSNG
TAGPGAAPFKEQVGLLHVGPGNGTPGGSVSSGATPQLIRKGSALLARQPSCLREQEHQQRLLLHEKPSTLVLSYDSQRGGVGVGVASGLLDNNERVSSV*
(SEQ ID NO: 198)

Name: GONADOTROPIN-RELEASING HORMONE RECEPTOR-like
Classification: G_protein_linked_receptor

FIGURE SHEET 89

INTERNATIONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7   C12N15/12   C07K14/435   C07K14/705   C07K16/18   C12N5/10
        C12Q1/68   G01N33/50

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7   C07K   G01N   C12N   C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the International search (name of data base and, where practical, search terms used)

SEQUENCE SEARCH, EPO-Internal, BIOSIS, WPI Data, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL SEQUENCE LIBRARY [Online] 6 January 2000 (2000-01-06) ADAMS, M. AND VENTER, J.C.: "Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces" XP002182628 accession no AC020076 ---	1,2,4,5
A	WO 94 08006 A (ZYMOGENETICS INC) 14 April 1994 (1994-04-14) the whole document ---	
	-/--	

| X | Further documents are listed in the continuation of box C. | | X | Patent family members are listed in annex. |

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the International filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the Invention

"X" document of particular relevance; the claimed Invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
13 November 2001	15. 02. 2002

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Holtorf, S

Application No
PCT/US 01/09341

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	LI X-J ET AL: "CLONING, FUNCTIONAL EXPRESSION, AND DEVELOPMENTAL REGULATION OF A NEUROPEPTIDE Y RECEPTOR FROM DROSOPHILA MELANOGASTER" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, US, vol. 267, no. 1, 5 January 1992 (1992-01-05), pages 9-12, XP000877443 ISSN: 0021-9258 the whole document	
A	WO 99 01468 A (DEN HEUVEL MARCEL VAN ;INGHAM PHILIP W (GB); ONTOGENY INC (US)) 14 January 1999 (1999-01-14) the whole document	
A	HAUSER FRANK ET AL: "Molecular cloning, genomic organization and developmental regulation of a novel receptor from Drosophila melanogaster structurally related to gonadotropin-releasing hormone receptors from vertebrates." BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 249, no. 3, 28 August 1998 (1998-08-28), pages 822-828, XP002182627 ISSN: 0006-291X the whole document	
A	FENG G ET AL: "CLONING AND FUNCTIONAL CHARACTERIZATION OF A NOVEL DOPAMINE RECEPTOR FROM DROSOPHILA MELANOGASTER" JOURNAL OF NEUROSCIENCE, NEW YORK, NY, US, vol. 15, no. 12, 15 June 1995 (1995-06-15), pages 3925-3933, XP002919142 ISSN: 0270-6474 the whole document	
P,X	ADAMS M D ET AL: "THE GENOME SEQUENCE OF DROSOPHILA MELANOGASTER" SCIENCE, AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE,, US, vol. 287, no. 5461, 24 March 2000 (2000-03-24), pages 2185-2195, XP000961051 ISSN: 0036-8075 the whole document	1,2,4,5

-/--

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/09341

Box I	Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted In accordance with the second and third sentences of Rule 6.4(a).

Box II	Observations where unity of Invention Is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report Is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 partially

Remark on Protest   ☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet (1)) (July 1998)

FURTHER INFORMATION CONTINUED FROM   PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-20 partially

Isolated protein consisting or comprising an amino acid sequence as characterized by SEQID3, or an allelic variant or an ortholog of said amino acid sequence·wherein said variant or ortholog is encoded by a nucleic acid molecule that hybridizes to the nucleic acid molecule as characterized by SEQID1 or 2; an antibody that binds to said protein; furthermore a nucleic acid molecule consisting or comprising of a nucleotide sequence that
1) encodes the amino acid sequence of SEQId3
2) encodes and allelic variant or an ortholog of an amino acid sequence of SEQId3 wherein said nucleotide sequence hybridizes to SEQID 1 or 2
3) encodes a fragment of said SEQID3
4) is the complement of the nucleotides of 1) to 3)

The recombinant expression of the same in host cells and methods for the detection of said proteins or said nucleic acids in a sample with the help of an agent that binds to said protein or an oligonucleotide and kits that contain such agent or oligonucleotide.
Furthermore, a method to identify an agent that binds to said protein by detecting a complex formed by an agent and the said protein.

Invention 2-66: claims 1-20 partially

as invention one but referring to the protein and nucleic acid sequences as characterized by SEQIDs
6,9,...,192,195,198; SEQIDs 4,7,....,190,193,196 and SEQIDs 5,8,....,191,194,197, respectively.

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	DATABASE EMBL SEQUENCE LIBRARY [Online] 24 March 2000 (2000-03-24) ADAMS, M.D:, ETAL.: "Drosophila melanogaster genomic scaffold 142000013386053 section 8 of 30 complete sequence" XP002182629 accession no. AE003491 and AE002593 ---	1,2,4,5
P,X	DATABASE TREMBLREL. DATABASE [Online] 1 May 2000 (2000-05-01) ADAMS, M.D., ET AL.: "The genome sequence of Drosophila melanogaster - cross-reference to EMBL accession no. AE003491, AAF48216.1" XP002182630 accession no. Q9VYH9 ---	1,2
E	EP 1 136 501 A (BAYER AG) 26 September 2001 (2001-09-26) the whole document -----	1-20

INTERNATIONAL SEARCH REPORT

Information on patent family members

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 9408006	A	14-04-1994	CA	2145866 A1	14-04-1994
			EP	0663006 A1	19-07-1995
			JP	8501942 T	05-03-1996
			WO	9408006 A1	14-04-1994
			US	5683884 A	04-11-1997
			US	5674981 A	07-10-1997
			US	5622839 A	22-04-1997
			US	5674689 A	07-10-1997
WO 9901468	A	14-01-1999	AU	8380898 A	25-01-1999
			WO	9901468 A2	14-01-1999
EP 1136501	A	26-09-2001	DE	10013618 A1	20-09-2001
			EP	1136501 A2	26-09-2001
			JP	2001299369 A	30-10-2001 |